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(54) Title: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

(57) Abstract: The invention provides proteins from gonococcus (*Neisseria gonorrhoeae*), including amino acid sequences, the corresponding nucleotide sequences, expression data, and serological data. The proteins are useful antigens for vaccines, immunogenic compositions, and/or diagnostics. They are also useful for distinguishing between gonococcus and meningococcus and, in particular, between gonococcus and serogroup B meningococcus.

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## GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

All documents cited herein are incorporated by reference in their entirety.

### TECHNICAL FIELD

This invention relates to proteins from the bacterium *Neisseria gonorrhoeae*, and more particularly to  
5 such proteins which do not have corresponding homologs or orthologs in serogroup B *N.meningitidis*.

### BACKGROUND ART

*Neisseria gonorrhoeae* is a bacterial pathogen. There is currently no effective vaccine against *N.gonorrhoeae* infection. It is an object of the invention to provide proteins and nucleic acid useful in vaccine study and/or manufacture.

10 *N.gonorrhoeae* is related to *N.meningitidis*. Sequence data are now available for serogroup B of meningococcus [e.g. WO99/24578; WO99/36544; WO99/57280; WO00/22430; WO00/66791; Tettelin *et al.* (2000) *Science* 287:1809-1815] and also for serogroup A [Parkhill *et al.* (2000) *Nature* 404:502-506]. It is a further object of the invention to provide proteins and nucleic acid useful in distinguishing between gonococcus and meningococcus and, in particular, between gonococcus and serogroup B meningococcus.

### 15 DISCLOSURE OF THE INVENTION

The invention provides proteins comprising the *N.gonorrhoeae* amino acid sequences disclosed in the examples (the even-numbered SEQ IDS 2 to 8622). 159 of these have no homolog in serogroup B meningococcus and these have been given a name in the form "NGSn".

It also provides proteins comprising amino acid sequences having sequence identity to the *N.gonorrhoeae*  
20 amino acid sequences disclosed in the examples. Depending on the particular sequence, the degree of sequence identity is preferably greater than 50% (e.g. 60%, 70%, 80%, 90%, 95%, 99% or more). These proteins include homologs, orthologs, allelic variants and functional mutants. Typically, 50% identity or more between two proteins is considered to be an indication of functional equivalence. Identity between proteins is preferably determined by the Smith-Waterman homology search algorithm as implemented in  
25 the MPSRCH program (Oxford Molecular), using an affine gap search with parameters *gap open penalty*=12 and *gap extension penalty*=1.

The invention further provides proteins comprising fragments of the *N.gonorrhoeae* amino acid sequences disclosed in the examples. The fragments should comprise at least *n* consecutive amino acids from the sequences and, depending on the particular sequence, *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18,  
30 20, 30, 40, 50, 60, 70, 80, 90, 100 or more). Preferably the fragments comprise one or more epitopes from the sequence. Other preferred fragments are (a) the N-terminal signal peptides of the proteins disclosed in the examples, and (b) the proteins disclosed in the examples, but without their N-terminal signal peptides.

The proteins of the invention can, of course, be prepared by various means (e.g. recombinant expression, purification from *Neisseria*, chemical synthesis *etc.*) and in various forms (e.g. native, fusions *etc.*). They  
35 are preferably prepared in substantially pure form (i.e. substantially free from other *N.gonorrhoeae* or host cell proteins).

The proteins of the invention are preferably *Neisserial* proteins, more preferably *N.gonorrhoeae* proteins.

The invention provides antibodies which bind to these proteins. These may be polyclonal or monoclonal and may be produced by any suitable means. The antibodies may include a detectable label.

The invention provides nucleic acid comprising the *N.gonorrhoeae* nucleotide sequences disclosed in the examples. In addition, the invention provides nucleic acid comprising nucleotide sequences having  
5 sequence identity to the *N.gonorrhoeae* nucleotide sequences disclosed in the examples.

Furthermore, the invention provides nucleic acid which can hybridise to the *N.gonorrhoeae* nucleic acid disclosed in the examples, preferably under "high stringency" conditions (e.g. 65°C in a 0.1xSSC, 0.5% SDS solution).

Nucleic acid comprising fragments of these sequences are also provided. These should comprise at least *n*  
10 consecutive nucleotides from the *N.gonorrhoeae* sequences and, depending on the particular sequence, *n* is 10 or more (e.g. 12, 14, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more).

The invention also provides nucleic acid encoding the proteins and protein fragments of the invention.

The invention includes nucleic acid comprising sequences complementary to those described above (e.g. for antisense or probing purposes).

15 Nucleic acid according to the invention can be prepared in many ways (e.g. by chemical synthesis, from genomic or cDNA libraries, from the organism itself *etc.*) and can take various forms (e.g. single stranded, double stranded, vectors, probes *etc.*).

In addition, the term "nucleic acid" includes DNA and RNA, and also their analogues, such as those containing modified backbones, and also peptide nucleic acids (PNA) *etc.*

20 The invention provides vectors comprising nucleotide sequences of the invention (e.g. cloning or expression vectors) and host cells transformed with such vectors.

The invention provides compositions comprising protein, antibody, and/or nucleic acid according to the invention. These compositions may be suitable as immunogenic compositions, for instance, or as diagnostic reagents, or as vaccines.

25 The invention also provides nucleic acid, protein, or antibody according to the invention for use as medicaments (e.g. as vaccines) or as diagnostic reagents. It also provides the use of nucleic acid, protein, or antibody according to the invention in the manufacture of: (i) a medicament for treating or preventing infection due to *Neisseria*; (ii) a diagnostic reagent for detecting the presence of *Neisseria* or of antibodies raised against *Neisseria*; and/or (iii) a reagent which can raise antibodies against *Neisseria*. Said *Neisseria*  
30 may be any species, but is preferably *N.gonorrhoeae*.

The invention also provides a method of treating a patient, comprising administering to the patient a therapeutically effective amount of nucleic acid, protein, and/or antibody of the invention.

According to further aspects, the invention provides various processes.

A process for producing proteins of the invention is provided, comprising the step of culturing a host cell  
35 of to the invention under conditions which induce protein expression.

A process for producing protein or nucleic acid of the invention is provided, wherein the protein or nucleic acid is synthesised in part or in whole using chemical means.

A process for detecting polynucleotides of the invention is provided, comprising the steps of: (a) contacting a nucleic probe according to the invention with a biological sample under hybridising conditions to form duplexes; and (b) detecting said duplexes.

A process for detecting proteins of the invention is provided, comprising the steps of: (a) contacting an antibody of the invention with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.

A process for distinguishing *N.gonorrhoeae* from *N.meningitidis* is provided, comprising the steps of: (a) contacting an antibody of the invention with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes. Alternatively, the steps may be (a) contacting nucleic acid of the invention with a biological sample under conditions suitable for the nucleic acid hybridisation; and (b) detecting any such hybridisation. Alternatively, the steps may be (a) contacting a protein of the invention with a biological sample (e.g. blood or serum) under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.

A summary of standard techniques and procedures which may be employed in order to perform the invention (e.g. to utilise the disclosed sequences for vaccination or diagnostic purposes) follows. This summary is not a limitation on the invention, but gives examples that may be used, but are not required.

#### General

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature eg. Sambrook *Molecular Cloning; A Laboratory Manual, Second Edition* (1989) or *Third Edition* (2000); *DNA Cloning, Volumes I and II* (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); *Transcription and Translation* (B.D. Hames & S.J. Higgins eds. 1984); *Animal Cell Culture* (R.I. Freshney ed. 1986); *Immobilized Cells and Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide to Molecular Cloning* (1984); the *Methods in Enzymology* series (Academic Press, Inc.), especially volumes 154 & 155; *Gene Transfer Vectors for Mammalian Cells* (J.H. Miller and M.P. Calos eds. 1987, Cold Spring Harbor Laboratory); Mayer and Walker, eds. (1987), *Immunochemical Methods in Cell and Molecular Biology* (Academic Press, London); Scopes, (1987) *Protein Purification: Principles and Practice*, Second Edition (Springer-Verlag, N.Y.), and *Handbook of Experimental Immunology, Volumes I-IV* (D.M. Weir and C. C. Blackwell eds 1986).

Standard abbreviations for nucleotides and amino acids are used in this specification.

#### Definitions

A composition containing X is "substantially free of" Y when at least 85% by weight of the total X+Y in the composition is X. Preferably, X comprises at least about 90% by weight of the total of X+Y in the composition, more preferably at least about 95% or even 99% by weight.

The term "comprising" means "including" as well as "consisting" e.g. a composition "comprising" X may consist exclusively of X or may include something additional e.g. X + Y.

The term "heterologous" refers to two biological components that are not found together in nature. The components may be host cells, genes, or regulatory regions, such as promoters. Although the heterologous components are not found together in nature, they can function together, as when a promoter heterologous to a gene is operably linked to the gene. Another example is where a *Neisseria* sequence is heterologous to a mouse host cell. A further examples  
5 would be two epitopes from the same or different proteins which have been assembled in a single protein in an arrangement not found in nature.

An "origin of replication" is a polynucleotide sequence that initiates and regulates replication of polynucleotides, such as an expression vector. The origin of replication behaves as an autonomous unit of polynucleotide replication within a cell, capable of replication under its own control. An origin of replication may be needed for a vector to  
10 replicate in a particular host cell. With certain origins of replication, an expression vector can be reproduced at a high copy number in the presence of the appropriate proteins within the cell. Examples of origins are the autonomously replicating sequences, which are effective in yeast; and the viral T-antigen, effective in COS-7 cells.

A "mutant" sequence is defined as DNA, RNA or amino acid sequence differing from but having sequence identity with the native or disclosed sequence. Depending on the particular sequence, the degree of sequence identity between  
15 the native or disclosed sequence and the mutant sequence is preferably greater than 50% (eg. 60%, 70%, 80%, 90%, 95%, 99% or more, calculated using the Smith-Waterman algorithm as described above). As used herein, an "allelic variant" of a nucleic acid molecule, or region, for which nucleic acid sequence is provided herein is a nucleic acid molecule, or region, that occurs essentially at the same locus in the genome of another or second isolate, and that, due to natural variation caused by, for example, mutation or recombination, has a similar but not identical nucleic acid  
20 sequence. A coding region allelic variant typically encodes a protein having similar activity to that of the protein encoded by the gene to which it is being compared. An allelic variant can also comprise an alteration in the 5' or 3' untranslated regions of the gene, such as in regulatory control regions (eg. see US patent 5,753,235).

#### Expression systems

The *Neisseria* nucleotide sequences can be expressed in a variety of different expression systems; for example those  
25 used with mammalian cells, baculoviruses, plants, bacteria, and yeast.

#### i. Mammalian Systems

Mammalian expression systems are known in the art. A mammalian promoter is any DNA sequence capable of binding mammalian RNA polymerase and initiating the downstream (3') transcription of a coding sequence (eg. structural gene) into mRNA. A promoter will have a transcription initiating region, which is usually placed proximal  
30 to the 5' end of the coding sequence, and a TATA box, usually located 25-30 base pairs (bp) upstream of the transcription initiation site. The TATA box is thought to direct RNA polymerase II to begin RNA synthesis at the correct site. A mammalian promoter will also contain an upstream promoter element, usually located within 100 to 200 bp upstream of the TATA box. An upstream promoter element determines the rate at which transcription is initiated and can act in either orientation [Sambrook et al. (1989) "Expression of Cloned Genes in Mammalian Cells."  
35 In *Molecular Cloning: A Laboratory Manual*, 2nd ed.].

Mammalian viral genes are often highly expressed and have a broad host range; therefore sequences encoding mammalian viral genes provide particularly useful promoter sequences. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter (Ad MLP), and herpes simplex virus promoter. In addition, sequences derived from non-viral genes, such as the murine metallothionein gene, also  
40 provide useful promoter sequences. Expression may be either constitutive or regulated (inducible), depending on the promoter can be induced with glucocorticoid in hormone-responsive cells.

The presence of an enhancer element (enhancer), combined with the promoter elements described above, will usually increase expression levels. An enhancer is a regulatory DNA sequence that can stimulate transcription up to 1000-fold when linked to homologous or heterologous promoters, with synthesis beginning at the normal RNA start site. Enhancers are also active when they are placed upstream or downstream from the transcription initiation site, in either normal or flipped orientation, or at a distance of more than 1000 nucleotides from the promoter [Maniatis et al. (1987) *Science* 236:1237; Alberts et al. (1989) *Molecular Biology of the Cell*, 2nd ed.]. Enhancer elements derived from viruses may be particularly useful, because they usually have a broader host range. Examples include the SV40 early gene enhancer [Dijkema et al (1985) *EMBO J.* 4:761] and the enhancer/promoters derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus [Gorman et al. (1982b) *Proc. Natl. Acad. Sci.* 79:6777] and from human cytomegalovirus [Boshart et al. (1985) *Cell* 41:521]. Additionally, some enhancers are regulatable and become active only in the presence of an inducer, such as a hormone or metal ion [Sassone-Corsi and Borelli (1986) *Trends Genet.* 2:215; Maniatis et al. (1987) *Science* 236:1237].

A DNA molecule may be expressed intracellularly in mammalian cells. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in mammalian cells. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The adenovirus tripartite leader is an example of a leader sequence that provides for secretion of a foreign protein in mammalian cells.

Usually, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. The 3' terminus of the mature mRNA is formed by site-specific post-transcriptional cleavage and polyadenylation [Birnstiel et al. (1985) *Cell* 41:349; Proudfoot and Whitelaw (1988) "Termination and 3' end processing of eukaryotic RNA. In *Transcription and splicing* (ed. B.D. Hames and D.M. Glover); Proudfoot (1989) *Trends Biochem. Sci.* 14:105]. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator/polyadenylation signals include those derived from SV40 [Sambrook et al (1989) "Expression of cloned genes in cultured mammalian cells." In *Molecular Cloning: A Laboratory Manual*].

Usually, the above described components, comprising a promoter, polyadenylation signal, and transcription termination sequence are put together into expression constructs. Enhancers, introns with functional splice donor and acceptor sites, and leader sequences may also be included in an expression construct, if desired. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (eg. plasmids) capable of stable maintenance in a host, such as mammalian cells or bacteria. Mammalian replication systems include those derived from animal viruses, which require trans-acting factors to replicate. For example, plasmids containing the replication systems of papovaviruses, such as SV40 [Gluzman (1981) *Cell* 23:175] or polyomavirus, replicate to extremely high copy number in the presence of the appropriate viral T antigen. Additional examples of mammalian replicons include those derived from bovine papillomavirus and Epstein-Barr virus. Additionally, the replicon may have two replicon systems, thus allowing it to be maintained, for example, in mammalian cells for expression and in a prokaryotic host

for cloning and amplification. Examples of such mammalian-bacteria shuttle vectors include pMT2 [Kaufman et al. (1989) *Mol. Cell. Biol.* 9:946] and pHEBO [Shimizu et al. (1986) *Mol. Cell. Biol.* 6:1074].

5 The transformation procedure used depends upon the host to be transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

10 Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to, Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (eg. Hep G2), and a number of other cell lines.

#### ii. Baculovirus Systems

15 The polynucleotide encoding the protein can also be inserted into a suitable insect expression vector, and is operably linked to the control elements within that vector. Vector construction employs techniques which are known in the art. Generally, the components of the expression system include a transfer vector, usually a bacterial plasmid, which contains both a fragment of the baculovirus genome, and a convenient restriction site for insertion of the heterologous gene or genes to be expressed; a wild type baculovirus with a sequence homologous to the baculovirus-specific fragment in the transfer vector (this allows for the homologous recombination of the heterologous gene in to the baculovirus genome); and appropriate insect host cells and growth media.

20 After inserting the DNA sequence encoding the protein into the transfer vector, the vector and the wild type viral genome are transfected into an insect host cell where the vector and viral genome are allowed to recombine. The packaged recombinant virus is expressed and recombinant plaques are identified and purified. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *inter alia*, Invitrogen, San Diego CA ("MaxBac" kit). These techniques are generally known to those skilled in the art and fully described in Summers & Smith, *Texas Agricultural Experiment Station Bulletin No. 1555* (1987) ("Summers & Smith").

25 Prior to inserting the DNA sequence encoding the protein into the baculovirus genome, the above described components, comprising a promoter, leader (if desired), coding sequence, and transcription termination sequence, are usually assembled into an intermediate transplacement construct (transfer vector). This may contain a single gene and operably linked regulatory elements; multiple genes, each with its own set of operably linked regulatory elements; or multiple genes, regulated by the same set of regulatory elements. Intermediate transplacement constructs are often maintained in a replicon, such as an extra-chromosomal element (e.g. plasmids) capable of stable maintenance in a host, such as a bacterium. The replicon will have a replication system, thus allowing it to be maintained in a suitable host for cloning and amplification.

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Currently, the most commonly used transfer vector for introducing foreign genes into AcNPV is pAc373. Many other vectors, known to those of skill in the art, have also been designed. These include, for example, pVL985 (which alters the polyhedrin start codon from ATG to ATT, and which introduces a BamHI cloning site 32 basepairs downstream from the ATT; see Luckow and Summers, *Virology* (1989) 17:31.

35

The plasmid usually also contains the polyhedrin polyadenylation signal (Miller et al. (1988) *Ann. Rev. Microbiol.*, 42:177) and a prokaryotic ampicillin-resistance (*amp*) gene and origin of replication for selection and propagation in *E. coli*.

Baculovirus transfer vectors usually contain a baculovirus promoter. A baculovirus promoter is any DNA sequence capable of binding a baculovirus RNA polymerase and initiating the downstream (5' to 3') transcription of a coding sequence (eg. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A baculovirus transfer vector may also have a second domain called an enhancer, which, if present, is usually distal to the structural gene. Expression may be either regulated or constitutive.

Structural genes, abundantly transcribed at late times in a viral infection cycle, provide particularly useful promoter sequences. Examples include sequences derived from the gene encoding the viral polyhedron protein, Friesen et al., (1986) "The Regulation of Baculovirus Gene Expression," in: *The Molecular Biology of Baculoviruses* (ed. Walter Doerfler); EPO Publ. Nos. 127 839 and 155 476; and the gene encoding the p10 protein, Vlak et al., (1988), *J. Gen. Virol.* 69:765.

DNA encoding suitable signal sequences can be derived from genes for secreted insect or baculovirus proteins, such as the baculovirus polyhedrin gene (Carbonell et al. (1988) *Gene*, 73:409). Alternatively, since the signals for mammalian cell posttranslational modifications (such as signal peptide cleavage, proteolytic cleavage, and phosphorylation) appear to be recognized by insect cells, and the signals required for secretion and nuclear accumulation also appear to be conserved between the invertebrate cells and vertebrate cells, leaders of non-insect origin, such as those derived from genes encoding human  $\alpha$ -interferon, Maeda et al., (1985), *Nature* 315:592; human gastrin-releasing peptide, Lebacqz-Verheyden et al., (1988), *Molec. Cell. Biol.* 8:3129; human IL-2, Smith et al., (1985) *Proc. Nat'l Acad. Sci. USA*, 82:8404; mouse IL-3, (Miyajima et al., (1987) *Gene* 58:273; and human glucocerebrosidase, Martin et al. (1988) *DNA*, 7:99, can also be used to provide for secretion in insects.

A recombinant polypeptide or polypeptide may be expressed intracellularly or, if it is expressed with the proper regulatory sequences, it can be secreted. Good intracellular expression of nonfused foreign proteins usually requires heterologous genes that ideally have a short leader sequence containing suitable translation initiation signals preceding an ATG start signal. If desired, methionine at the N-terminus may be cleaved from the mature protein by *in vitro* incubation with cyanogen bromide.

Alternatively, recombinant polypeptides or proteins which are not naturally secreted can be secreted from the insect cell by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in insects. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the translocation of the protein into the endoplasmic reticulum.

After insertion of the DNA sequence and/or the gene encoding the expression product precursor of the protein, an insect cell host is co-transformed with the heterologous DNA of the transfer vector and the genomic DNA of wild type baculovirus -- usually by co-transfection. The promoter and transcription termination sequence of the construct will usually comprise a 2-5kb section of the baculovirus genome. Methods for introducing heterologous DNA into the desired site in the baculovirus virus are known in the art. (See Summers & Smith *supra*; Ju et al. (1987); Smith et al., *Mol. Cell. Biol.* (1983) 3:2156; and Luckow and Summers (1989)). For example, the insertion can be into a gene such as the polyhedrin gene, by homologous double crossover recombination; insertion can also be into a restriction enzyme site engineered into the desired baculovirus gene. Miller et al., (1989), *Bioessays* 4:91. The DNA sequence, when cloned in place of the polyhedrin gene in the expression vector, is flanked both 5' and 3' by polyhedrin-specific sequences and is positioned downstream of the polyhedrin promoter.



The newly formed baculovirus expression vector is subsequently packaged into an infectious recombinant baculovirus. Homologous recombination occurs at low frequency (between about 1% and about 5%); thus, the majority of the virus produced after cotransfection is still wild-type virus. Therefore, a method is necessary to identify recombinant viruses. An advantage of the expression system is a visual screen allowing recombinant viruses to be distinguished. The polyhedrin protein, which is produced by the native virus, is produced at very high levels in the nuclei of infected cells at late times after viral infection. Accumulated polyhedrin protein forms occlusion bodies that also contain embedded particles. These occlusion bodies, up to 15  $\mu\text{m}$  in size, are highly refractile, giving them a bright shiny appearance that is readily visualized under the light microscope. Cells infected with recombinant viruses lack occlusion bodies. To distinguish recombinant virus from wild-type virus, the transfection supernatant is plaqued onto a monolayer of insect cells by techniques known to those skilled in the art. Namely, the plaques are screened under the light microscope for the presence (indicative of wild-type virus) or absence (indicative of recombinant virus) of occlusion bodies. "Current Protocols in Microbiology" Vol. 2 (Ausubel et al. eds) at 16.8 (Supp. 10, 1990); Summers & Smith, *supra*; Miller et al. (1989).

Recombinant baculovirus expression vectors have been developed for infection into several insect cells. For example, recombinant baculoviruses have been developed for, *inter alia*: *Aedes aegypti*, *Autographa californica*, *Bombyx mori*, *Drosophila melanogaster*, *Spodoptera frugiperda*, and *Trichoplusia ni* (WO 89/046699; Carbonell et al., (1985) *J. Virol.* 56:153; Wright (1986) *Nature* 321:718; Smith et al., (1983) *Mol. Cell. Biol.* 3:2156; and see generally, Fraser, et al. (1989) *In Vitro Cell. Dev. Biol.* 25:225).

Cells and cell culture media are commercially available for both direct and fusion expression of heterologous polypeptides in a baculovirus/expression system; cell culture technology is generally known to those skilled in the art. See, eg. Summers & Smith *supra*.

The modified insect cells may then be grown in an appropriate nutrient medium, which allows for stable maintenance of the plasmid(s) present in the modified insect host. Where the expression product gene is under inducible control, the host may be grown to high density, and expression induced. Alternatively, where expression is constitutive, the product will be continuously expressed into the medium and the nutrient medium must be continuously circulated, while removing the product of interest and augmenting depleted nutrients. The product may be purified by such techniques as chromatography, eg. HPLC, affinity chromatography, ion exchange chromatography, etc.; electrophoresis; density gradient centrifugation; solvent extraction, etc. As appropriate, the product may be further purified, as required, so as to remove substantially any insect proteins which are also present in the medium, so as to provide a product which is at least substantially free of host debris, eg. proteins, lipids and polysaccharides.

In order to obtain protein expression, recombinant host cells derived from the transformants are incubated under conditions which allow expression of the recombinant protein encoding sequence. These conditions will vary, dependent upon the host cell selected. However, the conditions are readily ascertainable to those of ordinary skill in the art, based upon what is known in the art.

### 35 iii. Plant Systems

There are many plant cell culture and whole plant genetic expression systems known in the art. Exemplary plant cellular genetic expression systems include those described in patents, such as: US 5,693,506; US 5,659,122; and US 5,608,143. Additional examples of genetic expression in plant cell culture has been described by Zenk, *Phytochemistry* 30:3861-3863 (1991). Descriptions of plant protein signal peptides may be found in addition to the references described above in Vaulcombe et al., *Mol. Gen. Genet.* 209:33-40 (1987); Chandler et al., *Plant Molecular Biology* 3:407-418 (1984); Rogers, *J. Biol. Chem.* 260:3731-3738 (1985); Rothstein et al., *Gene* 55:353-356 (1987);



- Whittier et al., *Nucleic Acids Research* 15:2515-2535 (1987); Wirsal et al., *Molecular Microbiology* 3:3-14 (1989); Yu et al., *Gene* 122:247-253 (1992). A description of the regulation of plant gene expression by the phytohormone, gibberellic acid and secreted enzymes induced by gibberellic acid can be found in R.L. Jones and J. MacMillin, *Gibberellins*: in: *Advanced Plant Physiology*, Malcolm B. Wilkins, ed., 1984 Pitman Publishing Limited, London, pp. 21-52. References that describe other metabolically-regulated genes: Sheen, *Plant Cell*, 2:1027-1038(1990); Maas et al., *EMBO J.* 9:3447-3452 (1990); Benkel and Hickey, *Proc. Natl. Acad. Sci.* 84:1337-1339 (1987).

Typically, using techniques known in the art, a desired polynucleotide sequence is inserted into an expression cassette comprising genetic regulatory elements designed for operation in plants. The expression cassette is inserted into a desired expression vector with companion sequences upstream and downstream from the expression cassette suitable for expression in a plant host. The companion sequences will be of plasmid or viral origin and provide necessary characteristics to the vector to permit the vectors to move DNA from an original cloning host, such as bacteria, to the desired plant host. The basic bacterial/plant vector construct will preferably provide a broad host range prokaryote replication origin; a prokaryote selectable marker; and, for *Agrobacterium* transformations, T DNA sequences for *Agrobacterium*-mediated transfer to plant chromosomes. Where the heterologous gene is not readily amenable to detection, the construct will preferably also have a selectable marker gene suitable for determining if a plant cell has been transformed. A general review of suitable markers, for example for the members of the grass family, is found in Wilmink and Dons, 1993, *Plant Mol. Biol. Rept.*, 11(2):165-185.

Sequences suitable for permitting integration of the heterologous sequence into the plant genome are also recommended. These might include transposon sequences and the like for homologous recombination as well as Ti sequences which permit random insertion of a heterologous expression cassette into a plant genome. Suitable prokaryote selectable markers include resistance toward antibiotics such as ampicillin or tetracycline. Other DNA sequences encoding additional functions may also be present in the vector, as is known in the art.

The nucleic acid molecules of the subject invention may be included into an expression cassette for expression of the protein(s) of interest. Usually, there will be only one expression cassette, although two or more are feasible. The recombinant expression cassette will contain in addition to the heterologous protein encoding sequence the following elements, a promoter region, plant 5' untranslated sequences, initiation codon depending upon whether or not the structural gene comes equipped with one, and a transcription and translation termination sequence. Unique restriction enzyme sites at the 5' and 3' ends of the cassette allow for easy insertion into a pre-existing vector.

A heterologous coding sequence may be for any protein relating to the present invention. The sequence encoding the protein of interest will encode a signal peptide which allows processing and translocation of the protein, as appropriate, and will usually lack any sequence which might result in the binding of the desired protein of the invention to a membrane. Since, for the most part, the transcriptional initiation region will be for a gene which is expressed and translocated during germination, by employing the signal peptide which provides for translocation, one may also provide for translocation of the protein of interest. In this way, the protein(s) of interest will be translocated from the cells in which they are expressed and may be efficiently harvested. Typically secretion in seeds are across the aleurone or scutellar epithelium layer into the endosperm of the seed. While it is not required that the protein be secreted from the cells in which the protein is produced, this facilitates the isolation and purification of the recombinant protein.

Since the ultimate expression of the desired gene product will be in a eucaryotic cell it is desirable to determine whether any portion of the cloned gene contains sequences which will be processed out as introns by the host's

splicosome machinery. If so, site-directed mutagenesis of the "intron" region may be conducted to prevent losing a portion of the genetic message as a false intron code, Reed and Maniatis, *Cell* 41:95-105, 1985.

The vector can be microinjected directly into plant cells by use of micropipettes to mechanically transfer the recombinant DNA. Crossway, *Mol. Gen. Genet*, 202:179-185, 1985. The genetic material may also be transferred into  
 5 the plant cell by using polyethylene glycol, Krens, et al., *Nature*, 296, 72-74, 1982. Another method of introduction of nucleic acid segments is high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface, Klein, et al., *Nature*, 327, 70-73, 1987 and Knudsen and Muller, 1991, *Planta*, 185:330-336 teaching particle bombardment of barley endosperm to create transgenic barley. Yet another method of introduction would be fusion of protoplasts with other entities, either minicells, cells, lysosomes or  
 10 other fusible lipid-surfaced bodies, Fraley, et al., *Proc. Natl. Acad. Sci. USA*, 79, 1859-1863, 1982.

The vector may also be introduced into the plant cells by electroporation. (Fromm et al., *Proc. Natl. Acad. Sci. USA* 82:5824, 1985). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the gene construct. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and form plant callus.

15 All plants from which protoplasts can be isolated and cultured to give whole regenerated plants can be transformed by the present invention so that whole plants are recovered which contain the transferred gene. It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to all major species of sugarcane, sugar beet, cotton, fruit and other trees, legumes and vegetables. Some suitable plants include, for example, species from the genera *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*,  
 20 *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersion*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Cichorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Hererocallis*, *Nemesia*, *Pelargonium*, *Panicum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Glycine*, *Lolium*, *Zea*, *Triticum*, *Sorghum*, and *Datura*.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts  
 25 containing copies of the heterologous gene is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced from the protoplast suspension. These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Shoots and roots normally develop simultaneously. Efficient  
 30 regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is fully reproducible and repeatable.

In some plant cell culture systems, the desired protein of the invention may be excreted or alternatively, the protein may be extracted from the whole plant. Where the desired protein of the invention is secreted into the medium, it may be collected. Alternatively, the embryos and embryoless-half seeds or other plant tissue may be mechanically  
 35 disrupted to release any secreted protein between cells and tissues. The mixture may be suspended in a buffer solution to retrieve soluble proteins. Conventional protein isolation and purification methods will be then used to purify the recombinant protein. Parameters of time, temperature pH, oxygen, and volumes will be adjusted through routine methods to optimize expression and recovery of heterologous protein.

#### iv. Bacterial Systems

40 Bacterial expression techniques are known in the art. A bacterial promoter is any DNA sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of a coding sequence (eg. structural gene)

into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A bacterial promoter may also have a second domain called an operator, that may overlap an adjacent RNA polymerase binding site at which RNA synthesis begins. The operator permits negative regulated (inducible) transcription, as a gene repressor protein may bind the operator and thereby inhibit transcription of a specific gene. Constitutive expression may occur in the absence of negative regulatory elements, such as the operator. In addition, positive regulation may be achieved by a gene activator protein binding sequence, which, if present is usually proximal (5') to the RNA polymerase binding sequence. An example of a gene activator protein is the catabolite activator protein (CAP), which helps initiate transcription of the lac operon in *Escherichia coli* (*E. coli*) [Raibaud *et al.* (1984) *Annu. Rev. Genet.* 18:173]. Regulated expression may therefore be either positive or negative, thereby either enhancing or reducing transcription.

Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose (*lac*) [Chang *et al.* (1977) *Nature* 198:1056], and maltose. Additional examples include promoter sequences derived from biosynthetic enzymes such as tryptophan (*trp*) [Goeddel *et al.* (1980) *Nuc. Acids Res.* 8:4057; Yelverton *et al.* (1981) *Nucl. Acids Res.* 9:731; US patent 4,738,921; EP-A-0036776 and EP-A-0121775]. The  $\beta$ -lactamase (*bla*) promoter system [Weissmann (1981) "The cloning of interferon and other mistakes." In *Interferon 3* (ed. I. Gresser)], bacteriophage lambda PL [Shimatake *et al.* (1981) *Nature* 292:128] and T5 [US patent 4,689,406] promoter systems also provide useful promoter sequences.

In addition, synthetic promoters which do not occur in nature also function as bacterial promoters. For example, transcription activation sequences of one bacterial or bacteriophage promoter may be joined with the operon sequences of another bacterial or bacteriophage promoter, creating a synthetic hybrid promoter [US patent 4,551,433]. For example, the *tac* promoter is a hybrid *trp-lac* promoter comprised of both *trp* promoter and *lac* operon sequences that is regulated by the *lac* repressor [Amann *et al.* (1983) *Gene* 25:167; de Boer *et al.* (1983) *Proc. Natl. Acad. Sci.* 80:21]. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. A naturally occurring promoter of non-bacterial origin can also be coupled with a compatible RNA polymerase to produce high levels of expression of some genes in prokaryotes. The bacteriophage T7 RNA polymerase/promoter system is an example of a coupled promoter system [Studier *et al.* (1986) *J. Mol. Biol.* 189:113; Tabor *et al.* (1985) *Proc Natl. Acad. Sci.* 82:1074]. In addition, a hybrid promoter can also be comprised of a bacteriophage promoter and an *E. coli* operator region (EPO-A-0 267 851).

In addition to a functioning promoter sequence, an efficient ribosome binding site is also useful for the expression of foreign genes in prokaryotes. In *E. coli*, the ribosome binding site is called the Shine-Dalgarno (SD) sequence and includes an initiation codon (ATG) and a sequence 3-9 nucleotides in length located 3-11 nucleotides upstream of the initiation codon [Shine *et al.* (1975) *Nature* 254:34]. The SD sequence is thought to promote binding of mRNA to the ribosome by the pairing of bases between the SD sequence and the 3' end of *E. coli* 16S rRNA [Steitz *et al.* (1979) "Genetic signals and nucleotide sequences in messenger RNA." In *Biological Regulation and Development: Gene Expression* (ed. R.F. Goldberg)]. To express eukaryotic genes and prokaryotic genes with weak ribosome-binding site [Sambrook *et al.* (1989) "Expression of cloned genes in *Escherichia coli*." In *Molecular Cloning: A Laboratory Manual*].

5 A DNA molecule may be expressed intracellularly. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide or by either *in vivo* or *in vitro* incubation with a bacterial methionine N-terminal peptidase (EPO-A-0 219 237).

10 Fusion proteins provide an alternative to direct expression. Usually, a DNA sequence encoding the N-terminal portion of an endogenous bacterial protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the bacteriophage lambda cell gene can be linked at the 5' terminus of a foreign gene and expressed in bacteria. The  
15 resulting fusion protein preferably retains a site for a processing enzyme (factor Xa) to cleave the bacteriophage protein from the foreign gene [Nagai *et al.* (1984) *Nature* 309:810]. Fusion proteins can also be made with sequences from the *lacZ* [Jia *et al.* (1987) *Gene* 60:197], *trpE* [Allen *et al.* (1987) *J. Biotechnol.* 5:93; Makoff *et al.* (1989) *J. Gen. Microbiol.* 135:11], and *Chey* [EP-A-0 324 647] genes. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. Another example is a ubiquitin fusion protein. Such a fusion  
20 protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (*eg.* ubiquitin specific processing-protease) to cleave the ubiquitin from the foreign protein. Through this method, native foreign protein can be isolated [Miller *et al.* (1989) *Bio/Technology* 7:698].

Alternatively, foreign proteins can also be secreted from the cell by creating chimeric DNA molecules that encode a fusion protein comprised of a signal peptide sequence fragment that provides for secretion of the foreign protein in  
25 bacteria [US patent 4,336,336]. The signal sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). Preferably there are processing sites, which can be cleaved either *in vivo* or *in vitro* encoded between the signal peptide fragment and the foreign gene.

30 DNA encoding suitable signal sequences can be derived from genes for secreted bacterial proteins, such as the *E. coli* outer membrane protein gene (*ompA*) [Masui *et al.* (1983), in: *Experimental Manipulation of Gene Expression*; Ghayeb *et al.* (1984) *EMBO J.* 3:2437] and the *E. coli* alkaline phosphatase signal sequence (*phoA*) [Oka *et al.* (1985) *Proc. Natl. Acad. Sci.* 82:7212]. As an additional example, the signal sequence of the alpha-amylase gene from various *Bacillus* strains can be used to secrete heterologous proteins from *B. subtilis* [Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EP-A-0 244 042].

Usually, transcription termination sequences recognized by bacteria are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Transcription termination sequences frequently include DNA sequences of about 50 nucleotides capable of forming stem loop structures that aid in  
35 terminating transcription. Examples include transcription termination sequences derived from genes with strong promoters, such as the *trp* gene in *E. coli* as well as other biosynthetic genes.

Usually, the above described components, comprising a promoter, signal sequence (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (*eg.* plasmids) capable of stable maintenance in  
40 a host, such as bacteria. The replicon will have a replication system, thus allowing it to be maintained in a prokaryotic host either for expression or for cloning and amplification. In addition, a replicon may be either a high or low copy

number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably contain at least about 10, and more preferably at least about 20 plasmids. Either a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host.

5 Alternatively, the expression constructs can be integrated into the bacterial genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to the bacterial chromosome that allows the vector to integrate. Integrations appear to result from recombinations between homologous DNA in the vector and the bacterial chromosome. For example, integrating vectors constructed with DNA from various *Bacillus* strains integrate into the *Bacillus* chromosome (EP-A- 0 127 328). Integrating vectors may also be comprised of bacteriophage or  
10 transposon sequences.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of bacterial strains that have been transformed. Selectable markers can be expressed in the bacterial host and may include genes which render bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin (neomycin), and tetracycline [Davies *et al.* (1978) *Annu. Rev. Microbiol.* 32:469]. Selectable markers may  
15 also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways.

Alternatively, some of the above described components can be put together in transformation vectors. Transformation vectors are usually comprised of a selectable market that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extra-chromosomal replicons or integrating vectors, have been  
20 developed for transformation into many bacteria. For example, expression vectors have been developed for, *inter alia*, the following bacteria: *Bacillus subtilis* [Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EP-A-0 036 259 and EP-A-0 063 953; WO 84/04541], *Escherichia coli* [Shimatake *et al.* (1981) *Nature* 292:128; Amann *et al.* (1985) *Gene* 40:183; Studier *et al.* (1986) *J. Mol. Biol.* 189:113; EP-A-0 036 776, EP-A-0 136 829 and EP-A-0 136 907], *Streptococcus cremoris* [Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655]; *Streptococcus lividans* [Powell *et al.*  
25 (1988) *Appl. Environ. Microbiol.* 54:655], *Streptomyces lividans* [US patent 4,745,056].

Methods of introducing exogenous DNA into bacterial hosts are well-known in the art, and usually include either the transformation of bacteria treated with  $\text{CaCl}_2$  or other agents, such as divalent cations and DMSO. DNA can also be introduced into bacterial cells by electroporation. Transformation procedures usually vary with the bacterial species to be transformed. See *eg.* [Masson *et al.* (1989) *FEMS Microbiol. Lett.* 60:273; Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EP-A-0 036 259 and EP-A-0 063 953; WO 84/04541, *Bacillus*], [Miller *et al.* (1988) *Proc. Natl. Acad. Sci.* 85:856; Wang *et al.* (1990) *J. Bacteriol.* 172:949, *Campylobacter*], [Cohen *et al.* (1973) *Proc. Natl. Acad. Sci.* 69:2110; Dower *et al.* (1988) *Nucleic Acids Res.* 16:6127; Kushner (1978) "An improved method for transformation of *Escherichia coli* with ColE1-derived plasmids. In *Genetic Engineering: Proceedings of the International Symposium on Genetic Engineering* (eds. H.W. Boyer and S. Nicosia); Mandel *et al.* (1970) *J. Mol. Biol.* 53:159; Taketo (1988) *Biochim. Biophys. Acta* 949:318; *Escherichia*], [Chassy *et al.* (1987) *FEMS Microbiol. Lett.* 44:173 *Lactobacillus*]; [Fiedler *et al.* (1988) *Anal. Biochem* 170:38, *Pseudomonas*]; [Augustin *et al.* (1990) *FEMS Microbiol. Lett.* 66:203, *Staphylococcus*], [Barany *et al.* (1980) *J. Bacteriol.* 144:698; Harlander (1987) "Transformation of *Streptococcus lactis* by electroporation, in: *Streptococcal Genetics* (ed. J. Ferretti and R. Curtiss III); Perry *et al.* (1981) *Infect. Immun.* 32:1295; Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655; Somkuti *et al.*  
30 (1987) *Proc. 4th Eur. Cong. Biotechnology* 1:412, *Streptococcus*].  
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### v. Yeast Expression

Yeast expression systems are also known to one of ordinary skill in the art. A yeast promoter is any DNA sequence capable of binding yeast RNA polymerase and initiating the downstream (3') transcription of a coding sequence (eg. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site (the "TATA Box") and a transcription initiation site. A yeast promoter may also have a second domain called an upstream activator sequence (UAS), which, if present, is usually distal to the structural gene. The UAS permits regulated (inducible) expression. Constitutive expression occurs in the absence of a UAS. Regulated expression may be either positive or negative, thereby either enhancing or reducing transcription.

Yeast is a fermenting organism with an active metabolic pathway, therefore sequences encoding enzymes in the metabolic pathway provide particularly useful promoter sequences. Examples include alcohol dehydrogenase (ADH) (EP-A-0 284 044), enolase, glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphate-dehydrogenase (GAP or GAPDH), hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, and pyruvate kinase (PyK) (EPO-A-0 329 203). The yeast *PHO5* gene, encoding acid phosphatase, also provides useful promoter sequences [Myanohara *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:1].

In addition, synthetic promoters which do not occur in nature also function as yeast promoters. For example, UAS sequences of one yeast promoter may be joined with the transcription activation region of another yeast promoter, creating a synthetic hybrid promoter. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region (US Patent Nos. 4,876,197 and 4,880,734). Other examples of hybrid promoters include promoters which consist of the regulatory sequences of either the *ADH2*, *GAL4*, *GAL10*, OR *PHO5* genes, combined with the transcriptional activation region of a glycolytic enzyme gene such as GAP or PyK (EP-A-0 164 556). Furthermore, a yeast promoter can include naturally occurring promoters of non-yeast origin that have the ability to bind yeast RNA polymerase and initiate transcription. Examples of such promoters include, *inter alia*, [Cohen *et al.* (1980) *Proc. Natl. Acad. Sci. USA* 77:1078; Henikoff *et al.* (1981) *Nature* 283:835; Hollenberg *et al.* (1981) *Curr. Topics Microbiol. Immunol.* 96:119; Hollenberg *et al.* (1979) "The Expression of Bacterial Antibiotic Resistance Genes in the Yeast *Saccharomyces cerevisiae*," in: *Plasmids of Medical, Environmental and Commercial Importance* (eds. K.N. Timmis and A. Puhler); Mercerau-Puigalon *et al.* (1980) *Gene* 11:163; Panthier *et al.* (1980) *Curr. Genet.* 2:109;].

A DNA molecule may be expressed intracellularly in yeast. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Fusion proteins provide an alternative for yeast expression systems, as well as in mammalian, baculovirus, and bacterial expression systems. Usually, a DNA sequence encoding the N-terminal portion of an endogenous yeast protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the yeast or human superoxide dismutase (SOD) gene, can be linked at the 5' terminus of a foreign gene and expressed in yeast. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. See eg. EP-A-0 196 056. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (eg. ubiquitin-specific processing protease) to cleave the ubiquitin from the foreign protein. Through this method, therefore, native foreign protein can be isolated (eg. WO 88/024066).

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provide for secretion in yeast of the foreign protein. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell.

DNA encoding suitable signal sequences can be derived from genes for secreted yeast proteins, such as the yeast invertase gene (EP-A-0 012 873; JPO. 62,096,086) and the A-factor gene (US patent 4,588,684). Alternatively, leaders of non-yeast origin, such as an interferon leader, exist that also provide for secretion in yeast (EP-A-0 060 057).

- 10 A preferred class of secretion leaders are those that employ a fragment of the yeast alpha-factor gene, which contains both a "pre" signal sequence, and a "pro" region. The types of alpha-factor fragments that can be employed include the full-length pre-pro alpha factor leader (about 83 amino acid residues) as well as truncated alpha-factor leaders (usually about 25 to about 50 amino acid residues) (US Patents 4,546,083 and 4,870,008; EP-A-0 324 274). Additional leaders employing an alpha-factor leader fragment that provides for secretion include hybrid alpha-factor
- 15 leaders made with a presequence of a first yeast, but a pro-region from a second yeast alphafactor. (eg. see WO 89/02463.)

Usually, transcription termination sequences recognized by yeast are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator

20 sequence and other yeast-recognized termination sequences, such as those coding for glycolytic enzymes.

- Usually, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (eg. plasmids) capable of stable maintenance in a host, such as yeast or bacteria. The replicon may have two replication systems, thus allowing it to be maintained, for
- 25 example, in yeast for expression and in a prokaryotic host for cloning and amplification. Examples of such yeast-bacteria shuttle vectors include YEp24 [Botstein *et al.* (1979) *Gene* 8:17-24], pCM1 [Brake *et al.* (1984) *Proc. Natl. Acad. Sci USA* 81:4642-4646], and YRp17 [Stinchcomb *et al.* (1982) *J. Mol. Biol.* 158:157]. In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid
- 30 will preferably have at least about 10, and more preferably at least about 20. Enter a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host. See eg. Brake *et al.*, *supra*.

- Alternatively, the expression constructs can be integrated into the yeast genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to a yeast chromosome that allows the vector to
- 35 integrate, and preferably contain two homologous sequences flanking the expression construct. Integrations appear to result from recombinations between homologous DNA in the vector and the yeast chromosome [Orr-Weaver *et al.* (1983) *Methods in Enzymol.* 101:228-245]. An integrating vector may be directed to a specific locus in yeast by selecting the appropriate homologous sequence for inclusion in the vector. See Orr-Weaver *et al.*, *supra*. One or more expression construct may integrate, possibly affecting levels of recombinant protein produced [Rine *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:6750]. The chromosomal sequences included in the vector can occur either as a single
- 40 segment in the vector, which results in the integration of the entire vector, or two segments homologous to adjacent



segments in the chromosome and flanking the expression construct in the vector, which can result in the stable integration of only the expression construct.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of yeast strains that have been transformed. Selectable markers may include biosynthetic genes that can be expressed in the yeast host, such as *ADE2*, *HIS4*, *LEU2*, *TRP1*, and *ALG7*, and the G418 resistance gene, which confer resistance in yeast cells to tunicamycin and G418, respectively. In addition, a suitable selectable marker may also provide yeast with the ability to grow in the presence of toxic compounds, such as metal. For example, the presence of *CUP1* allows yeast to grow in the presence of copper ions [Butt *et al.* (1987) *Microbiol. Rev.* 51:351].

Alternatively, some of the above described components can be put together into transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extrachromosomal replicons or integrating vectors, have been developed for transformation into many yeasts. For example, expression vectors have been developed for, *inter alia*, the following yeasts: *Candida albicans* [Kurtz, *et al.* (1986) *Mol. Cell. Biol.* 6:142], *Candida maltosa* [Kunze, *et al.* (1985) *J. Basic Microbiol.* 25:141], *Hansenula polymorpha* [Gleeson, *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302], *Kluyveromyces fragilis* [Das, *et al.* (1984) *J. Bacteriol.* 158:1165], *Kluyveromyces lactis* [De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:737; Van den Berg *et al.* (1990) *Bio/Technology* 8:135], *Pichia guilliermondii* [Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141], *Pichia pastoris* [Cregg, *et al.* (1985) *Mol. Cell. Biol.* 5:3376; US Patent Nos. 4,837,148 and 4,929,555], *Saccharomyces cerevisiae* [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163], *Schizosaccharomyces pombe* [Beach and Nurse (1981) *Nature* 300:706], and *Yarrowia lipolytica* [Davidow, *et al.* (1985) *Curr. Genet.* 10:380471 Gaillardin, *et al.* (1985) *Curr. Genet.* 10:49].

Methods of introducing exogenous DNA into yeast hosts are well-known in the art, and usually include either the transformation of spheroplasts or of intact yeast cells treated with alkali cations. Transformation procedures usually vary with the yeast species to be transformed. See *eg.* [Kurtz *et al.* (1986) *Mol. Cell. Biol.* 6:142; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; *Candida*]; [Gleeson *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302; *Hansenula*]; [Das *et al.* (1984) *J. Bacteriol.* 158:1165; De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:1165; Van den Berg *et al.* (1990) *Bio/Technology* 8:135; *Kluyveromyces*]; [Cregg *et al.* (1985) *Mol. Cell. Biol.* 5:3376; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; US Patent Nos. 4,837,148 and 4,929,555; *Pichia*]; [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163 *Saccharomyces*]; [Beach and Nurse (1981) *Nature* 300:706; *Schizosaccharomyces*]; [Davidow *et al.* (1985) *Curr. Genet.* 10:39; Gaillardin *et al.* (1985) *Curr. Genet.* 10:49; *Yarrowia*].

### Antibodies

As used herein, the term "antibody" refers to a polypeptide or group of polypeptides composed of at least one antibody combining site. An "antibody combining site" is the three-dimensional binding space with an internal surface shape and charge distribution complementary to the features of an epitope of an antigen, which allows a binding of the antibody with the antigen. "Antibody" includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, humanised antibodies, altered antibodies, univalent antibodies, Fab proteins, and single domain antibodies.

Antibodies against the proteins of the invention are useful for affinity chromatography, immunoassays, and distinguishing/identifying *Neisseria* proteins.



Antibodies to the proteins of the invention, both polyclonal and monoclonal, may be prepared by conventional methods. In general, the protein is first used to immunize a suitable animal, preferably a mouse, rat, rabbit or goat. Rabbits and goats are preferred for the preparation of polyclonal sera due to the volume of serum obtainable, and the availability of labeled anti-rabbit and anti-goat antibodies. Immunization is generally performed by mixing or emulsifying the protein in saline, preferably in an adjuvant such as Freund's complete adjuvant, and injecting the mixture or emulsion parenterally (generally subcutaneously or intramuscularly). A dose of 50-200 µg/injection is typically sufficient. Immunization is generally boosted 2-6 weeks later with one or more injections of the protein in saline, preferably using Freund's incomplete adjuvant. One may alternatively generate antibodies by *in vitro* immunization using methods known in the art, which for the purposes of this invention is considered equivalent to *in vivo* immunization. Polyclonal antisera is obtained by bleeding the immunized animal into a glass or plastic container, incubating the blood at 25°C for one hour, followed by incubating at 4°C for 2-18 hours. The serum is recovered by centrifugation (eg. 1,000g for 10 minutes). About 20-50 ml per bleed may be obtained from rabbits.

Monoclonal antibodies are prepared using the standard method of Kohler & Milstein [*Nature* (1975) 256:495-96], or a modification thereof. Typically, a mouse or rat is immunized as described above. However, rather than bleeding the animal to extract serum, the spleen (and optionally several large lymph nodes) is removed and dissociated into single cells. If desired, the spleen cells may be screened (after removal of nonspecifically adherent cells) by applying a cell suspension to a plate or well coated with the protein antigen. B-cells expressing membrane-bound immunoglobulin specific for the antigen bind to the plate, and are not rinsed away with the rest of the suspension. Resulting B-cells, or all dissociated spleen cells, are then induced to fuse with myeloma cells to form hybridomas, and are cultured in a selective medium (eg. hypoxanthine, aminopterin, thymidine medium, "HAT"). The resulting hybridomas are plated by limiting dilution, and are assayed for production of antibodies which bind specifically to the immunizing antigen (and which do not bind to unrelated antigens). The selected MAb-secreting hybridomas are then cultured either *in vitro* (eg. in tissue culture bottles or hollow fiber reactors), or *in vivo* (as ascites in mice).

If desired, the antibodies (whether polyclonal or monoclonal) may be labeled using conventional techniques. Suitable labels include fluorophores, chromophores, radioactive atoms (particularly <sup>32</sup>P and <sup>125</sup>I), electron-dense reagents, enzymes, and ligands having specific binding partners. Enzymes are typically detected by their activity. For example, horseradish peroxidase is usually detected by its ability to convert 3,3',5,5'-tetramethylbenzidine (TMB) to a blue pigment, quantifiable with a spectrophotometer. "Specific binding partner" refers to a protein capable of binding a ligand molecule with high specificity, as for example in the case of an antigen and a monoclonal antibody specific therefor. Other specific binding partners include biotin and avidin or streptavidin, IgG and protein A, and the numerous receptor-ligand couples known in the art. It should be understood that the above description is not meant to categorize the various labels into distinct classes, as the same label may serve in several different modes. For example, <sup>125</sup>I may serve as a radioactive label or as an electron-dense reagent. HRP may serve as enzyme or as antigen for a MAb. Further, one may combine various labels for desired effect. For example, MAbs and avidin also require labels in the practice of this invention: thus, one might label a MAb with biotin, and detect its presence with avidin labeled with <sup>125</sup>I, or with an anti-biotin MAb labeled with HRP. Other permutations and possibilities will be readily apparent to those of ordinary skill in the art, and are considered as equivalents within the scope of the instant invention.

### Pharmaceutical Compositions

Pharmaceutical compositions can comprise either polypeptides, antibodies, or nucleic acid of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

- 5 The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgement of the clinician.

For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

- 15 A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

- 20 Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

- 25 Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

### Delivery Methods

Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals; in particular, human subjects can be treated.

- 35 Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal or transcutaneous applications (eg. see WO98/20734), needles, and gene guns or hypodermic syringes. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Vaccines

Vaccines according to the invention may either be prophylactic (*ie.* to prevent infection) or therapeutic (*ie.* to treat disease after infection).

Such vaccines comprise immunising antigen(s), immunogen(s), polypeptide(s), protein(s) or nucleic acid, usually in combination with "pharmaceutically acceptable carriers," which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or liposomes), and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the antigen or immunogen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, *H. pylori*, *etc.* pathogens.

Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, *etc.*; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59™ (WO 90/14837; Chapter 10 in *Vaccine design: the subunit and adjuvant approach*, eds. Powell & Newman, Plenum Press 1995), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA), (b) SAF, containing 10% Squalane, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) Ribi™ adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (Detox™); (3) saponin adjuvants, such as Stimulon™ (Cambridge Bioscience, Worcester, MA) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (*eg.* IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, *etc.*), interferons (*eg.* gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), *etc.*; and (6) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59™ are preferred.

As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-*sn*-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), *etc.*

The immunogenic compositions (*eg.* the immunising antigen/immunogen/polypeptide/protein/ nucleic acid, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, *etc.* Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles.

Typically, the immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

Immunogenic compositions used as vaccines comprise an immunologically effective amount of the antigenic or immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By "immunologically effective amount", it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (eg. nonhuman primate, primate, etc.), the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

- 10 The immunogenic compositions are conventionally administered parenterally, eg. by injection, either subcutaneously, intramuscularly, or transdermally/transcutaneously (eg. WO98/20734). Additional formulations suitable for other modes of administration include oral and pulmonary formulations, suppositories, and transdermal applications. Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.
- 15 As an alternative to protein-based vaccines, DNA vaccination may be used [eg. Robinson & Torres (1997) *Seminars in Immunol* 9:271-283; Donnelly et al. (1997) *Annu Rev Immunol* 15:617-648; later herein].

#### Gene Delivery Vehicles

Gene therapy vehicles for delivery of constructs including a coding sequence of a therapeutic of the invention, to be delivered to the mammal for expression in the mammal, can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches in *in vivo* or *ex vivo* modality. Expression of such coding sequence can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence *in vivo* can be either constitutive or regulated.

The invention includes gene delivery vehicles capable of expressing the contemplated nucleic acid sequences. The gene delivery vehicle is preferably a viral vector and, more preferably, a retroviral, adenoviral, adeno-associated viral (AAV), herpes viral, or alphavirus vector. The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picornavirus, poxvirus, or togavirus viral vector. See generally, Jolly (1994) *Cancer Gene Therapy* 1:51-64; Kimura (1994) *Human Gene Therapy* 5:845-852; Connelly (1995) *Human Gene Therapy* 6:185-193; and Kaplitt (1994) *Nature Genetics* 6:148-153.

Retroviral vectors are well known in the art and we contemplate that any retroviral gene therapy vector is employable in the invention, including B, C and D type retroviruses, xenotropic retroviruses (for example, NZB-X1, NZB-X2 and NZB9-1 (see O'Neill (1985) *J. Virol.* 53:160) polytropic retroviruses eg. MCF and MCF-MLV (see Kelly (1983) *J. Virol.* 45:291), spumaviruses and lentiviruses. See RNA Tumor Viruses, Second Edition, Cold Spring Harbor Laboratory, 1985.

Portions of the retroviral gene therapy vector may be derived from different retroviruses. For example, retrovector LTRs may be derived from a Murine Sarcoma Virus, a tRNA binding site from a Rous Sarcoma Virus, a packaging signal from a Murine Leukemia Virus, and an origin of second strand synthesis from an Avian Leukosis Virus.

These recombinant retroviral vectors may be used to generate transduction competent retroviral vector particles by introducing them into appropriate packaging cell lines (see US patent 5,591,624). Retrovirus vectors can be constructed for site-specific integration into host cell DNA by incorporation of a chimeric integrase enzyme into the

retroviral particle (see WO96/37626). It is preferable that the recombinant viral vector is a replication defective recombinant virus.

Packaging cell lines suitable for use with the above-described retrovirus vectors are well known in the art, are readily prepared (see WO95/30763 and WO92/05266), and can be used to create producer cell lines (also termed vector cell lines or "VCLs") for the production of recombinant vector particles. Preferably, the packaging cell lines are made from human parent cells (eg. HT1080 cells) or mink parent cell lines, which eliminates inactivation in human serum.

Preferred retroviruses for the construction of retroviral gene therapy vectors include Avian Leukosis Virus, Bovine Leukemia Virus, Murine Leukemia Virus, Mink-Cell Focus-Inducing Virus, Murine Sarcoma Virus, Reticuloendotheliosis Virus and Rous Sarcoma Virus. Particularly preferred Murine Leukemia Viruses include 4070A and 1504A (Hartley and Rowe (1976) *J Virol* 19:19-25), Abelson (ATCC No. VR-999), Friend (ATCC No. VR-245), Graffi, Gross (ATCC No. VR-590), Kirsten, Harvey Sarcoma Virus and Rauscher (ATCC No. VR-998) and Moloney Murine Leukemia Virus (ATCC No. VR-190). Such retroviruses may be obtained from depositories or collections such as the American Type Culture Collection ("ATCC") in Rockville, Maryland or isolated from known sources using commonly available techniques.

Exemplary known retroviral gene therapy vectors employable in this invention include those described in patent applications GB2200651, EP0415731, EP0345242, EP0334301, WO89/02468; WO89/05349, WO89/09271, WO90/02806, WO90/07936, WO94/03622, WO93/25698, WO93/25234, WO93/11230, WO93/10218, WO91/02805, WO91/02825, WO95/07994, US 5,219,740, US 4,405,712, US 4,861,719, US 4,980,289, US 4,777,127, US 5,591,624. See also Vile (1993) *Cancer Res* 53:3860-3864; Vile (1993) *Cancer Res* 53:962-967; Ram (1993) *Cancer Res* 53 (1993) 83-88; Takamiya (1992) *J Neurosci Res* 33:493-503; Baba (1993) *J Neurosurg* 79:729-735; Mann (1983) *Cell* 33:153; Cane (1984) *Proc Natl Acad Sci* 81:6349; and Miller (1990) *Human Gene Therapy* 1.

Human adenoviral gene therapy vectors are also known in the art and employable in this invention. See, for example, Berkner (1988) *Biotechniques* 6:616 and Rosenfeld (1991) *Science* 252:431, and WO93/07283, WO93/06223, and WO93/07282. Exemplary known adenoviral gene therapy vectors employable in this invention include those described in the above referenced documents and in WO94/12649, WO93/03769, WO93/19191, WO94/28938, WO95/11984, WO95/00655, WO95/27071, WO95/29993, WO95/34671, WO96/05320, WO94/08026, WO94/11506, WO93/06223, WO94/24299, WO95/14102, WO95/24297, WO95/02697, WO94/28152, WO94/24299, WO95/09241, WO95/25807, WO95/05835, WO94/18922 and WO95/09654. Alternatively, administration of DNA linked to killed adenovirus as described in Curiel (1992) *Hum. Gene Ther.* 3:147-154 may be employed. The gene delivery vehicles of the invention also include adenovirus associated virus (AAV) vectors. Leading and preferred examples of such vectors for use in this invention are the AAV-2 based vectors disclosed in Srivastava, WO93/09239. Most preferred AAV vectors comprise the two AAV inverted terminal repeats in which the native D-sequences are modified by substitution of nucleotides, such that at least 5 native nucleotides and up to 18 native nucleotides, preferably at least 10 native nucleotides up to 18 native nucleotides, most preferably 10 native nucleotides are retained and the remaining nucleotides of the D-sequence are deleted or replaced with non-native nucleotides. The native D-sequences of the AAV inverted terminal repeats are sequences of 20 consecutive nucleotides in each AAV inverted terminal repeat (ie. there is one sequence at each end) which are not involved in HP formation. The non-native replacement nucleotide may be any nucleotide other than the nucleotide found in the native D-sequence in the same position. Other employable exemplary AAV vectors are pWP-19, pWN-1, both of which are disclosed in Nahreini (1993) *Gene* 124:257-262. Another example of such an AAV vector is psub201 (see Samulski (1987) *J. Virol.* 61:3096). Another exemplary AAV vector is the Double-D ITR vector. Construction of the Double-D ITR vector is disclosed in

US Patent 5,478,745. Still other vectors are those disclosed in Carter US Patent 4,797,368 and Muzyczka US Patent 5,139,941, Chartejee US Patent 5,474,935, and Kotin WO94/288157. Yet a further example of an AAV vector employable in this invention is SSV9AFABTKneo, which contains the AFP enhancer and albumin promoter and directs expression predominantly in the liver. Its structure and construction are disclosed in Su (1996) *Human Gene Therapy* 7:463-470. Additional AAV gene therapy vectors are described in US 5,354,678, US 5,173,414, US 5,139,941, and US 5,252,479.

The gene therapy vectors of the invention also include herpes vectors. Leading and preferred examples are herpes simplex virus vectors containing a sequence encoding a thymidine kinase polypeptide such as those disclosed in US 5,288,641 and EP0176170 (Roizman). Additional exemplary herpes simplex virus vectors include HFEM/ICP6-LacZ disclosed in WO95/04139 (Wistar Institute), pHSVlac described in Geller (1988) *Science* 241:1667-1669 and in WO90/09441 and WO92/07945, HSV Us3::pgC-lacZ described in Fink (1992) *Human Gene Therapy* 3:11-19 and HSV 7134, 2 RH 105 and GAL4 described in EP 0453242 (Breakefield), and those deposited with the ATCC with accession numbers VR-977 and VR-260.

Also contemplated are alpha virus gene therapy vectors that can be employed in this invention. Preferred alpha virus vectors are Sindbis viruses vectors. Togaviruses, Semliki Forest virus (ATCC VR-67; ATCC VR-1247), Middleberg virus (ATCC VR-370), Ross River virus (ATCC VR-373; ATCC VR-1246), Venezuelan equine encephalitis virus (ATCC VR923; ATCC VR-1250; ATCC VR-1249; ATCC VR-532), and those described in US patents 5,091,309, 5,217,879, and WO92/10578. More particularly, those alpha virus vectors described in US Serial No. 08/405,627, filed March 15, 1995, WO94/21792, WO92/10578, WO95/07994, US 5,091,309 and US 5,217,879 are employable. Such alpha viruses may be obtained from depositories or collections such as the ATCC in Rockville, Maryland or isolated from known sources using commonly available techniques. Preferably, alphavirus vectors with reduced cytotoxicity are used (see USSN 08/679640).

DNA vector systems such as eukaryotic layered expression systems are also useful for expressing the nucleic acids of the invention. See WO95/07994 for a detailed description of eukaryotic layered expression systems. Preferably, the eukaryotic layered expression systems of the invention are derived from alphavirus vectors and most preferably from Sindbis viral vectors.

Other viral vectors suitable for use in the present invention include those derived from poliovirus, for example ATCC VR-58 and those described in Evans, *Nature* 339 (1989) 385 and Sabin (1973) *J. Biol. Standardization* 1:115; rhinovirus, for example ATCC VR-1110 and those described in Arnold (1990) *J Cell Biochem* L401; pox viruses such as canary pox virus or vaccinia virus, for example ATCC VR-111 and ATCC VR-2010 and those described in Fisher-Hoch (1989) *Proc Natl Acad Sci* 86:317; Flexner (1989) *Ann NY Acad Sci* 569:86, Flexner (1990) *Vaccine* 8:17; in US 4,603,112 and US 4,769,330 and WO89/01973; SV40 virus, for example ATCC VR-305 and those described in Mulligan (1979) *Nature* 277:108 and Madzak (1992) *J Gen Virol* 73:1533; influenza virus, for example ATCC VR-797 and recombinant influenza viruses made employing reverse genetics techniques as described in US 5,166,057 and in Enami (1990) *Proc Natl Acad Sci* 87:3802-3805; Enami & Palese (1991) *J Virol* 65:2711-2713 and Luytjes (1989) *Cell* 59:110, (see also McMichael (1983) *NEJ Med* 309:13, and Yap (1978) *Nature* 273:238 and *Nature* (1979) 277:108); human immunodeficiency virus as described in EP-0386882 and in Buchschacher (1992) *J. Virol.* 66:2731; measles virus, for example ATCC VR-67 and VR-1247 and those described in EP-0440219; Aura virus, for example ATCC VR-368; Bebaru virus, for example ATCC VR-600 and ATCC VR-1240; Cabassou virus, for example ATCC VR-922; Chikungunya virus, for example ATCC VR-64 and ATCC VR-1241; Fort Morgan Virus, for example ATCC VR-924; Getah virus, for example ATCC VR-369 and ATCC VR-1243; Kyzylagach virus,

for example ATCC VR-927; Mayaro virus, for example ATCC VR-66; Mucambo virus, for example ATCC VR-580 and ATCC VR-1244; Ndumu virus, for example ATCC VR-371; Pixuna virus, for example ATCC VR-372 and ATCC VR-1245; Tonate virus, for example ATCC VR-925; Trinit virus, for example ATCC VR-469; Una virus, for example ATCC VR-374; Whataroa virus, for example ATCC VR-926; Y-62-33 virus, for example ATCC VR-375; O'Nyong virus, Eastern encephalitis virus, for example ATCC VR-65 and ATCC VR-1242; Western encephalitis virus, for example ATCC VR-70, ATCC VR-1251, ATCC VR-622 and ATCC VR-1252; and coronavirus, for example ATCC VR-740 and those described in Hamre (1966) *Proc Soc Exp Biol Med* 121:190.

Delivery of the compositions of this invention into cells is not limited to the above mentioned viral vectors. Other delivery methods and media may be employed such as, for example, nucleic acid expression vectors, polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example see US Serial No. 08/366,787, filed December 30, 1994 and Curiel (1992) *Hum Gene Ther* 3:147-154 ligand linked DNA, for example see Wu (1989) *J Biol Chem* 264:16985-16987, eucaryotic cell delivery vehicles cells, for example see US Serial No.08/240,030, filed May 9, 1994, and US Serial No. 08/404,796, deposition of photopolymerized hydrogel materials, hand-held gene transfer particle gun, as described in US Patent 5,149,655, ionizing radiation as described in US5,206,152 and in WO92/11033, nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip (1994) *Mol Cell Biol* 14:2411-2418 and in Woffendin (1994) *Proc Natl Acad Sci* 91:1581-1585.

Particle mediated gene transfer may be employed, for example see US Serial No. 60/023,867. Briefly, the sequence can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, as described in Wu & Wu (1987) *J. Biol. Chem.* 262:4429-4432, insulin as described in Hucked (1990) *Biochem Pharmacol* 40:253-263, galactose as described in Plank (1992) *Bioconjugate Chem* 3:533-539, lactose or transferrin.

Naked DNA may also be employed. Exemplary naked DNA introduction methods are described in WO 90/11092 and US 5,580,859. Uptake efficiency may be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method may be improved further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm.

Liposomes that can act as gene delivery vehicles are described in US 5,422,120, WO95/13796, WO94/23697, WO91/14445 and EP-524,968. As described in USSN. 60/023,867, on non-viral delivery, the nucleic acid sequences encoding a polypeptide can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then be incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, insulin, galactose, lactose, or transferrin. Other delivery systems include the use of liposomes to encapsulate DNA comprising the gene under the control of a variety of tissue-specific or ubiquitously-active promoters. Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al* (1994) *Proc. Natl. Acad. Sci. USA* 91(24):11581-11585. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in US 5,149,655; use of ionizing radiation for activating transferred gene, as described in US 5,206,152 and WO92/11033



Exemplary liposome and polycationic gene delivery vehicles are those described in US 5,422,120 and 4,762,915; in WO 95/13796; WO94/23697; and WO91/14445; in EP-0524968; and in Stryer, Biochemistry, pages 236-240 (1975) W.H. Freeman, San Francisco; Szoka (1980) *Biochem Biophys Acta* 600:1; Bayer (1979) *Biochem Biophys Acta* 550:464; Rivnay (1987) *Meth Enzymol* 149:119; Wang (1987) *Proc Natl Acad Sci* 84:7851; Plant (1989) *Anal Biochem* 176:420.

A polynucleotide composition can comprises therapeutically effective amount of a gene therapy vehicle, as the term is defined above. For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

#### Delivery Methods

Once formulated, the polynucleotide compositions of the invention can be administered (1) directly to the subject; (2) delivered *ex vivo*, to cells derived from the subject; or (3) *in vitro* for expression of recombinant proteins. The subjects to be treated can be mammals or birds. Also, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal or transcutaneous applications (eg. see WO98/20734), needles, and gene guns or hypodermic sprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in eg. WO93/14778. Examples of cells useful in *ex vivo* applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells.

Generally, delivery of nucleic acids for both *ex vivo* and *in vitro* applications can be accomplished by the following procedures, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

#### Polynucleotide and polypeptide pharmaceutical compositions

In addition to the pharmaceutically acceptable carriers and salts described above, the following additional agents can be used with polynucleotide and/or polypeptide compositions.

##### A. Polypeptides

One example are polypeptides which include, without limitation: asialoglycoprotein (ASOR); transferrin; asialoglycoproteins; antibodies; antibody fragments; ferritin; interleukins; interferons, granulocyte, macrophage colony stimulating factor (GM-CSF), granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), stem cell factor and erythropoietin. Viral antigens, such as envelope proteins, can also be used. Also, proteins from other invasive organisms, such as the 17 amino acid peptide from the circumsporozoite protein of *Plasmodium falciparum* known as RII.

##### B. Hormones, Vitamins, etc.

Other groups that can be included are, for example: hormones, steroids, androgens, estrogens, thyroid hormone, or vitamins, folic acid.



C. Polyalkylenes, Polysaccharides, etc.

Also, polyalkylene glycol can be included with the desired polynucleotides/polypeptides. In a preferred embodiment, the polyalkylene glycol is polyethylene glycol. In addition, mono-, di-, or polysaccharides can be included. In a preferred embodiment of this aspect, the polysaccharide is dextran or DEAE-dextran. Also, chitosan and poly(lactide-co-glycolide)

D. Lipids, and Liposomes

The desired polynucleotide/polypeptide can also be encapsulated in lipids or packaged in liposomes prior to delivery to the subject or to cells derived therefrom.

Lipid encapsulation is generally accomplished using liposomes which are able to stably bind or entrap and retain nucleic acid. The ratio of condensed polynucleotide to lipid preparation can vary but will generally be around 1:1 (mg DNA:micromoles lipid), or more of lipid. For a review of the use of liposomes as carriers for delivery of nucleic acids, see, Hug and Sleight (1991) *Biochim. Biophys. Acta*. 1097:1-17; Straubinger (1983) *Meth. Enzymol.* 101:512-527.

Liposomal preparations for use in the present invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner (1987) *Proc. Natl. Acad. Sci. USA* 84:7413-7416); mRNA (Malone (1989) *Proc. Natl. Acad. Sci. USA* 86:6077-6081); and purified transcription factors (Debs (1990) *J. Biol. Chem.* 265:10189-10192), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, NY. (See, also, Felgner *supra*). Other commercially available liposomes include transfectace (DDAB/DOPE) and DOTAP/DOPE (Boehringer). Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, *eg.* Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; WO90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, AL), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art. See *eg.* Straubinger (1983) *Meth. Immunol.* 101:512-527; Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; Papahadjopoulos (1975) *Biochim. Biophys. Acta* 394:483; Wilson (1979) *Cell* 17:77; Deamer & Bangham (1976) *Biochim. Biophys. Acta* 443:629; Ostro (1977) *Biochem. Biophys. Res. Commun.* 76:836; Fraley (1979) *Proc. Natl. Acad. Sci. USA* 76:3348; Enoch & Strittmatter (1979) *Proc. Natl. Acad. Sci. USA* 76:145; Fraley (1980) *J. Biol. Chem.* (1980) 255:10431; Szoka & Papahadjopoulos (1978) *Proc. Natl. Acad. Sci. USA* 75:145; and Schaefer-Ridder (1982) *Science* 215:166.

E. Lipoproteins

In addition, lipoproteins can be included with the polynucleotide/polypeptide to be delivered. Examples of lipoproteins to be utilized include: chylomicrons, HDL, IDL, LDL, and VLDL. Mutants, fragments, or fusions of

these proteins can also be used. Also, modifications of naturally occurring lipoproteins can be used, such as acetylated LDL. These lipoproteins can target the delivery of polynucleotides to cells expressing lipoprotein receptors. Preferably, if lipoproteins are including with the polynucleotide to be delivered, no other targeting ligand is included in the composition.

- 5 Naturally occurring lipoproteins comprise a lipid and a protein portion. The protein portion are known as apoproteins. At the present, apoproteins A, B, C, D, and E have been isolated and identified. At least two of these contain several proteins, designated by Roman numerals, AI, AII, AIV; CI, CII, CIII.

A lipoprotein can comprise more than one apoprotein. For example, naturally occurring chylomicrons comprises of A, B, C & E, over time these lipoproteins lose A and acquire C & E. VLDL comprises A, B, C & E apoproteins, LDL  
10 comprises apoprotein B; and HDL comprises apoproteins A, C, & E.

The amino acid of these apoproteins are known and are described in, for example, Breslow (1985) *Annu Rev. Biochem* 54:699; Law (1986) *Adv. Exp Med. Biol.* 151:162; Chen (1986) *J Biol Chem* 261:12918; Kane (1980) *Proc Natl Acad Sci USA* 77:2465; and Utermann (1984) *Hum Genet* 65:232.

- 15 Lipoproteins contain a variety of lipids including, triglycerides, cholesterol (free and esters), and phospholipids. The composition of the lipids varies in naturally occurring lipoproteins. For example, chylomicrons comprise mainly triglycerides. A more detailed description of the lipid content of naturally occurring lipoproteins can be found, for example, in *Meth. Enzymol.* 128 (1986). The composition of the lipids are chosen to aid in conformation of the apoprotein for receptor binding activity. The composition of lipids can also be chosen to facilitate hydrophobic interaction and association with the polynucleotide binding molecule.

- 20 Naturally occurring lipoproteins can be isolated from serum by ultracentrifugation, for instance. Such methods are described in *Meth. Enzymol.* (*supra*); Pitas (1980) *J. Biochem.* 255:5454-5460 and Mahey (1979) *J Clin. Invest* 64:743-750. Lipoproteins can also be produced by *in vitro* or recombinant methods by expression of the apoprotein genes in a desired host cell. See, for example, Atkinson (1986) *Annu Rev Biophys Chem* 15:403 and Radding (1958) *Biochim Biophys Acta* 30: 443. Lipoproteins can also be purchased from commercial suppliers, such as Biomedical  
25 Technologies, Inc., Stoughton, Massachusetts, USA. Further description of lipoproteins can be found in Zuckermann *et al.* PCT/US97/14465.

#### F. Polycationic Agents

Polycationic agents can be included, with or without lipoprotein, in a composition with the desired polynucleotide/polypeptide to be delivered.

- 30 Polycationic agents, typically, exhibit a net positive charge at physiological relevant pH and are capable of neutralizing the electrical charge of nucleic acids to facilitate delivery to a desired location. These agents have both *in vitro*, *ex vivo*, and *in vivo* applications. Polycationic agents can be used to deliver nucleic acids to a living subject either intramuscularly, subcutaneously, *etc.*

- The following are examples of useful polypeptides as polycationic agents: polylysine, polyarginine, polyornithine,  
35 and protamine. Other examples include histones, protamines, human serum albumin, DNA binding proteins, non-histone chromosomal proteins, coat proteins from DNA viruses, such as (X174, transcriptional factors also contain domains that bind DNA and therefore may be useful as nucleic acid condensing agents. Briefly, transcriptional factors such as C/EBP, c-jun, c-fos, AP-1, AP-2, AP-3, CPF, Prot-1, Sp-1, Oct-1, Oct-2, CREP, and TFIID contain basic domains that bind DNA sequences.

- 40 Organic polycationic agents include: spermine, spermidine, and putrescine.

The dimensions and of the physical properties of a polycationic agent can be extrapolated from the list above, to construct other polypeptide polycationic agents or to produce synthetic polycationic agents.

Synthetic polycationic agents which are useful include, for example, DEAE-dextran, polybrene. Lipofectin™, and lipofectAMINE™ are monomers that form polycationic complexes when combined with  
5 polynucleotides/polypeptides.

#### Immunodiagnostic Assays

Neisseria antigens of the invention can be used in immunoassays to detect antibody levels (or, conversely, anti-Neisseria antibodies can be used to detect antigen levels). Immunoassays based on well defined, recombinant antigens can be developed to replace invasive diagnostics methods. Antibodies to Neisseria proteins within biological samples,  
10 including for example, blood or serum samples, can be detected. Design of the immunoassays is subject to a great deal of variation, and a variety of these are known in the art. Protocols for the immunoassay may be based, for example, upon competition, or direct reaction, or sandwich type assays. Protocols may also, for example, use solid supports, or may be by immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the labels may be, for example, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays which amplify the  
15 signals from the probe are also known; examples of which are assays which utilize biotin and avidin, and enzyme-labeled and mediated immunoassays, such as ELISA assays.

Kits suitable for immunodiagnosis and containing the appropriate labeled reagents are constructed by packaging the appropriate materials, including the compositions of the invention, in suitable containers, along with the remaining reagents and materials (for example, suitable buffers, salt solutions, etc.) required for the conduct of the assay, as well  
20 as suitable set of assay instructions.

#### Nucleic Acid Hybridisation

"Hybridization" refers to the association of two nucleic acid sequences to one another by hydrogen bonding. Typically, one sequence will be fixed to a solid support and the other will be free in solution. Then, the two sequences will be placed in contact with one another under conditions that favor hydrogen bonding. Factors that affect this  
25 bonding include: the type and volume of solvent; reaction temperature; time of hybridization; agitation; agents to block the non-specific attachment of the liquid phase sequence to the solid support (Denhardt's reagent or BLOTTO); concentration of the sequences; use of compounds to increase the rate of association of sequences (dextran sulfate or polyethylene glycol); and the stringency of the washing conditions following hybridization. See Sambrook *et al.* [*supra*] Volume 2, chapter 9, pages 9.47 to 9.57.

"Stringency" refers to conditions in a hybridization reaction that favor association of very similar sequences over sequences that differ. For example, the combination of temperature and salt concentration should be chosen that is approximately 120 to 200°C below the calculated T<sub>m</sub> of the hybrid under study. The temperature and salt conditions can often be determined empirically in preliminary experiments in which samples of genomic DNA immobilized on filters are hybridized to the sequence of interest and then washed under conditions of different stringencies. See  
30 Sambrook *et al.* at page 9.50.

Variables to consider when performing, for example, a Southern blot are (1) the complexity of the DNA being blotted and (2) the homology between the probe and the sequences being detected. The total amount of the fragment(s) to be studied can vary a magnitude of 10, from 0.1 to 1µg for a plasmid or phage digest to 10<sup>-9</sup> to 10<sup>-4</sup> g for a single copy gene in a highly complex eukaryotic genome. For lower complexity polynucleotides, substantially shorter blotting,  
40 hybridization, and exposure times, a smaller amount of starting polynucleotides, and lower specific activity of probes

can be used. For example, a single-copy yeast gene can be detected with an exposure time of only 1 hour starting with 1 µg of yeast DNA, blotting for two hours, and hybridizing for 4-8 hours with a probe of  $10^8$  cpm/µg. For a single-copy mammalian gene a conservative approach would start with 10 µg of DNA, blot overnight, and hybridize overnight in the presence of 10% dextran sulfate using a probe of greater than  $10^8$  cpm/µg, resulting in an exposure time of ~24 hours.

Several factors can affect the melting temperature ( $T_m$ ) of a DNA-DNA hybrid between the probe and the fragment of interest, and consequently, the appropriate conditions for hybridization and washing. In many cases the probe is not 100% homologous to the fragment. Other commonly encountered variables include the length and total G+C content of the hybridizing sequences and the ionic strength and formamide content of the hybridization buffer. The effects of all of these factors can be approximated by a single equation:

$$T_m = 81 + 16.6(\log_{10} C_i) + 0.4[\%(G + C)] - 0.6(\% \text{ formamide}) - 600/n - 1.5(\% \text{ mismatch}).$$

where  $C_i$  is the salt concentration (monovalent ions) and  $n$  is the length of the hybrid in base pairs (slightly modified from Meinkoth & Wahl (1984) *Anal. Biochem.* 138: 267-284).

In designing a hybridization experiment, some factors affecting nucleic acid hybridization can be conveniently altered. The temperature of the hybridization and washes and the salt concentration during the washes are the simplest to adjust. As the temperature of the hybridization increases (*ie.* stringency), it becomes less likely for hybridization to occur between strands that are nonhomologous, and as a result, background decreases. If the radiolabeled probe is not completely homologous with the immobilized fragment (as is frequently the case in gene family and interspecies hybridization experiments), the hybridization temperature must be reduced, and background will increase. The temperature of the washes affects the intensity of the hybridizing band and the degree of background in a similar manner. The stringency of the washes is also increased with decreasing salt concentrations.

In general, convenient hybridization temperatures in the presence of 50% formamide are 42°C for a probe with is 95% to 100% homologous to the target fragment, 37°C for 90% to 95% homology, and 32°C for 85% to 90% homology. For lower homologies, formamide content should be lowered and temperature adjusted accordingly, using the equation above. If the homology between the probe and the target fragment are not known, the simplest approach is to start with both hybridization and wash conditions which are nonstringent. If non-specific bands or high background are observed after autoradiography, the filter can be washed at high stringency and reexposed. If the time required for exposure makes this approach impractical, several hybridization and/or washing stringencies should be tested in parallel.

### 30 Nucleic Acid Probe Assays

Methods such as PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes according to the invention can determine the presence of cDNA or mRNA. A probe is said to "hybridize" with a sequence of the invention if it can form a duplex or double stranded complex, which is stable enough to be detected.

The nucleic acid probes will hybridize to the *Neisseria* nucleotide sequences of the invention (including both sense and antisense strands). Though many different nucleotide sequences will encode the amino acid sequence, the native *Neisseria* sequence is preferred because it is the actual sequence present in cells. mRNA represents a coding sequence and so a probe should be complementary to the coding sequence; single-stranded cDNA is complementary to mRNA, and so a cDNA probe should be complementary to the non-coding sequence.

The probe sequence need not be identical to the *Neisseria* sequence (or its complement) — some variation in the sequence and length can lead to increased assay sensitivity if the nucleic acid probe can form a duplex with target

nucleotides, which can be detected. Also, the nucleic acid probe can include additional nucleotides to stabilize the formed duplex. Additional Neisseria sequence may also be helpful as a label to detect the formed duplex. For example, a non-complementary nucleotide sequence may be attached to the 5' end of the probe, with the remainder of the probe sequence being complementary to a Neisseria sequence. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the a Neisseria sequence in order to hybridize therewith and thereby form a duplex which can be detected.

The exact length and sequence of the probe will depend on the hybridization conditions (e.g. temperature, salt condition etc.). For example, for diagnostic applications, depending on the complexity of the analyte sequence, the nucleic acid probe typically contains at least 10-20 nucleotides, preferably 15-25, and more preferably at least 30 nucleotides, although it may be shorter than this. Short primers generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

Probes may be produced by synthetic procedures, such as the triester method of Matteucci *et al.* [*J. Am. Chem. Soc.* (1981) 103:3185], or according to Urdea *et al.* [*Proc. Natl. Acad. Sci. USA* (1983) 80: 7461], or using commercially available automated oligonucleotide synthesizers.

The chemical nature of the probe can be selected according to preference. For certain applications, DNA or RNA are appropriate. For other applications, modifications may be incorporated eg. backbone modifications, such as phosphorothioates or methylphosphonates, can be used to increase *in vivo* half-life, alter RNA affinity, increase nuclease resistance etc. [eg. see Agrawal & Iyer (1995) *Curr Opin Biotechnol* 6:12-19; Agrawal (1996) *TIBTECH* 14:376-387]; analogues such as peptide nucleic acids may also be used [eg. see Corey (1997) *TIBTECH* 15:224-229; Buchardt *et al.* (1993) *TIBTECH* 11:384-386].

Alternatively, the polymerase chain reaction (PCR) is another well-known means for detecting small amounts of target nucleic acid. The assay is described in Mullis *et al.* [*Meth. Enzymol.* (1987) 155:335-350] & US patents 4,683,195 & 4,683,202. Two "primer" nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers can comprise sequence that does not hybridize to the sequence of the amplification target (or its complement) to aid with duplex stability or, for example, to incorporate a convenient restriction site. Typically, such sequence will flank the desired Neisseria sequence.

A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a threshold amount of target nucleic acids are generated by the polymerase, they can be detected by more traditional methods, such as Southern blots. When using the Southern blot method, the labelled probe will hybridize to the Neisseria sequence (or its complement).

Also, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al* [*supra*]. mRNA, or cDNA generated from mRNA using a polymerase enzyme, can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labelled probe and then washed to remove any unhybridized probe. Next, the duplexes containing the labeled probe are detected. Typically, the probe is labelled with a radioactive moiety.

## BRIEF DESCRIPTION OF DRAWINGS

There are no drawings.

## MODES FOR CARRYING OUT THE INVENTION

The following examples describe nucleic acid sequences which have been identified in *N.gonorrhoeae*, along with their inferred translation products.

The examples are generally in the following format:

- 5      ○ a nucleotide sequence which has been identified in *N.gonorrhoeae*. The strain used is FA1090 [Dempsey *et al.* (1991) *J. Bacteriol.* 173:5476-5486]
- the inferred translation product of this sequence
- a computer analysis (*e.g.* PSORT output) of the translation product, indicating antigenicity
- homologous sequences (where relevant)
- 10     ○ results of expression and purification (where relevant)

These examples typically include details of sequence homology between species and strains. Proteins that are similar in sequence are generally similar in both structure and function, and the homology often indicates a common evolutionary origin. Comparison with sequences of proteins of known function is widely used as a guide for the assignment of putative protein function to a new sequence and has proved particularly useful in whole-genome analyses.

Open reading frames (ORFs) within nucleotide sequences were predicted using the GLIMMER program [Salzberg *et al.* (1998) *Nucleic Acids Res* 26:544-8]. All predicted open-reading frames longer than 60 aa were screened against the meningococcus serotype B ('MenB') ORFs (accession NC002183) using the BLASTP algorithm [Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-410]. ORFs were considered to be gonococcus-specific if they showed sequence identity to a MenB ORF lower than 60% over the whole protein length, or matching the MenB ORF over less than 30% of the length.

Open reading frames are usually shown with a N-terminal methionine. Where this is not the case (*e.g.* SEQ IDs 12, 18, 20, 32, 54, 62, 66, 84, 98, 102, 104, 112, 116, 118, 126, 128, 130, 134, 136, 138, 146, 152, 162, 186, 228, 238, 240, 278, 280, 288, 290, 298, 300, 308, 314), a non-ATG start codon is present, but the N-terminus amino acid will be methionine when translated using this start codon. If an upstream start codon is used, however, the "native" amino acid will be translated (*e.g.* if the sequence is expressed with N-terminus fusion sequences). Even where the first amino acid is not shown as methionine, the invention encompasses sequences in which the first amino acid is methionine.

Various tests can be used to assess the *in vivo* immunogenicity of the proteins identified in the examples. For example, the proteins can be expressed recombinantly and used to screen patient sera by immunoblot. A positive reaction between the protein and patient serum indicates that the patient has previously mounted an immune response to the protein in question *i.e.* the protein is an immunogen. This method can also be used to identify immunodominant proteins.

The recombinant protein can also be conveniently used to prepare antibodies *e.g.* in a mouse. These can be used for direct confirmation that a protein is located on the cell-surface. Labelled antibody (*e.g.* fluorescent labelling for FACS) can be incubated with intact bacteria and the presence of label on the bacterial surface confirms the location of the protein.

For protein expression of 14 antigens, sequences were amplified using the following primers:

		Sequences	Restriction site
NGS5	Fwd	CGCGGATCCCATATG-TGGGCAGAACACCGGC	NdeI
	Rev	CCCGCTCGAG-GTTTTTCAGCAGGGGGATTG	XhoI
NGS7	Fwd	CGCGGATCCCATATG-GCCGGTAAAGAGCAATTTAC	NdeI
	Rev	CCCGCTCGAG-AGCCAAGAAGAACCCGTTAT	XhoI
NGS13	Fwd	CGCGGATCCGCTAGC-TGCGTTGCCGACCCCG	NheI
	Rev	CCCGCTCGAG-CATGTGCCGTGCGGCGT	XhoI
NGS36	Fwd	CGCGGATCCGCTAGC-GACACCCCGAACAAATACC	NheI
	Rev	CCCGCTCGAG-AAACCTGCCCTTGATGCC	XhoI
NGS37	Fwd	CGCGGATCCCATATG-GTAGAAGTTAAAGGCGGGG	NdeI
	Rev	CCCGCTCGAG-TTTTTTCGCGCCGCCGAA	XhoI
NGS38	Fwd	CGCGGATCCCATATG-GCCGACGAACGCCGCC	NdeI
	Rev	CCCGCTCGAG-AAACCGATATTTAAACCCCAACAGCC	XhoI
NGS39	Fwd	CGCGGATCCGCTAGC-AACCAAGAAGGGATTACCG	NheI
	Rev	CCCGCTCGAG-TTTTTTGAGCATAATGACTTTTGCCCT	XhoI
NGS67	Fwd	CGCGGATCCCATATG-CGTGCGCACGGACACG	NdeI
	Rev	CCCGCTCGAG-GGCGGCGAGTTTTTCGC	XhoI
NGS106	Fwd	CGCGGATCCCATATG-GCAAACAGCGGAACGATAG	NdeI
	Rev	CCCGCTCGAG-AAAATCCTGCGGGATCGGT	XhoI
NGS115	Fwd	CGCGGATCCCATATG-GGGGGCGGCTCCGGC	NdeI
	Rev	CCCGCTCGAG-TTCGGCCAACAATGCTTCC	XhoI
NGSΔG115	Fwd	CGCGGATCCCATATG-GATGCCCAATCTTCACAAAG	NdeI
	Rev	CCCGCTCGAG-TTCGGCCAACAATGCTTCC	XhoI
NGS118	Fwd	CGCGGATCCCATATG-ACCGCCCTTCCCTCTGA	NdeI
	Rev	CCCGCTCGAG-CGGCTGCCATTTCGCGTT	XhoI
NGS122	Fwd	CGCGGATCCCATATG-AACCCGAACGATGCGTTTT	NdeI
	Rev	CCCGCTCGAG-AGGGTAAAACTTATTCAAATCGGCAA	XhoI
NGS144	Fwd	CGCGGATCCCATATG-GCTTCTGAAAATTCTGTAGC	NdeI
	Rev	CCCGCTCGAG-GAACACGCTTTTCATTACACCCA	XhoI
NGS151	Fwd	CGCGGATCCCATATG-CACGGTATGCATAAGAGCA	NdeI
	Rev	CCCGCTCGAG-TTGCTGATGCGGCTTTATTCG	XhoI

### Example 1

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1> which encodes amino acid sequence <SEQ ID 2; NGS1>. Analysis of this protein sequence reveals the following:

5 GvH: Examining signal sequence (von Heijne)  
Signal Score (-7.5): -5.47  
Possible cleavage site: 36  
>>> Seems to have no N-terminal signal seq.  
Amino Acid Composition of Predicted Mature Form:  
10 calculated from 1  
ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 4.72 threshold: 0.0

-32-

PERIPHERAL Likelihood = 4.72  
 modified ALOM score: -1.44  
 Rule: cytoplasmic protein

5 \*\*\* Reasoning Step: 2

----- Final Results -----

10 bacterial cytoplasm --- Certainty= 0.326(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

15 >sp|P45941|YQCF\_BACSU HYPOTHETICAL 21.5 KD PROTEIN IN CWLA-CISA INTERGENIC REGION  
 pir|E69949 hypothetical protein yqcF - Bacillus subtilis  
 dbj|BAA06963.1| (D32216) ORF95 [Bacillus subtilis]  
 dbj|BAA12427.1| (D84432) YqcF [Bacillus subtilis]  
 emb|CAB14528.1| (Z99117) yqcF [Bacillus subtilis]  
 20 Length = 192

Score = 35.5 bits (81), Expect = 0.45  
 Identities = 36/162 (22%), Positives = 77/162 (47%), Gaps = 5/162 (3%)

25 Query: 19 DSGSQYKLNIAAIPSSPNRDLKTYITLGLSKHDLNYK---SRFEILFVCSLKYDENQIFP 75  
 D ++I ++ P + +Y TLGLS H +NY+ + I V +++ +  
 Sbjct: 29 DDKNSSIDILSVSDQPQEGITSYSTLGLSDHSINYEVNGTPLRIEIVAAMESASDIYAN 88

30 Query: 76 FLRWLAETIENKKILLRGQVVYLPRISIVNS-TKMDALYVSAPFYFDDDFQVCYGEHYNI 134  
 L A II + G + S + + T M + PF +++D ++ + N+  
 Sbjct: 89 VLSTCAFNIINSNFTCAPGVIFKNVISMVYDQETDMKHIMFVPPFLWEEDLELLEFSNKNV 148

Query: 135 VFPLLVPYKQAEELVEKKGWNAFEQFLLDNEVGNLSDMNRK 176  
 + + +P+ + E ++ EK G + + Q LL+++ ++ D+ R+  
 35 Sbjct: 149 TWLMALPISEGELQVAEKHG-SDYLQDLLESKQIDIFDIKRE 189

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## Example 2

40 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 3> which encodes amino acid sequence <SEQ ID 4; NGS2>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -7.2  
 Possible cleavage site: 18

45 >>> Seems to have no N-terminal signal seq.

Amino Acid Composition of Predicted Mature Form:  
 calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 5.89 threshold: 0.0

50 PERIPHERAL Likelihood = 5.89  
 modified ALOM score: -1.68

Rule: cytoplasmic protein

55 \*\*\* Reasoning Step: 2

----- Final Results -----

60 bacterial cytoplasm --- Certainty= 0.367(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>



The protein has homology with the following sequences in the databases:

```

5  >emb|CAC01359.1| (AL390975) hypothetical protein SCP8.21 [Streptomyces coelicolor A3(2)]
    Length = 198

    Score = 37.1 bits (85), Expect = 0.15
    Identities = 29/107 (27%), Positives = 51/107 (47%), Gaps = 3/107 (2%)

10  Query: 73  ETPEHIETLAMLASASMHYPDQFQLGKTVNIGRPWVEQSSFRHFLISLPYPYQGELEY-- 130
    +T + + LA+LA++          G ++++G P   + F  L++ P   ++LE
    Sbjct: 88  DTDKVLRLPLAVLAASPQVEGVIVAPGASLDVGEPLWPGAPFTSVLVAEPGGLVEDLELDA 147

    Query: 131 -MDNVRFFWLLPITQTERLFLNTHSVEELETKFDEAGIDYLDINRAS 176
    +D VRF LLP+T E +   H   L+ ++   G D D +R S
15  Sbjct: 148 PLDPVRFLPLLPMTPNAAWKRVHGAPALQERWLNHGTDLRDPSRRS 194
  
```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 3

20 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 5> which encodes amino acid sequence <SEQ ID 6; NGS3>. Analysis of this protein sequence reveals the following:

```

    GvH: Examining signal sequence (von Heijne)
    Signal Score (-7.5): -1.69
    Possible cleavage site: 32
25  >>> Seems to have a cleavable N-term signal seq.
    Amino Acid Composition of Predicted Mature Form:
    calculated from 33
    ALOM: Finding transmembrane regions (Klein et al.)
    count: 5 value: -10.56 threshold: 0.0
30  INTEGRAL Likelihood = -10.56 Transmembrane 182 - 198 ( 171 - 201)
    INTEGRAL Likelihood = -7.86 Transmembrane 251 - 267 ( 244 - 273)
    INTEGRAL Likelihood = -7.48 Transmembrane 142 - 158 ( 136 - 167)
    INTEGRAL Likelihood = -6.32 Transmembrane 55 - 71 ( 50 - 82)
    INTEGRAL Likelihood = -2.97 Transmembrane 100 - 116 ( 99 - 117)
35  PERIPHERAL Likelihood = 4.72
    modified ALOM score: 2.61
    Rule: cytoplasmic membrane protein

    *** Reasoning Step: 2
40  ----- Final Results -----

    bacterial inner membrane --- Certainty= 0.522(Affirmative) < succ>
    bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
45  bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
    bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>
  
```

The protein has homology with the following sequences in the databases:

```

50  >sp|P19845|NOSY_PSEST MEMBRANE PROTEIN NOSY PRECURSOR
    pir|S13585 nosY protein precursor - Pseudomonas stutzeri
    emb|CAA37717.1| (X53676) nosY [Pseudomonas stutzeri]
    Length = 276

    Score = 163 bits (413), Expect = 2e-39
55  Identities = 117/275 (42%), Positives = 174/275 (62%), Gaps = 2/275 (0%)

    Query: 1  MNPVWIITGKEARDSLRNRWVLA AVLLLAALALSLGFLGSSPTGSVKVDPLTVTVVSLSS 60
    MN VW I KE D LRNRW+LA LL A LA+ + +LG++ +G +   + T+ SL+S
    Sbjct: 1  MNQVWNIARKELSDGLRNRWLLAISLLFAVLAVGIAWLGAASGQLGFTSIPATIASLAS 60
60
  
```

Query: 61 LSIFLIPLIAMLLSYDALIGEIERGTALLLSYPIWRNQILAGKFVGHLLIILALATTAGY 120  
 L+ FL+PLIA+LL+YDA++GE E GT+ LLL+YP+ R QIL GKFVGH +ILALA G+  
 Sbjct: 61 LATFLMPLIALLLAYDAIVGEDEGTLMLLLTYPLGRGQILLGKFVGHGLILALAVLIGF 120

5 Query: 121 GLAGITLQLANGGFDIAA-WKPFALLIAASVILGAAFLSMGYLISAKVKERGTAAGISIG 179  
 G A + + L G ++ + F + +S +LG FL+ Y++S KV E+ +AAG+++G  
 Sbjct: 121 GCAALAIALLVEGVELGMLFWAFGRFMISSTLLGWVFLAFAYVLSGKVNKSSAAGLALG 180

10 Query: 180 VWLFFVVFIDMALLGILVADSKQVITAPVTVLLFNPTDIYRLNLTYENTAMYAGMA 239  
 VW F V+ +L L+ S+ ++ +LL NPTDIYRL+NL+G+E + G+  
 Sbjct: 181 VW-FLFVLVFDLVLLALLVLVSEGKFNPELLPWLLLNPTDIYRLINLSGFEGSGSAMGVL 239

Query: 240 GLSGQIGLTVPVLLTAQVLWVIIPVLAAGIFRRR 274  
 L + + VL + W+ + L+LA IFR+R  
 15 Sbjct: 240 SLGADLPVPAAVLWLCLLAWIGVSLLLAYAIRRR 274

A homolog (amino acids 226-276) was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS3 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

20 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 4

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 7> which encodes amino acid sequence <SEQ ID 8; NGS4>. Analysis of this protein sequence reveals the following:

25 GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): 1.53  
 Possible cleavage site: 58  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 30 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 0.63 threshold: 0.0  
 PERIPHERAL Likelihood = 0.63  
 modified ALOM score: -0.63  
 35 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 ----- Final Results -----  
 40 bacterial cytoplasm --- Certainty= 0.103(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

45 The protein has homology with the following sequences in the databases:

>sp|Q59746|NOSZ\_RHIME NITROUS-OXIDE REDUCTASE PRECURSOR (N(2)OR) (N2O REDUCTASE)  
 gb|AAC44023.1| (U47133) nitrous-oxide reductase [Sinorhizobium meliloti]  
 prf||2209347B nitrous-oxide reductase [Rhizobium meliloti]  
 50 Length = 639  
 Score = 660 bits (1704), Expect = 0.0  
 Identities = 344/536 (64%), Positives = 407/536 (75%), Gaps = 23/536 (4%)  
 55 Query: 1 MSDEKLEQNGLSRRSFLGTAA--ASGAGIAGAGLLGLAGCSKDGEQAAANASGAAPVAKA 58  
 MS+E+ + L+RR LGT A A+ + G L L+G G A A+A  
 Sbjct: 1 MSNEETKMR-LNRRQMLGTTAFMAAAGAVGAGGALTLSG-----GTATPARA 46

-35-

Query: 59 QGESKPGQLSSEVGPGELEDQYYGFLSGGQSGEMRLIGLPSMRELMRIPVFNMDSATGWGR 118  
 Q S S EV PGELD+YY F S QSGE+R++G PSMRE+MRIPVFN SATGWG+  
 Sbjct: 47 QETSQS---SYEVKPGELDEYYVFFSSGQSGEIRIVGAPSMREMMRIPVFNRCSATGWGQ 103

5 Query: 119 TNESLKVNLGNITEETRKFLKDSGLRCYPNGDLHHPHLSFTDQTYDGRYAYANDKANNRV 178  
 TNES KV+ + ET +FLKD G Y NGDLHHPH SFTD TYDGRY YANDK+N+RV  
 Sbjct: 104 TNESRKVMTEGLLPETVEFLKDQG-GLYLNGLHHPHPSFTDGTYDGRYLYANDKNSRV 162

10 Query: 179 CRVRLDVMKADKIIDIPNDSGIHGLRPQRYPKTGYVVFANGEHITPVSGVGK-LDDAKTWN 237  
 .CR+RLDVMK DKII +PN +HGLR Q+YPKTGYVF NGE PV GK + D ++  
 Sbjct: 163 CRIRLDVMKCDKIIQLPNQHTVHGLRVQKYPKTGYVFCNGEDAVFPVNDGKTMGDKNSYQ 222

15 Query: 238 AVYTAIDGETMEIAWQVLVDGNLDNGDADYQGYKSFATCYNSEALTVQGASSNEQDWCV 297  
 A++TA+DGETME+AWQV+VDGNLDN DADYQGYK FATCYNSE T+ ++EQDW V  
 Sbjct: 223 AIFTAVDGETMEVAWQVMVDGNLDNVDADYQGYKCFATCYNSEEGFTLADMMASEQDWVV 282

20 Query: 298 VFDLKAIEEGIKAGDFKEVNGVKMLDGRABAKSKYTRYIPVPNSPHGCNASPDGKYIMPN 357  
 +F+LK IEE + GD+KE+ GV +LDGR S YTRY+PVPNSPHG N +PDG +++ N  
 Sbjct: 283 IFNLKRIEEAVAKGDYKEIGGVPLDGR--KGSPTYTRYVPVPNSPHGINTAPDGIHVVAN 340

25 Query: 358 GKLPTVTVLDVSKLDDLFAKIKERDVVVAEPQLGLGPLHTAFDGRGNAYTTLFIDSQM 417  
 GKL PTVTV DV K DDLF KI+ RD VVAEP+LGLGPLHTA+DG+GNAYTTLFIDSQ+  
 Sbjct: 341 GKLSPTVTVFDVRKFDLFDLDDKIQRDTTVVAEPELGLGPLHTAYDGKGNAYTTLFIDSQV 400

30 Query: 418 VKWNIDDAIKAYKGEKIDPIKQKLDVHYQPGHNHTTMTGETKEADGQWLVS LNKF SKDRFL 477  
 KWN I+DA +AY GEK+DPI+ KLDVHYQPGHNHT+MG+TKEADG+WL+SLNKF SKDR+L  
 Sbjct: 401 CKWNIEDAKRAYAGEKVDPIRHKLVDVHYQPGHNHTSMGQTKEADGKWLISLNKF SKDRYL 460

Query: 478 NAGPLKPECDQLIGISGDEMRLVHDNPTFAEPHDLCLVAASKLNPGKTWDRKDPWF 533  
 N GPLKPE DQLI ISGDEM LVHDNPTFAEPHD +V ASK+NP W+R DP+F  
 Sbjct: 461 NVGPLKPENQQLIDISGDEMVLVDNPTFAEPHDATIVHASKINPVHVWNRDDPFF 516

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### 35 Example 5

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 9> which encodes amino acid sequence <SEQ ID 10; NGS5>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): 1.09  
 Possible cleavage site: 19  
 >>> Seems to have a cleavable N-term signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 20

40 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 7.43 threshold: 0.0  
 PERIPHERAL Likelihood = 7.43  
 modified ALOM score: -1.99  
 Score for OM-PP discrimination: 4.97  
 Rule: outer membrane or periplasmic protein

45 Score for OM-PP discrimination: 4.97  
 Rule: outer membrane or periplasmic protein

50 \*\*\* Reasoning Step: 2

55 Outer membrane? Score: 0.496525

----- Final Results -----

60 bacterial outer membrane --- Certainty= 0.781(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.138(Affirmative) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology with sequences in the databases.

The protein was expressed in *E.coli* as an insoluble 43.56kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
5 useful antigens for vaccines or diagnostics.

#### Example 6

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 11> which encodes amino acid sequence  
<SEQ ID 12; NGS6>. Analysis of this protein sequence reveals the following:

```

10  GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -3.93
      Possible cleavage site: 36
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
15  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 6.42 threshold: 0.0
      PERIPHERAL Likelihood = 6.42
      modified ALOM score: -1.78
20  Rule: cytoplasmic protein

      *** Reasoning Step: 2

      ----- Final Results -----

25      bacterial cytoplasm --- Certainty= 0.447(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

30  The protein has homology with the following sequences in the databases:

      >pir||F83173 outer membrane protein OprC PA3790 [imported] - Pseudomonas
      aeruginosa (strain PA01)
      dbj|BAA05664.1| (D28119) outer membrane protein C [Pseudomonas aeruginosa]
      gb|AAG07177.1|AE004797_12 (AE004797) outer membrane protein OprC [Pseudomonas
35  aeruginosa]
      Length = 723

      Score = 77.9 bits (191), Expect = 1e-13
      Identities = 58/188 (30%), Positives = 89/188 (46%), Gaps = 13/188 (6%)

40  Query: 49 VKDLIIFDRAHGQSGTASKDGGIITRNVDARLETAQAYARYNFNPHWAAGIKAAYNYGHN 108
      V+D I+F G G++++ NVDAR+ + A Y +W AY +G N
      Sbjct: 546 VQDFILFSYREGMMGSSTQ-----ATNVDARIMGGELGASYQLTGNWKT DASLAYAWGKN 600

45  Query: 109 ETDGRPPYQIRPFEEAAVQADYKNYFAHGSYNIGAATRFVAKQTRGDFDMASGLGIDKREA 168
      +D R QI P EA Y+ G ++ G+ R VA Q R D + +G D ++
      Sbjct: 601 SSDDRALPQIPPLEARFGLTYE----EGDWSAGSLWRVVAPQNRIARDQGNVVGKDFDKS 656

      Query: 169 AKGFTVADVYAGVNIKDKYGLRLGVNNVFNKKYVEYI--SGDHVLALSPS-VVYAPGRTY 225
      A GF V + + L GV+N+F+K Y E++ +GD S + V PGRT+
50  Sbjct: 657 A-GFGVFSLNGAYRVTRNVKLSAGVDNLFDKDYTEHLNKAGDAGFGFSANETVPEPGRTF 715

      Query: 226 WLSLHAAF 233
      W + +F
55  Sbjct: 716 WTKVDFSF 723

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 7

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 13> which encodes amino acid sequence

5 <SEQ ID 14; NGS7>. Analysis of this protein sequence reveals the following:

```

GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): 4.94
      Possible cleavage site: 26
>>> Seems to have a cleavable N-term signal seq.
10 Amino Acid Composition of Predicted Mature Form:
      calculated from 27
ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 0.79 threshold: 0.0
      PERIPHERAL Likelihood = 0.79
15 modified ALOM score: -0.66
      Score for OM-PP discrimination: -18.85
      Rule: outer membrane or periplasmic protein
      Score for OM-PP discrimination: -18.85
      Rule: outer membrane or periplasmic protein
20
*** Reasoning Step: 2
      Periplasmic space? Score: 1.8846
25
----- Final Results -----
      bacterial periplasmic space --- Certainty= 0.929(Affirmative) < succ>
      bacterial outer membrane --- Certainty= 0.211(Affirmative) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>
30      bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

>pir|D72405 hypothetical protein - Thermotoga maritima (strain MSB8)
gb|AAD35294.1|AE001705_5 (AE001705) hypothetical protein [Thermotoga maritima]
35      Length = 300

      Score = 81.8 bits (201), Expect = 1e-14
      Identities = 72/289 (24%), Positives = 124/289 (41%), Gaps = 17/289 (5%)
40
Query: 38 PAMPSVTIAVAALQGKLAQADVSLKIWRSPDQLRAGVASGQFKVMMSPSNVGNLRNQG 97
      P P++ V + GK+ DV ++IW++P++ A + S + + P VG NL +G
Sbjct: 24 PLGPALIPVVPIMDGKIP--TDVKIEIWKNPEEAVAKIVSKEVDFAVLPTVVGANLYGKG 81

Query: 98 QKVGVMNILTNGITQLVCKGSAIASP-QDLVGKKILVPP-KNDMPDIVLQALLKKLKIDA 155
      ++ +V + + LV A + L G+++ P + D++++ L K +
45 Sbjct: 82 VRIKLVGVHEWKVFYLVASDDATFDGWESLRGQEVYTPHGRGQTVDVLRYFLSKAGLTL 141

Query: 156 HK-VSITYAATPPEAVGLFPSKGYHAVILPEPMATASLLKGKTIGINVVHGFDLVKAWGQ 214
      + V I YA P E V L F S LPEP + L +GK + D K WG+
50 Sbjct: 142 DRDVKILYAP-PQEIVLAFKSGVKYAAALPEPFVSMCLDRGKVV-----LDFQKEWGK 193

Query: 215 AFDTKPLIPMAGIIANEEYFHAHKAQFDIFHQDLKALNWILANRQNAKIGKNYLPAPPE 274
      IP+AG+ E K + + L +++ W+ N ++ L P
55 Sbjct: 194 ELGVPGRIPRIAGLFVRE---GVDKETVEKVEKALIDSIRWMKENLDETQVLSSEKLGIPA 250

Query: 275 PALVMGLDGARLTVSKGSEVKNEILKFYEILMQFNPELLGGKLPDNGFF 323
      L L+ + + E+ F + L + PE K+PD GF+
Sbjct: 251 KILKSSLERIEFEYVPVEKCREEVETFLKKLNELYPEGF-EKIPDEGFF 298

```

60 The protein was expressed in *E.coli* as an insoluble 32.89kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 8

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 15> which encodes amino acid sequence

5 <SEQ ID 16; NGS8>. Analysis of this protein sequence reveals the following:

```

GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): 2.39
      Possible cleavage site: 15
>>> Seems to have a cleavable N-term signal seq.
10 Amino Acid Composition of Predicted Mature Form:
    calculated from 16
ALOM: Finding transmembrane regions (Klein et al.)
      count: 4 value: -8.23 threshold: 0.0
15 INTEGRAL    Likelihood = -8.23    Transmembrane 49 - 65 ( 41 - 73)
    INTEGRAL    Likelihood = -7.38    Transmembrane 83 - 99 ( 75 - 106)
    INTEGRAL    Likelihood = -7.06    Transmembrane 110 - 126 ( 100 - 133)
    INTEGRAL    Likelihood = -4.41    Transmembrane 164 - 180 ( 163 - 187)
    PERIPHERAL  Likelihood = 5.89
      modified ALOM score: 2.15
20 Rule: cytoplasmic membrane protein

*** Reasoning Step: 2

----- Final Results -----
25 bacterial inner membrane --- Certainty= 0.429(Affirmative) < succ>
    bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
    bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
    bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>
30

The protein has homology with the following sequences in the databases:

>sp|P38044|NRTB_SYNPF NITRATE TRANSPORT PERMEASE PROTEIN NRTB
  pir||S30892 nitrate transport protein nrtB - Synechococcus sp. (strain PCC
    7942)
35 emb|CAA43810.1| (X61625) nitrate transporter [Synechococcus sp.]
  prf||1908370A nitrate transporter [Synechococcus sp.]
    Length = 279

Score = 67.5 bits (164), Expect = 1e-10
40 Identities = 54/202 (26%), Positives = 96/202 (46%), Gaps = 7/202 (3%)

Query: 4 VALWAWGSAVFGEFMLPAPVEVFQKSL--DLLKHFQEN-----EIGISLWRSVVGISVAL 56
      +A+W SA+ G+ LP P+ V + +++ F +N +G+ + S+ +++
Sbjct: 36 LAIWQVISAILGQDRLPGPINVVANTWMPYIIVEPFFDNGGTSKGLGLQILISLQ RVAIGY 95

45 Query: 57 IAGLAAGLVAGLVAGSFKTAMALLKPVITILLAMPPIIWWVMALFWFGFNGPSVLFITIV 116
      + G++ G V G K L PVI +L +PP+ W ++L F N S +F I +
Sbjct: 96 LLAAGTGLVGGVLGMSKFLGKGLDPVIQVLRTPPLAWFPISLMVFQDANTS AIFVIFI 155

50 Query: 117 LVAPLTFASAAVGMASVKNQHEELFDAYKLGRLLKIRYLYIPHLTGVISSVGVAVAMGV 176
      + AVG+ + + + KL + I + IP YV + + +AV +
Sbjct: 156 TAIWPIIINTAVGINQIPDDYNNVARVLKLSKKDYILNIPSTVPYVFPAGLRIAVGLAW 215

55 Query: 177 KAVIMAELLGASKGVGARIADA 198
      A++ AE+L A G+G I DA
Sbjct: 216 LAIVAAEMLKADGGIGYFIWDA 237

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

**Example 9**

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 17> which encodes amino acid sequence <SEQ ID 18; NGS9>. Analysis of this protein sequence reveals the following:

```

5   GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -5.07
      Possible cleavage site: 29
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 1 value: -1.81 threshold: 0.0
      INTEGRAL Likelihood = -1.81 Transmembrane 97 - 113 ( 96 - 113)
      PERIPHERAL Likelihood = 4.24
      modified ALOM score: 0.86
15  Rule: cytoplasmic membrane protein

      *** Reasoning Step: 2

```

```

      ----- Final Results -----
20      bacterial inner membrane --- Certainty= 0.172(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>
25

```

The protein has homology with the following sequences in the databases:

```

>sp|P97027|SSUB_BACSU PUTATIVE ALIPHATIC SULFONATES TRANSPORT ATP-BINDING PROTEIN
SSUB
30  pir|G69816 nitrate ABC transporter (binding protein) homolog ygaL - B.subtilis
    emb|CAB07520.1| (Z93102) hypothetical 30.6 kd protein [Bacillus subtilis]
    emb|CAB12711.1| (Z99108) similar to nitrate ABC transporter (binding protein)
      [Bacillus subtilis]
      Length = 274

35  Score = 99.5 bits (247), Expect = 3e-20
      Identities = 68/181 (37%), Positives = 102/181 (55%), Gaps = 9/181 (4%)

Query: 4  LFGPSGCGKTTVLRLLIAGLETTPKSGTIRNTPH-----KTGFLFQENRLPENLTAMQNI 56
          L GPSGCGK+T+L++IAGL++ G++ + GF+PQE+RL LT QNI
40  Sbjct: 56  LIGPSGCGKSTLLKIIAGLDSEYDGSVEINGRSVTAPGIQQGFIFQEHRLFPWLTVEQNI 115

Query: 57  A--IFMDNPEGEIIVALAAKVGLTAGDLNKYPTELSSGGMARVAFRLRLLCGCDLALLDE 114
          A ++ +P + V ++ G YP ELSSGM++RVA R LL ++ LLDE
45  Sbjct: 116 AADLNLDKDPKVQKQVDLEIIVRLKGSEKAYPRELSSGMSQRVAITRALLREPEVILLDE 175

Query: 115 PFVGLDRDLRDILVAMLVKIERQGMACILVTHDRFEAARLSHEIMLLSAKGMNVQNVIT 174
          PF LD R L +L++ ++ ILVTHD E+ L +E+ +L AK + ++
50  Sbjct: 176 PFGALDAFTRKHLQDVLLDIWRKKKTMTILVTHDIDESVYLGNELAILKAKPGKIHLMP 235

Query: 175 L 175
          +
55  Sbjct: 236 I 236

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

**Example 10**

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 19> which encodes amino acid sequence <SEQ ID 20; NGS10>. Analysis of this protein sequence reveals the following:



-40-

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): 2.27  
 Possible cleavage site: 26  
 >>> Seems to have no N-terminal signal seq.  
 5 Amino Acid Composition of Predicted Mature Form:  
     calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
     count: 0 value: 5.14 threshold: 0.0  
 10 PERIPHERAL Likelihood = 5.14  
     modified ALOM score: -1.53

\*\*\* Reasoning Step: 2

imb2 HYPID: 2 CFP: 0.1

15 ----- Final Results -----

    bacterial inner membrane --- Certainty= 0.100(Affirmative) < succ>  
     bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 20      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
     bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

25 >pir||A82615 surface protein XF1981 [imported] - Xylella fastidiosa (strain  
     9a5c)  
     gb|AAF84783.1|AE004017\_6 (AE004017) surface protein [Xylella fastidiosa]  
         Length = 1190

    Score = 50.2 bits (119), Expect = 2e-05  
 30      Identities = 59/210 (28%), Positives = 92/210 (43%), Gaps = 5/210 (2%)

Query: 17   SIGTSAEANAPGALALGGSSEASKKFSIABGYLASSDGYGALIGSAAKI-KQLEKGTIN 75  
           ++G    A+A GA A+G + AS K S A G A +   G++A+G AK   + +  
 35 Sbjct: 876   AVGVGTLASAEAGATAVGSAAASGKGSTAIGRNAVASADGSVALGDGAKDGARGAESYTG 935

Query: 76   HIVGNDNKGLYVDADGNVTRITVRTESEKDILSRYGQTYGAVALGFRSSSHNLFA----S 131  
           G N +   + G+ +K   RT S                   L +   N +  
 Sbjct: 936   KYSGLQNNVTGTVSVGDASKGETRTVSNVADAKEATDAVNLRQLDRVAQDANRYVDNKIE 995

40 Query: 132   SFGAFSTATAIESLAVGDSSQSTGYRSATFGSHSRALAEESLALGYETRANAYGSVALGA 191  
           S    T + SL   + + G +   G + A   +S+A+G +   A+A +VA+G  
 Sbjct: 996   SLSEGQTFVKVNSLNN SATPIAAGVDATAIGVGATASGADSIAMGNKASASADNAVAIGN 1055

Query: 192   ESVANEENTVSVSSDTLKRKIVNVADGTED 221  
           SVA+   NTVSV S   +R++ NVA GT D  
 45 Sbjct: 1056   HSVADRANTVSVGSAGSERQVTNVAAGTAD 1085

>sp|P10858|YADA\_YERPS INVASIN PRECURSOR (OUTER MEMBRANE ADHESIN)  
 50 pir||S04534 invasin precursor - Yersinia pseudotuberculosis plasmid pIBI  
     emb|CAA32088.1| (X13883) YopI preprotein (AA 1 - 434) [Yersinia  
     pseudotuberculosis]  
     prf||1411295A invasin [Yersinia pseudotuberculosis]  
         Length = 434

55      Score = 42.1 bits (98), Expect = 0.006  
     Identities = 35/134 (26%), Positives = 68/134 (50%), Gaps = 28/134 (20%)

Query: 116   AVALGFRSSSHNLFASSFGAFSTATAIESLAVGDSSQSTGYRSATFGSHSRA----- 167  
           ++A+G + +   A + G+ S AT + S+A+G S++ G + T+G+ S A  
 60 Sbjct: 107   SIAIGATAEAAKPAAVAVGSGSIATGVNSVAIGPLSKALGDSAVTYGASSTAQKDGVAIG 166

Query: 168   -----LAEESLALGYETRANAYGSVALGA-----ESVANEENTVSVSSDT 207  
           ++   +A+G+ ++ +A SVA+G                   S + EN+VS+ ++  
 Sbjct: 167   ARASASDTGVAVGFNSKVDAQNSVAIGHSSHVAADHGYSIAIGDHSKTDRENSVSIGHS 226

65 Query: 208   LKRKIVNVADGTED 221  
           L R++ ++A GTED

Sbjct: 227 LNRQLTHLAAGTED 240

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## 5 Example 11

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 21> which encodes amino acid sequence <SEQ ID 22; NGS11>. Analysis of this protein sequence reveals the following:

```

10  GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -0.16
      Possible cleavage site: 60
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
15  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 4.67 threshold: 0.0
      PERIPHERAL Likelihood = 4.67
      modified ALOM score: -1.43
      Rule: cytoplasmic protein

20  *** Reasoning Step: 2

      ----- Final Results -----

      bacterial cytoplasm --- Certainty= 0.297 (Affirmative) < succ>
25  bacterial periplasmic space --- Certainty= 0.000 (Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000 (Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000 (Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

30  >sp|P10858|YADA_YERPS INVASIN PRECURSOR (OUTER MEMBRANE ADHESIN)
      pir|S04534|invasin precursor - Yersinia pseudotuberculosis plasmid pIBI
      emb|CAA32088.1|(X13883) Yop1 preprotein (AA 1 - 434) [Yersinia
      pseudotuberculosis]
      prf||1411295A|invasin [Yersinia pseudotuberculosis]
      Length = 434

35  Score = 41.3 bits (96), Expect = 0.007
      Identities = 27/71 (38%), Positives = 48/71 (67%), Gaps = 4/71 (5%)

40  Query: 16 QLNRLSKRTNVRVGASAAALASL-KPAQLGKNDKFAFSLGFGSYKNAQAVAMGAVFKPAEN 74
      +L++L KR ++ AS+AAL SL +P +GK + F+ G G Y+++QA+A+G+ ++ E+
      Sbjct: 353 RLDKLDKRVDKGLASSAALNSLFQPYGVGVKNV---FTAGVGGYRSSQALAIGSGYRVNES 409

      Query: 75 VLLNVAGSFAG 85
      V L ++AG
45  Sbjct: 410 VALKAGVAYAG 420

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## Example 12

50 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 23> which encodes amino acid sequence <SEQ ID 24; NGS12>. Analysis of this protein sequence reveals the following:

```

      GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -1.29
      Possible cleavage site: 61
55  >>> Seems to have a cleavable N-term signal seq.

```

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Amino Acid Composition of Predicted Mature Form:  
calculated from 62

ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 6.36 threshold: 0.0

5 PERIPHERAL Likelihood = 6.36  
modified ALOM score: -1.77

Score for OM-PP discrimination: 6.03

Rule: outer membrane or periplasmic protein

10 Score for OM-PP discrimination: 6.03

Rule: outer membrane or periplasmic protein

\*\*\* Reasoning Step: 2

Outer membrane? Score: 0.602784

15

----- Final Results -----

20 bacterial outer membrane --- Certainty= 0.867(Affirmative) < succ>  
bacterial periplasmic space --- Certainty= 0.158(Affirmative) < succ>  
bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>  
bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology with sequences in the databases.

25 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
useful antigens for vaccines or diagnostics.

### Example 13

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 25> which encodes amino acid sequence  
<SEQ ID 26; NGS13>. Analysis of this protein sequence reveals the following:

30 GvH: Examining signal sequence (von Heijne)  
Signal Score (-7.5): -3.64  
Possible cleavage site: 51

>>> May be a lipoprotein

Amino Acid Composition of Predicted Mature Form:  
calculated from 21

35 ALOM: Finding transmembrane regions (Klein et al.)  
count: 1 value: -1.01 threshold: 0.0

INTEGRAL Likelihood = -1.01 Transmembrane 36 - 52 ( 36 - 52)

PERIPHERAL Likelihood = 5.14

modified ALOM score: 0.70

40 Rule: inner or outer membrane protein

Rule: inner or outer membrane protein

Rule: cytoplasmic membrane protein

45 \*\*\* Reasoning Step: 2

Lipoprotein?

Inner membrane?

50 ----- Final Results -----

55 bacterial outer membrane --- Certainty= 0.790(Affirmative) < succ>  
bacterial inner membrane --- Certainty= 0.742(Affirmative) < succ>  
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

>gb|AAC33455.1| (AF067083) outer membrane protein homolog [Vitreoscilla sp.]  
Length = 217

60 Score = 236 bits (602), Expect = 2e-61

Identities = 134/217 (61%), Positives = 166/217 (75%)

```

5  Query: 1  MTFFKPSTVVLTAASALALSGCVADPVTGQQSPNKSAMYGLGGAAVCGIVGALTHSGKGAR 60
    M +K +++ T +A+ALS C DP+TGQ N + + LGGAA CGIVGALTH KGAR
    Sbjct: 1  MKAWKKFSLMATVAVALSACATDPMTGQVDRNNTVLGALGGAATCGIVGALTHSGKGAR 60

10 Query: 61  NSALACGAIGAGVGGYMDYQEQRLRQNLQAGTQIEIQRQGNQIRLVMPESVTFATGSAALG 120
    NSALACGAIGAGVG YMD+QE++LRQ+LA TQ+E+ R G++IRLVMPES+TFATGS L
    Sbjct: 61  NSALACGAIGAGVGAYMDHQERQLRQSLANTQVEVNRVGDIEIRLVMPESITFATGSYQLN 120

15 Query: 121  GSAQYALNTAAQTLVQYPTDTTLTINGHTDNTGSDAVNNPLSQHRAQAVAYYLQTRGVAAS 180
    SA +LN+ + L QY DTT+ I GHTD+TGSDA+N PLS++RA AVA YL +R VA++
    Sbjct: 121  SSASTSLNSVSSVLAQYTTDTTINIVGHTDSTGSDAINEPLSRNRASAVANYLVSERNVASN 180

20 Query: 181  RLTVYGYGSHMPVASNATVEGRAQNRRVEILINPDQR 217
    R+T G G PVASN TV GRA+NRRVEI +NP QR
    Sbjct: 181  RITTVGAGCRQFVASNNTVAGRAENRRVEITVNPIQR 217

    >gb|AAD40344.1|U88088_22 (U88088) OmpA [Pseudomonas alcaligenes]
    Length = 220

    Score = 130 bits (328), Expect = 1e-29
    Identities = 90/219 (41%), Positives = 127/219 (57%), Gaps = 6/219 (2%)

25 Query: 7  STVVLTAASALALSGCVA---DPVTGQQSPNKSAMYGLGGAAVCGIVGALTHSGKGARN 63
    S + + L+GC + + T + + A L GA ++G + +GA A
    Sbjct: 3  SVIAASLVIFTLTGCASIQNEDGTTKNTALYGAGGALAGAVAGALIGK-ENRAQGALIGA 61

30 Query: 64  LACGAIGAGVGGYMDYQEQRLRQNLQAGTQIEIQRQGNQIRLVMPESVTFATGSAALGSA 123
    G++GAG G Y D QE LR+ + G+ ++++RQG++I +VMP ++TFATG A + +
    Sbjct: 62  AVAGSLGAGYGYADKQEAEELREQMKSGVQVERQGDIEIVIMPGAITFATGKAEIQPNF 121

35 Query: 124  QYALNTAAQTLVQYPTDTTLTINGHTDNTGSDAVNNPLSQHRAQAVAYYLQTRGVAASRLT 183
    LN A + YPD+ L + GHTD+ GS N LSQ RAQ+VA +L+ GV R+
    Sbjct: 122  ANTNLQLAGSFRNYPDSRLIVTGHTDSVGSYEANELLSQRRASQAQFLRGNGVQTDRIE 181

40 Query: 184  VYGYGSHMPVASNATVEGRAQNRRVEILINPDQRAVNAA 222
    V G G + PVASNAT EGRAQNRRVEI + P RAV A
    Sbjct: 182  VIGAGPNQFVASNATAEGRAQNRRVEIKLAP--RAVQQA 218
  
```

The protein was expressed in *E.coli* as a soluble 22.55kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 14

45 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 27> which encodes amino acid sequence <SEQ ID 28; NGS14>. Analysis of this protein sequence reveals the following:

```

50 GvH: Examining signal sequence (von Heijne)
    Signal Score (-7.5): -5.32
    Possible cleavage site: 40
    >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
        calculated from 1
    ALOM: Finding transmembrane regions (Klein et al.)
        count: 0 value: 3.39 threshold: 0.0
55 PERIPHERAL Likelihood = 3.39
    modified ALOM score: -1.18
    Rule: cytoplasmic protein
  
```

60 \*\*\* Reasoning Step: 2

----- Final Results -----

5           bacterial cytoplasm --- Certainty= 0.254(Affirmative) < succ>  
           bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
           bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
           bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## 10 Example 15

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 29> which encodes amino acid sequence <SEQ ID 30; NGS15>. Analysis of this protein sequence reveals the following:

15       GvH: Examining signal sequence (von Heijne)  
           Signal Score (-7.5): -1.75  
           Possible cleavage site: 45  
       >>> Seems to have no N-terminal signal seq.  
       Amino Acid Composition of Predicted Mature Form:  
           calculated from 1  
       ALOM: Finding transmembrane regions (Klein et al.)  
       count: 0 value: 5.89 threshold: 0.0  
       PERIPHERAL Likelihood = 5.89  
       modified ALOM score: -1.68  
       Rule: cytoplasmic protein  
       \*\*\* Reasoning Step: 2  
       ----- Final Results -----  
           bacterial cytoplasm --- Certainty= 0.232(Affirmative) < succ>  
           bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
           bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
           bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

35       >sp|P10487|RCI1\_ECOLI SHUFFLON-SPECIFIC DNA RECOMBINASE  
       pir||S03815 probable integrase - Escherichia coli  
       dbj|BAA77989.1| (AB027308) shufflon-specific DNA recombinase [Plasmid R64]  
           Length = 384  
       Score = 67.1 bits (163), Expect = 3e-10  
       Identities = 75/301 (24%), Positives = 125/301 (40%), Gaps = 34/301 (11%)  
       Query: 68 KVKMMTLSEAMRKYLNETLGAGRSKKMGL---RFLMEFPPIGGIGIDKLKRSDFAEHVMQR 124  
               +++ M+LS A+ KYL           +           + +PI   +D++ D A + R  
       45       Sbjct: 5 RIRKMSLSRALDKYLKTVSVHKKGHQQEFYRSNVIKRYPIALRNMDIITVDIATYRDVR 64  
       Query: 125 RRGIPELDIAPIAASTALQELQYIRSVLKHAFYVWGLEIGWQELDFAANGLKRSNMVAKS 184  
               I       PI +T EL + S+ A WG                   N ++ S  
       50       Sbjct: 65 LAEINPRTGKPITGNTVRLELALLSSLFNIARVEWG-----TCRTNPVELVRKPKVS 116  
       Query: 185 AIRDRLPTTEELQTLTYFLRQWQSRKSSIPMHLIMWLAIYTSRRQDEICRLLFDDWHKN 244  
               + RDR T+ E + L+ YF           R+ ++ +++I LA+ T+ RQ EI L W  
       Sbjct: 117 SGRDRRLTSSEERRLSRYF-----REKNLMLYVIFHLALETAMRQGEILAL---RWEHI 167  
       55       Query: 245 DCTRPVRLKPNPSTGNNKEFDILPMALPVIDELPEESVRKRLANKGLADSLVPCNGK 304  
               D V L P G++++ + A + +P                   + ++  
       Sbjct: 168 DLRHGVHL--PETKNHGRSDVPLSRRARNFLQMP-----VNLHGNVFDYTAS 214  
       60       Query: 305 SVSAAWTRACKVLGIKDLRFHDLRHEAATRMABDG-FTIPQMQRVTLHDGWNLSQRYVSVR 364  
               AW A + L I+DL FHLRHEA +R E G + ++ ++ H N L+RY +R

Sbjct: 215 GFKNAWRIATQRLRIEDLHFHDLRHEAISRFELGSLNVMEIAAISGHRSMNMLKRYTHLR 275

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## 5 Example 16

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 31> which encodes amino acid sequence <SEQ ID 32; NGS16>. Analysis of this protein sequence reveals the following:

```

10  GvH: Examining signal sequence (von Heijne)
      signal Score (-7.5): -3.64
      Possible cleavage site: 20
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
          calculated from 1
15  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 4.67 threshold: 0.0
      PERIPHERAL Likelihood = 4.67
      modified ALOM score: -1.43
      Rule: cytoplasmic protein
      *** Reasoning Step: 2
20  ----- Final Results -----
          bacterial cytoplasm --- Certainty= 0.262(Affirmative) < succ>
          bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
          bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
25  bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

30  >sp|P10484|T1M1_ECOLI TYPE I RESTRICTION ENZYME ECOR124II M PROTEIN (M.ECOR124II)
      pir||S02166 type I site-specific deoxyribonuclease (EC 3.1.21.3) EcoR124/3
          chain hsdM - Escherichia coli plasmid R124/3
      emb|CAA31541.1| (X13145) hsdM protein (AA 1-520) [Escherichia coli]
          Length = 520
      Score = 44.4 bits (104), Expect = 0.002
      Identities = 65/235 (27%), Positives = 99/235 (41%), Gaps = 55/235 (23%)
35  Query: 107 NRKKAGGYAEYITGGSRLRLVAAKVRRYCGEHPGVFDGAAGSG-----QLEQYIEPS 158
          N K+GG E+ T + +L+A ++D AAGSG Q + +I
      Sbjct: 191 NAGKSGG--EFFTPQHVSKLIAQLAMHGQTHVNKIYDPAAGSGSLLLQAKKQFDNHIIEE 248
40  Query: 159 DFRAVEIQAEACKALLQNYPAKVYNTSLFL-----YTDGEPQDC 198
          F EI N+ + ++FL + D +P D
      Sbjct: 249 GFFGQEI-----NHTTYNLARMNMFLEHNINYDKFDIKLGNTLTTEPHFRDEKPFDA 298
45  Query: 199 TVMNPPFSIKLKDLSEDEKSRIAQEPWKKSGV-----ADEIFVLKGLE--NARRFGFF 250
          V NPP+S+K + D+ + I E + +GV AD FVL L +A+
      Sbjct: 299 IVSNPPYSVKW--IGSDDPTLINDER-FAPAGVLAPKSKADFAFVLHALNYLSAKGRAAI 355
      Query: 251 ILFPGIAYR-KSEQRPRE-IIGNRLAE--LNRIQNAFEDTFIEVLLLVIDKDKTD 301
          + FPGI YR +EQ+ R+ ++ N E ++ N F T I V +LV+ K KTD
50  Sbjct: 356 VCFPGIFYRGGAEQKIRQYLVDDNYVETVISLAPNLFFGTITAVNIVLSKHKTD 410

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

**Example 17**

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 33> which encodes amino acid sequence <SEQ ID 34; NGS17>. Analysis of this protein sequence reveals the following:

```

5   GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -5.29
      Possible cleavage site: 16
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
          calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 2.60 threshold: 0.0
      PERIPHERAL Likelihood = 2.60
      modified ALOM score: -1.02
15  Rule: cytoplasmic protein

      *** Reasoning Step: 2

      ----- Final Results -----

20      bacterial cytoplasm --- Certainty= 0.284(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

25  The protein has homology with the following sequences in the databases:

      >ref|NP_052389.1| translocator YopD [Yersinia enterocolitica]
      sp|P37132|YOPD_YEREN YOPD PROTEIN
      gb|AAD16812.1| (AF102990) translocator YopD [Yersinia enterocolitica]
30      Length = 306

      Score = 32.1 bits (72), Expect = 8.2
      Identities = 29/93 (31%), Positives = 43/93 (46%), Gaps = 17/93 (18%)

35  Query: 13  MLAAKRAAKESTRQERAVKRAGTVRNVDNRNLSARSKAQKENIARMLSGAKVSEDEALTC 72
      +L  R A+E  Q+R ++  T+          AQKE +A M+SGAK+  A+
      Sbjct: 89  LLELARKAREMGLQORDIENKATI-----SAQKEQVAEMVSGAKLMIAMAVVS 136

      Query: 73  GIMMRLSLQDMRYACNQELINF AEHIVKQVQRL 105
      GIM  S  ++  +E+  IVKQ Q L
40  Sbjct: 137  GIMAATSTVASAFSIAKEV-----KIVKQEQIL 164

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

**Example 18**

45 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 35> which encodes amino acid sequence <SEQ ID 36; NGS18>. Analysis of this protein sequence reveals the following:

```

      GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -2.56
      Possible cleavage site: 38
50  >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
          calculated from 1
      ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 4.56 threshold: 0.0
55  PERIPHERAL Likelihood = 4.56
      modified ALOM score: -1.41
      Rule: cytoplasmic protein

```



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\*\*\* Reasoning Step: 2

----- Final Results -----

5                   bacterial cytoplasm --- Certainty= 0.397(Affirmative) < succ>  
                   bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
                   bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
                   bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

10   The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

**Example 19**

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 37> which encodes amino acid sequence  
 15 <SEQ ID 38; NGS19>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
       Signal Score (-7.5): -4.12  
       Possible cleavage site: 43  
     >>> Seems to have no N-terminal signal seq.  
 20   Amino Acid Composition of Predicted Mature Form:  
       calculated from 1  
   ALOM: Finding transmembrane regions (Klein et al.)  
         count: 0   value: 8.49 threshold: 0.0  
         PERIPHERAL Likelihood = 8.49  
 25   modified ALOM score: -2.20  
   Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

----- Final Results -----

30                   bacterial cytoplasm --- Certainty= 0.250(Affirmative) < succ>  
                   bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
                   bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 35                   bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

>ref|NP\_043483.1| orf14 [Bacteriophage HP1]  
 40   sp|P51716|YO14\_BPHP1 HYPOTHETICAL 14.9 KD PROTEIN IN REP-HOL INTERGENIC REGION  
   (ORF14)  
   pir||S69520 hypothetical protein 14 - phage HP1  
   gb|AAB09199.1| (U24159) orf14 [Bacteriophage HP1]  
       Length = 133  
 45   Score = 73.3 bits (179), Expect = 1e-12  
   Identities = 44/129 (34%), Positives = 74/129 (57%), Gaps = 6/129 (4%)  
   Query: 1   MFIPALHKDEHSAYGVITPDLPGCFSCGDTVEEAVANARSAAYMHIDGMIEDGGFKNLA 60  
           M P + K + Y V++PD+PGCFS GDT+ EA+ NA+ A   HI+GM+ED + L  
 50   Sbjct: 1   MLYPICIEK-VNDGYVVSVPDVPDVGCFSGAGDTLSEAMLNKAEAISFHIEGMLEDD--EELP 57  
   Query: 61   VSS-IADLSQEPDYHGATWVMIEIDPAKISRQQIRFNVSWFQYLLDRVDEY--TSANHET 117  
           S+ I    +P+Y    +++D   + + + N++ P LL R+D++ T ++  
   Sbjct: 58   KSNPIEQYINQPEYKDFIVTVVDVLDLTHLMGKAEKINITVPALLLHRIDQFIATHPEYKN 117  
 55   Query: 118 RSGFLAKAA 126  
           RS FL++ A  
   Sbjct: 118 RSNFLSOLA 126

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 20

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 39> which encodes amino acid sequence <SEQ ID 40; NGS20>. Analysis of this protein sequence reveals the following:

```

5  GvH: Examining signal sequence (von Heijne)
    Signal Score (-7.5): -0.1
    Possible cleavage site: 19
10 >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
        calculated from 1
    ALOM: Finding transmembrane regions (Klein et al.)
        count: 0 value: 7.58 threshold: 0.0
        PERIPHERAL Likelihood = 7.58
15 modified ALOM score: -2.02
    Rule: cytoplasmic protein

    *** Reasoning Step: 2

20 ----- Final Results -----

        bacterial cytoplasm --- Certainty= 0.057(Affirmative) < succ>
        bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
        bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
25 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### 30 Example 21

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 41> which encodes amino acid sequence <SEQ ID 42; NGS21>. Analysis of this protein sequence reveals the following:

```

35 GvH: Examining signal sequence (von Heijne)
    Signal Score (-7.5): -3.52
    Possible cleavage site: 52
    >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
        calculated from 1
    ALOM: Finding transmembrane regions (Klein et al.)
40 count: 0 value: 5.83 threshold: 0.0
        PERIPHERAL Likelihood = 5.83
        modified ALOM score: -1.67
    Rule: cytoplasmic protein

45 *** Reasoning Step: 2

    ----- Final Results -----

        bacterial cytoplasm --- Certainty= 0.311(Affirmative) < succ>
50 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
        bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
        bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

>ref|NP_040628.1| cI (repressor;237) [bacteriophage lambda]
ref|NP_061378.1| phage lambda repressor protein CI [Escherichia coli]
sp|P03034|RPC1_LAMB REPRESSOR PROTEIN CI
pir||RFBPL repressor protein cI - phage lambda
5 emb|CAA24991.1| (X00166) coding sequence cI gene [bacteriophage lambda]
gb|AAA96581.1| (J02459) cI (repressor;237) [bacteriophage lambda]
emb|CAB96428.1| (AJ277653) phage lambda repressor protein CI [Escherichia coli]
    Length = 237

10 Score = 62.5 bits (151), Expect = 5e-09
    Identities = 36/85 (42%), Positives = 51/85 (59%)

Query: 2 KKRELNEIETAECAELKRIFNSKKEELKLTQYKLAEAVGVTSQSAVNHYLNGTNALNASTA 61
      KK+ L + + + LK I+ KK EL L+Q +A+ +G+ QS V NG NALNA A
15 Sbjct: 4 KKKPLTQEQLEDARRLKAIEYKKKKNELGLSQESVADKMGMGQSGVGALFNGINALNAYNA 63

Query: 62 SQFAKILQIPVSDPSLRRLAEIISM 86
      + AKIL++ V +PS +A EI M
20 Sbjct: 64 ALLAKILKVSVEEFSPSIARBIYEM 88

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 22

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 43> which encodes amino acid sequence  
 25 <SEQ ID 44; NGS22>. Analysis of this protein sequence reveals the following:

```

GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -2.6
      Possible cleavage site: 43
>>> Seems to have no N-terminal signal seq.
30 Amino Acid Composition of Predicted Mature Form:
    calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 7.74 threshold: 0.0
      PERIPHERAL Likelihood = 7.74
35 modified ALOM score: -2.05
Rule: cytoplasmic protein

*** Reasoning Step: 2

40 ----- Final Results -----

      bacterial cytoplasm --- Certainty= 0.072(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
45      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

>pir||S30432 hypothetical protein - Streptomyces clavuligerus plasmid pSCL
    Length = 307

50 Score = 43.6 bits (102), Expect = 0.002
    Identities = 25/86 (29%), Positives = 49/86 (56%), Gaps = 2/86 (2%)

Query: 6 MGMAFKT-GIPRGQRFVLVKLCDNCANDDGLCYPSQETLAEDTGFAETA VRQH IKWLKDNN 64
      MGM F G+ ++ +L+ + + G C+PS++ L +D G + + V++ + L N
55 Sbjct: 1 MGMVFAAEGLDGSEKLLLLGYTNWTD PYGYCWPS EDR LVDDCGTSRSTVQRTKRKL VKKN 60

Query: 65 FIKSARRQGR-ERKSDIYRIN VALL 89
      ++S RR+ + E S++ R+N+ LL
60 Sbjct: 61 LLRSVRRKNSKGEFISNLSRVNLP LL 86

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 23

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 45> which encodes amino acid sequence  
5 <SEQ ID 46; NGS23>. Analysis of this protein sequence reveals the following:

```

GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -2.8
      Possible cleavage site: 59
>>> Seems to have no N-terminal signal seq.
10 Amino Acid Composition of Predicted Mature Form:
      calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 0.05 threshold: 0.0
      PERIPHERAL Likelihood = 0.05
15 modified ALOM score: -0.51
      Rule: cytoplasmic protein

*** Reasoning Step: 2

20 ----- Final Results -----

      bacterial cytoplasm --- Certainty= 0.195(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
25      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

>sp|P07905|DNAC_ECOLI DNA REPLICATION PROTEIN DNAC
pir||XMECNC DNA replication protein dnaC - Escherichia coli (strain K-12)
30      Length = 245

      Score = 110 bits (275), Expect = 2e-23
      Identities = 75/224 (33%), Positives = 116/224 (51%), Gaps = 23/224 (10%)

35 Query: 50  EAADEMAAYAETLRRGAMRDA-----LEKRIGRSGIAPRFRNCRIENYAV--SDS 97
      + +E+ A+ + +GA+R A          +++ RSGI P +NC ENY V
Sbjct: 24  KTGEELLAWQK--EQGAIRSAALERENRAMQMORTFNRS GIRPLHQNCSFENYRVECEGQ 81

40 Query: 98  IPGMARAKAAAAEYAAANFADVLQTGRSMIFSGRRGTGKNHLACGIAREVIAAGKSALVIT 157
      + +++A+ E+ N A          S IFSG+ GTGKNHLA I E++ GKS L+IT
Sbjct: 82  MNALSKARQYVEEFDGNIA-----SFIFSGKPGTGKNHLAAAI CNELLRLGRKSVLIIT 134

Query: 158  VGDMLRTVKDSF--GGGGEAGAVGIFVKPDLLVLDEFGAGSLSETDGRILFSVFNARYER 215
      V D++ +KD+F G E +          DLLV+DE G + S+ + I+ +V+ R
45 Sbjct: 135 VADIMSAMKDTFRNSGTSEEQLNDLSNVDLLVIDEIGVQTESKYEKVIINQIVDRRSSS 194

Query: 216  LMPMLVLTLNLTAFAFRENTDARIRDRLRDGGGKLIPFDWESYRA 259
      P +LTN E + R+ DR+R G + F+W+SYR+
50 Sbjct: 195 KRPTGMLTNSNMEEMTKLLGERVMDRMLGNSLWVIFNWDYSYS 238

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 24

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 47> which encodes amino acid sequence  
55 <SEQ ID 48; NGS24>. Analysis of this protein sequence reveals the following:

-51-

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -5.76  
 Possible cleavage site: 26  
 >>> Seems to have no N-terminal signal seq.  
 5 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 1.43 threshold: 0.0  
 10 PERIPHERAL Likelihood = 1.43  
 modified ALOM score: -0.79  
 Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

15 ----- Final Results -----

bacterial cytoplasm --- Certainty= 0.112(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 20 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

>ref|NP\_053228.1| pXO2-73 [Bacillus anthracis]  
 gb|AAF13678.1|AF188935\_76 (AF188935) pXO2-73 [Bacillus anthracis]  
 25 Length = 541

Score = 125 bits (315), Expect = 9e-28  
 Identities = 139/535 (25%), Positives = 254/535 (46%), Gaps = 70/535 (13%)

30 Query: 14 PVLFIGTGMSLRYL DNSYTW DGLLSKIAIDLFGDDREYLN IKSRYCEDGRFQYEEIAEEL 73  
 P LFIG+G S RYL N W GL+ K + +L + EY Y + E+AE +  
 Sbjct: 19 PFLFIGSGFSKRYL-NLEDWAGLMKKFS-NLMPYEFY-----YSSTANKDWAEEV AELM 70

35 Query: 74 QSKFDKVL---ENDPDGRFKEINDKFFENMRAGNTLSRFKIYISTLLSQLNYK----DNSN 127  
 F + E + KE D R + S K+ ++ L+ + YK + ++  
 Sbjct: 71 AKDFHPIWKEQQFENNRRKEFKD-----RISSKQSPLKVEVAKYLN SIEYKYGLDEKND 124

40 Query: 128 TELSELKKARKNVGSIITTN YDKLAQDIFEFNPL---IGN-DILLSNPFY--GSVYKIHGC 181  
 E++ LKK + IITTN+D L + IFB + IG ++L S+P +YKIHGC  
 Sbjct: 125 KEIAALKKIV--IDGIITTNWDL LLEQIFEEQEMQVYIGQKELLF SHPLEINEIYKIHGC 182

45 Query: 182 VDDPSKIIITKDYEFKEKYELIRAQLLSLFIHNPIIFLGYNVGDENIKEILKTIFTYV 241  
 P +++T DY+ + EK + A+LL++FI +P+IFLGY++ D+NI++ILK I +  
 Sbjct: 183 SSIPDSLVLTTSDYKGYNEKNAYLA AKLLTVFIEHPVIFLGYSISDDNIQQILKAITRCL 242

50 Query: 242 EQNSPSANKIRNRFLLVEYEPESNNEDIVEHDIDIT-GFSTIRINKIKTDNFSQIYKALA 300  
 +Q++ K R L+ E ED E++ +T G T+ I ++KT+++ +IY ALA  
 Sbjct: 243 DQDNIHKLKDR----LIFVERAGQEEDSFENNSSLTIGKITVPITRVKTNDEYKIYNALA 298

55 Query: 301 ELTLPISAMDVRKFQSI AKIETGCGNIKVSF---TEDMDNLNNSDKVVAIGSTKTISYNF 357  
 + S +R+ +S E+ + + + D+ + + V+ +G K +  
 Sbjct: 299 QNKRKFSMKMMRQMSQIYELVKTNDPEEKIYVVDGEYDDTQDIEFVIGLG-VKNVVEEM 357

Query: 358 QTTSEMMSN-----YFKIIEENS-----QLLKLIDKHSIASTQYFPI-- 395  
 Q+ E+ ++ + +++ +E ++K+ + S QY P+  
 Sbjct: 358 QSNHEISASKELSEHG YGGISDIELFNELLSDEPKYDYDSIVKISLPQILRSNQYVPLFR 417

60 Query: 396 YGFSRICSDIHKEAVLKRQKEKLDHFIEBINRCKNNHSSIQSILDDENISDTYKND AI 455  
 Y D ++ +K + K + F+ E ++ N S + + + + +  
 Sbjct: 418 YVLESSVEDELLDSKIKNKLKMYTDFLTETQKKNIKNLSWDWQFKNLDEV LKGFDPDIKV 477

65 Query: 456 AWG----IWNQNQLSEDEVENYL---KNFVNKKN----THYKRLLCMFDYKKYADT 499  
 A + L+ D++++L FV +KN T +RL ++D+ KY +  
 Sbjct: 478 AIEQIPLL GQKNLNCDDLKDFLIKNSKFVKEKNTPERTGIRRLFRIYDWLKYGQS 532

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 25

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 49> which encodes amino acid sequence  
5 <SEQ ID 50; NGS25>. Analysis of this protein sequence reveals the following:

```

GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): 4.76837e-07
      Possible cleavage site: 56
>>> May be a lipoprotein
10 Amino Acid Composition of Predicted Mature Form:
      calculated from 21
      ALOM: Finding transmembrane regions (Klein et al.)
          count: 0 value: 6.68 threshold: 0.0
          PERIPHERAL Likelihood = 6.68
15 modified ALOM score: -1.84
      Rule: inner or outer membrane protein
      Rule: inner or outer membrane protein

*** Reasoning Step: 2

20 Lipoprotein?
      Inner membrane?

----- Final Results -----
25
      bacterial outer membrane --- Certainty= 0.790(Affirmative) < succ>
      bacterial inner membrane --- Certainty= 0.700(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>
30

```

The protein has homology with the following sequences in the databases:

```

>gi|7433005|pir|B70313 cytochrome-c peroxidase (EC 1.11.1.5) - Aquifex aeolicus
gi|2982865|gb|AAC06485.1| (AE000675) cytochrome c peroxidase [Aquifex aeolicus]
35      Length = 355

      Score = 345 bits (885), Expect = 7e-94
      Identities = 180/336 (53%), Positives = 237/336 (69%), Gaps = 12/336 (3%)

40 Query: 59 EDQDLLKRAQGVFQPLPTVEEMQKIRPFTEEQVKLGHLWYEPRLSKGNTVSCNSCHNLA 118
      +D++LLK A+ F+PLP V E + P T E+VKLG L+Y+PRLSK +SCN+CHNLA
      Sbjct: 22 DDKELLKMARQYFKPLPKVAENPQ-NPVTPEKVKLGKMLYYDPRLSKSGLISCNTCHNLA 80

      Query: 119 SAGVDNMPTSQGHKGQFGGRNSPTALNALLGSQFWDGRAADVEEQAGGPLVNPVEMAND 178
      GVDN+PTS GH+ G RN+PT NAA+ +QFWDGRA DVEEQA GP+VNP+EMAN
45 Sbjct: 81 RYGVDNLPTSIGHRWAIGPRNAPTIVYNAIHLAQFWDGRAKDVEEQALGPVNPPIEMAN- 139

      Query: 179 SQEAAAIAKVPPEYQEMFKAFP-EDGAVSFKNITTALGAFERTLLTPTKWDEYLKGNV 237
      ++E A + +PEY E+FKKAFP E V ++NI A+GAFERTL+TP+++DE+LKGN
50 Sbjct: 140 TEENAVKTLKSIPEYVELFKKAFPNEKDPVKYENIGKAIGAFERTLMTPSRFDEFLKGNT 199

      Query: 238 NALSEQERKGVRAFMDNGCIACHNGVNLGGTTTFQKFGLVQGPYWK-----FIEDP--KR 289
      AL+EQE++G++ F++ GC+ACHNG +GG F KFG++ YWK + P K
      Sbjct: 200 KALTEQEKRLKTFIEVGCVACHNGPGVGGNMFAKFGMIT-EYWKVTYPYVLVGKPAIKV 258

55 Query: 290 DKGRADVTKKTEDEFFFRVPLGRNVAKTYPYFHNGSVWELDKAVTIMKAQLGKDIPKED 349
      D GR VTKK ED F F+VP LRN+ TYPYFH+GSVW L+ AV IM K QLKG++ +
      Sbjct: 259 DFGRFVTKKEEDMFVFKVPSLRNIEHTYPYFHDGSVWSLEDAVRIMAKTQLGKELTDQQ 318

      Query: 350 VDNIVVFLNALSGNVSESARTMPPLTAPMESKPD 385
      V +IV FL AL+G + + A +PEL + KP+
60 Sbjct: 319 VKDIVAFLKALTGKIPKHALEVPPELPPSTDKTPKPE 354

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 26

- 5 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 51> which encodes amino acid sequence <SEQ ID 52; NGS26>. Analysis of this protein sequence reveals the following:

```

GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): 0.610001
Possible cleavage site: 15
10 >>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 5.04 threshold: 0.0
15 PERIPHERAL Likelihood = 5.04
modified ALOM score: -1.51
Rule: cytoplasmic protein

*** Reasoning Step: 2

20 ----- Final Results -----

bacterial cytoplasm --- Certainty= 0.127(Affirmative) < succ>
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
25 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

30 >pir||T13296 hypothetical protein 8 - Streptococcus phage phi-01205
gb|AAC79524.1| (U88974) ORF8 [Streptococcus thermophilus temperate bacteriophage
01205]
Length = 157

Score = 62.5 bits (151), Expect = 2e-09
35 Identities = 53/161 (32%), Positives = 86/161 (52%), Gaps = 8/161 (4%)

Query: 5 TLYRCAADVQAALDYYFDSETEREDTLEAV--IGQFEVKAQSVIAYIKNQBITKMLEGH 62
TLY + + D ET + DTLEA+ +E K + + IK+ E + +
Sbjct: 3 TLYELTDQLLEIYNMDVDDDET-KLDTLEAIDWTTDYENKVEGYVKVKSLEADIEARKNE 61

40 Query: 63 IRQMTGKLKAAKARNQSLKDYLRNMQAAGITEIKADDGTFKASFRKSEAVVILDEAQIP 122
+++ G K+ +++ LK LA +M G T + D FK FRKSEAVV+ +E ++P
Sbjct: 62 KKRLDGLNKSDQSKIDKLKTALAVSMAETGQTRV--DTTLFKVGFRKSEAVVV-NEEKLP 118

45 Query: 123 AEFMREAVKTEPDKTAIRKAIESGRQVAGAKIEGRKNLQIR 163
E+ K PDK +++ ++SG+ + GA +E R+NL IR
Sbjct: 119 KEYQIATYK--PDKKTLKELLKSGKHIEGATLEERRNLNIR 157

```

- 50 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 27

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 53> which encodes amino acid sequence <SEQ ID 54; NGS27>. Analysis of this protein sequence reveals the following:

```

55 GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): -5.45

```



-54-

Possible cleavage site: 49  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 5 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 1.80 threshold: 0.0  
 PERIPHERAL Likelihood = 1.80  
 modified ALOM score: -0.86  
 Rule: cytoplasmic protein  
 10 \*\*\* Reasoning Step: 2  
 ----- Final Results -----  
 15 bacterial cytoplasm --- Certainty= 0.559 (Affirmative) < succ>  
 motifs:  
 Subtilase\_Asp (S,T,A,I,V)x(L,I,V,M,F) (L,I,V,M)D(D,S,T,A)G(L,I,V,M,F,C)x  
 (A)x(L)(I)D(D)G(I)x(2)(D)  
 20 79: DDDFL AALIDDGIVFD V

A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS27 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
 25 useful antigens for vaccines or diagnostics.

#### Example 28

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 55> which encodes amino acid sequence <SEQ ID 56; NGS28>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 30 Signal Score (-7.5): -0.19  
 Possible cleavage site: 61  
 >>> Seems to have a cleavable N-term signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 62  
 35 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 0.69 threshold: 0.0  
 PERIPHERAL Likelihood = 0.69  
 modified ALOM score: -0.64  
 Score for OM-PP discrimination: -24.78  
 40 Rule: outer membrane or periplasmic protein  
 Score for OM-PP discrimination: -24.78  
 Rule: outer membrane or periplasmic protein  
 \*\*\* Reasoning Step: 2  
 45 Periplasmic space? Score: 2.47798  
 Periplasmic space? Score: 2.47798  
 ----- Final Results -----  
 50 bacterial periplasmic space --- Certainty= 0.916 (Affirmative) < succ>

The protein has homology with the following sequences in the databases:

55 >prf||1306286A mobilization protein B [Escherichia coli]  
 Length = 529  
 Score = 34.7 bits (78), Expect = 2.4  
 Identities = 24/69 (34%), Positives = 31/69 (44%), Gaps = 12/69 (17%)

-55-

Query: 344 QLRARQQEIPVDYARTAVCGRIPFRRHSRPTLRSRTLGAQRRRIVPNVGQAGGIRAD--- 400  
 +LRA Q++P D+ +T V P R R + GA GQ G IR D  
 Sbjct: 440 RLRAAGQDLDPADFVKTTVLDTNTPIRWFYRAASQESRSGA-----GQTGEIRVDVER 490

5 Query: 401 RTPNTQRGT 409  
 R P +RGT  
 Sbjct: 491 RGPAGRRGT 499

A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS28 protein and  
 10 nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
 useful antigens for vaccines or diagnostics.

### Example 29

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 57> which encodes amino acid sequence  
 15 <SEQ ID 58; NGS29>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -3.61  
 Possible cleavage site: 31  
 >>> Seems to have no N-terminal signal seq.  
 20 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 4.03 threshold: 0.0  
 PERIPHERAL Likelihood = 4.03  
 25 modified ALOM score: -1.31  
 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 30 ----- Final Results -----  
 bacterial cytoplasm --- Certainty= 0.106(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

35 emb|CAB83930.1| (AL162753) hypothetical protein NMA0640 [Neisseria meningitidis  
 Z2491]  
 Length = 387  
 Score = 653 bits (1685), Expect = 0.0  
 40 Identities = 324/388 (83%), Positives = 351/388 (89%), Gaps = 1/388 (0%)  
 Query: 1 MNITIAAPYCSLPSEPHFNRFWYLAELLSQSHDVLLITSNFKHYDKSFRRPEDAKAASQG 60  
 MNITI APYCSLPSEP+FNRFWYLAELLSQSHDVLLITS F+HYDKSFRR EDA A S G  
 Sbjct: 1 MNITIVAFYCSLPSEPFYFNRFWYLAERLSQSHDVLLITSRFRHYDKSFRRHEDAAATSNG 60  
 45 Query: 61 RLKVMLLEESGYSKNVSLGRVTSNHRFVKHFKEWLENCRPGEQDVVYSAYPLIATNLLLG 120  
 RL+V LL+E GY KNVSL RV SH FV++ +WL + + EQD+VYSAYPL+ATNLLLG  
 Sbjct: 61 RLRVKLLDEPGYRKNVSLARVASHRVFVRNLARWLHSPQAAEQDIVYSAYPLMATNLLLG 120  
 50 Query: 121 KHKARLGYKLIVDVQDVWPESFSSVVPFLKKIPHNLLPFASRANRAYRYADALVAVSQTY 180  
 KHKARLGYKLIVDVQDVWPESFSSVVPFLKK+PH LLPFASRANRAYR ADAL+AVSQTY  
 Sbjct: 121 KHKARLGYKLIVDVQDVWPESFSSVVPFLKKVPHKLLPFASRANRAYRCADALIAVSQTY 180  
 55 Query: 181 LDRAKEANPNVPGEVVYIGADFAAIAPPPFRSKTVRFFYLGTLSSYNDVETVCKGVRKL 240  
 LDRAKEANPNVPGE VYIG DFAAIA PPRFRSKTVR FYLGTLSSY+YDVETVCKGVRKL  
 Sbjct: 181 LDRAKEANPNVPGETVYIGTDFAAIA-PPRFRSKTVRLFYLGTLSSYDVETVCKGVRKL 239  
 Query: 241 LDDGENVELHIMGGGPDLDRLKQYACDGKIFYGYIPYAEMMSVAKGCDIAVNATHSYAMQ 300  
 LDDGENVELHIMGGGPD++LKQY IKFYGY+PY+EMMS+AK CDIAVNATHS+AMQ

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Sbjct: 240 LDDGENVELHIMGGPDLEKLRQYENRAIKFYGYLPYSEMMSLAKACDIAVNAIHSAMQ 299

Query: 301 SITNKLSDYMALQKPILNSQVHDEVAEVLTLPHENYRSGDVGDFVQAAKDILKRKNDPV 360  
S+TNKLSDYMALQKPILNSQ + EV ++L LLPHENYRSGDVD FVQAAK+ILKRK+DPV

5 Sbjct: 300 SVTNKLSDYMALQKPILNSQNAEVLDLLNLLPHENYRSGDVDSFVQAAKNILKRKDDPV 359

Query: 361 QSDEIVRRFRHDISYRKIVNLIERLANE 388  
QSDEIVRRFR DISYRKIVNLIERLA+E

10 Sbjct: 360 QSDEIVRRFRDISYRKIVNLIERLAHE 387

>emb|CAB58324.1| (AL121855) hypothetical protein SCF62.09 [Streptomyces  
coelicolor  
A3(2)]  
Length = 407

15 Score = 54.7 bits (130), Expect = 2e-06  
Identities = 57/243 (23%), Positives = 105/243 (42%), Gaps = 24/243 (9%)

Query: 99 RPGEQDVVYSAYP---LIATNLLLGKHKARLGYKLIVDVQDVWPESFSSVVPFLKKIPHN 155  
R G DVV++ P L L L R G ++ D D+ PE + S K ++

20 Sbjct: 81 RVGFPVDVHACNPPDLLFLPALWL---KRRGARFVFDQHDLIPELYLSRFGRGKDLLYR 136

Query: 156 LLPFASRANRAYRYADALVAVSQTYLDRAKEANPNVPGEVVYIGA-----DFAAIAPPPR 210  
+ R YR AD ++A ++Y D A P +V + + F + P P

25 Sbjct: 137 AVCALERWT--YRAADVVLATNESYKDVAIRRGRRPDDVVFVRSAPATDRFQFVPEPE 194

Query: 211 F-RSKTVRFFYLGTLSYNYDVETVCKGVRKLLDDGENVELH--IMGGPDLDRLKQYA-- 265  
R K YLG + V+ ++ KL D+ + H +G G D + + +

30 Sbjct: 195 LKRGPHELLCYLGVMGPQDGVLYALRALAKLRDEVGRTDWHAVFVGSGDAFDAMVELSRS 254

Query: 266 ---CDGIKFGYIPIYAEMMSVAKGCDIAVNAIHSYAMQSIT--NKLSDYMALQKPILNSQ 320  
+ ++F G IP A+++ D+ ++ + ++ NK+ +YMA+ +PI++

35 Sbjct: 255 LGLDEQVRFTGRIPDADLVRHLSTADVCLSPDPRNPLNDVSTMNKVLEYMAMGRPIVSFD 314

Query: 321 VHD 323  
+ +

Sbjct: 315 LRE 317

As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS29 protein and  
40 nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
useful antigens for vaccines or diagnostics.

### Example 30

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 59> which encodes amino acid sequence  
45 <SEQ ID 60; NGS30>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -4.8  
Possible cleavage site: 46  
>>> Seems to have no N-terminal signal seq.  
Amino Acid Composition of Predicted Mature Form:  
50 calculated from 1  
ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 1.54 threshold: 0.0  
PERIPHERAL Likelihood = 1.54  
modified ALOM score: -0.81  
55 Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

----- Final Results -----

60

bacterial cytoplasm --- Certainty= 0.113(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

```

5   fastidiosa (strain 9a5c)
    gb|AAF84279.1|AE003977_2 (AE003977) conserved hypothetical protein [Xylella
    fastidiosa]
      Length = 376

    Score = 73.6 bits (179), Expect = 3e-12
10   Identities = 82/354 (23%), Positives = 143/354 (40%), Gaps = 35/354 (9%)

    Query: 1   MKIILTTSMGLGGTETATVRLGRLLKRHGHDIIILASSDG-PFVGEAQASGIRWQPVDFY 59
          MKI+ T + +G GG E   R   ++ GH + L   G P   A+ +G+   ++ +
    Sbjct: 1   MKILHTEAATGCGGEETIYIRHMLSMQAQGHMALLCQPGAPLSTMARNAGLPVYHINMH 60

15   Query: 60  RGGLAGYLKSTFAYARMLRREQPDIIIDCMARVVPACALAAKIVSPKTKIICHSHGLDAA 119
          G   L               +L+RE D+++               A AA++ +T++I S L A
    Sbjct: 61  --GPWRVLNGIHTVQHLLQRETDFDVNTTSHVDTLIAAAAARLT--RTRLIVRSRHLMAP 116

20   Query: 120 TYPKTAKLFDKLGAYIIGNCKHEREKLI RHGFPAGRIAYA-----YNTPEFHFHRK 170
          K+   + L   +I   +H R+ LI+ G   RI               +T PE   +++
    Sbjct: 117 I--KSQLTYTYLPHRVITVSQHVRDLLIKQGIQPTRIGIVPPITAQPPWMDTDPEHAWQR 174

25   Query: 171 TEK-----ECAVLGTL SRLDTVRAVHMLDLILKKMVGRNIPVRLNMAGIGEE 217
          ++               ++G ++ L   +   +LD +   +   N   + L +AG GE
    Sbjct: 175 LQQTRHVVRTELGFNDNDIIVGCVAVLREAKGHRELLDALAPLCQANPRHLVVIAGDGEP 234

    Query: 218 -MDNLKAQAKRLGIEDKVTFLGGVRDLTG YFKEVDILVNTPHCVGDHGAGVGNNILEAGL 276
          M +L A K L +E ++ LG   D               DI   +   G   LEA
30   Sbjct: 235 VMQHLLAHRKTLTLETQIHLLGYRHDAPRLMSGFDIFA-----LATQKEAAGTVFLBAAQ 289

    Query: 277 YDTPVVVTYNMAGISEMVITGQTYGCI PF GDDEAFIEAVDTLIKHPELRSQMGKA 330
          P++   + G+ EM+ G   +   G+ A   A+ TL+ + + R MG+A
35   Sbjct: 290 AGIPIIATRVGGVPEMLQEGTNAILVTPGNQTALTNALHTLVTTNNQQRHSMGRA 343

```

A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS30 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### 40 Example 31

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 61> which encodes amino acid sequence <SEQ ID 62; NGS31>. Analysis of this protein sequence reveals the following:

```

    GvH: Examining signal sequence (von Heijne)          Signal Score (-7.5): -5.36
    Possible cleavage site: 16
45   >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
        calculated from 1
    ALOM: Finding transmembrane regions (Klein et al.)
        count: 0 value: 3.50 threshold: 0.0
50   PERIPHERAL Likelihood = 3.50
        modified ALOM score: -1.20
    Rule: cytoplasmic protein

    *** Reasoning Step: 2
55   ----- Final Results -----

```

bacterial cytoplasm --- Certainty= 0.299(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

gb|AAB49297.1| (U84350) hypothetical hydroxylase a [Amycolatopsis orientalis]  
Length = 491

5      Score = 111 bits (278), Expect = 1e-23  
      Identities = 87/269 (32%), Positives = 123/269 (45%), Gaps = 15/269 (5%)

Query: 1    LKNGAAPSWSGSRYTEFDF----TDKFSGPGTVYQVRRVFDKILIEBAKQGVEVRFGH 56  
          +K G F WG+R + F + K + YQV RA FD IL++ A +GV VR G

10    Sbjct: 73 IKRGGTFRWGARPEPWTFHFGISAKMAGSTSHAYQVERAKFDDILLKNAKSGVVRREGC 132

Query: 57    GVTAFDNSGDFARLNIETDT-GESYELTAKFVLDASGY-GRVLPRLNLNLETPSHLPPRQT 114  
          V      G+      TD G ++E++A+FV+DASG R+ ++ S

15    Sbjct: 133 SVNDVVEDGERVTGARVTDADGNAHEVSARFVIDASGNKSRLYTKVNGSRNYSEFFRSLA 192

Query: 115    HFTHIDDNITHPKFDRNKILITTHPQHRDVWIWLIFFGDNRCSVGVV---GTPDKLAGES 171  
          F + +      P+      IL      W W IP D    SVG V      DK+ G+

      Sbjct: 193 LFGYFEGGKRLPEPVSGNLSVAFDSG---WFWYIPLSDTLTSVGAVVRREDADKIQGDR 249

20    Query: 172 ETVLKKFVYECPMLSEILDKAVWENDFPFRSIQ---GYSANVKSLLHGRHFALLGNAAEFL 228  
          E L + ECP++SE L A + ++ YS S L+G+AA F+

      Sbjct: 250 EKALNTLIAECPLISEYLSNATRVTTGRYGELRVKDYDYSYQQDSYWRPGMVLVGDAACFV 309

25    Query: 229 DPVFSSGVTTIALHSARLAADLLTKQLKGE 257  
          DPVFSSGV +A +SA LAA + L G+

      Sbjct: 310 DPVFSSGVHLATYSALLAARSINSVLGAD 338

30    A homolog (amino acids 280-341) was found in serogroup A *N.meningitidis* but not in serogroup B, so  
      NGS31 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B  
      *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
useful antigens for vaccines or diagnostics.

### Example 32

35    A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 63> which encodes amino acid sequence  
      <SEQ ID 64; NGS32>. Analysis of this protein sequence reveals the following:

      Signal Score (-7.5): -3.49  
      Possible cleavage site: 38  
      >>> Seems to have no N-terminal signal seq.  
      Amino Acid Composition of Predicted Mature Form:  
40    calculated from 1  
      ALOM: Finding transmembrane regions (Klein et al.)  
          count: 0 value: 7.80 threshold: 0.0  
          PERIPHERAL Likelihood = 7.80  
45    modified ALOM score: -2.06  
      Rule: cytoplasmic protein

      \*\*\* Reasoning Step: 2

50    ----- Final Results -----  
          bacterial cytoplasm --- Certainty= 0.278(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

55    fastidiosa (strain 9a5c)  
      gb|AAF83310.1|AE003899\_2 (AE003899) phage-related repressor protein [Xylella  
      fastidiosa]  
          Length = 143

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Score = 87.0 bits (214), Expect = 2e-16  
 Identities = 40/71 (56%), Positives = 54/71 (75%)

5 Query: 1 MFSGEQLGQAISEAIKRNVSQKEVADHFGVKQPSVSGWIKNGRIDKKHLDKLIDYFSDV 60  
 M +GEQLG+AI +A++ K V+ ++A+HFGVK PSV GWIK GRI K+ L L YFSDV  
 Sbjct: 1 MLTGEQLGRAIKQAMQLKGVTPTKMAEHFGVKAPSVYGWIKRISKEKLPSLWSYFSDV 60

10 Query: 61 VTPSHFGIETF 71  
 V P+H+G+E +  
 Sbjct: 61 VGPTHWGLEAW 71

>sp|P18680|RPC1\_BPHK0 26 KD REPRESSOR PROTEIN (REGULATORY PROTEIN CI)  
 emb|CAA34222.1| (X16093) cI gene product (AA 1-208) [Bacteriophage HK022]  
 15 Length = 235

Score = 80.5 bits (197), Expect = 2e-14  
 Identities = 60/200 (30%), Positives = 99/200 (49%), Gaps = 15/200 (7%)

20 Query: 22 QKEVADHFGVKQPSVSGWIKNGRIDKKHLDKLIDYFSDVVTPSHF-----GIETFRV 73  
 Q ++A V ++S W I +K DK+ S + T + + GI +  
 Sbjct: 29 QADLAVRLKVTTPKAISKWFNGESIPRK--DKMESLASVLGTTAAYLHGYADDDGITVNL 86

25 Query: 74 LKSNEQSSIRFPRLNAEATCGAGT-INDHYIEVVDYVTVAAWAREKLGGNLNK-IQVIT 131  
 +SN+ R L+ +A+ G GT +++ +IE + + AR G + ++VIT  
 Sbjct: 87 SRSNDY--YRVDVLDVQASAGPGTMVSNEFIEKIRALEYTTTEQARILFNGRPQESVKVIT 144

Query: 132 ARGDSMEPTIENGDMFVDTAVEAFDGDGLYLLWYIDGLKAKRLQSTVGGGLMIISDNSS 191  
 RGDSME TI GD +FVD ++ FDGDG+Y+ Y + KRLQ L +ISDN++  
 30 Sbjct: 145 VRGDSMEGTINPGDEIFVDVSITCFDGDGIYVFYVGKTMHVKRLQMQ-KNRLAVISDNAA 203

Query: 192 YRTETVRGEDLNAVRIIGRI 211  
 Y + + + I+ ++  
 35 Sbjct: 204 YDRWYIEEGEEQLHILAKV 223

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 33

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 65> which encodes amino acid sequence  
 40 <SEQ ID 66; NGS33>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -4.87  
 Possible cleavage site: 31  
 >>> Seems to have no N-terminal signal seq.  
 45 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 4.88 threshold: 0.0  
 PERIPHERAL Likelihood = 4.88  
 50 modified ALOM score: -1.48  
 Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

55 ----- Final Results -----

bacterial cytoplasm --- Certainty= 0.313(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

60 gb|AAF31132.1| (AF069529) Gp54 [Bacteriophage HK97]  
 Length = 273

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Score = 47.4 bits (111), Expect = 3e-04  
 Identities = 33/123 (26%), Positives = 52/123 (41%), Gaps = 20/123 (16%)

5 Query: 221 NGGLSGKPKNANVPRRRKTHGVPLQEIADLYNEVLGGRLPSVQVLNDTRKRAIANRWCEM 280  
 NGG G+ K P R R K + + + Y N + G R L P + N + R K R + +  
 Sbjct: 160 NGGGDGQVK----PERRKAERIDYESFLNAYNTEVGDRLPHAVAVNEKRKRRL-KKIIPQ 214

10 Query: 281 LGTAAPNGKVRFGDKETGLAWFAGFFRKVA--MNPFFWMGENQTGFAVGFDWIFKAGNFVK 338  
 L T + G F + R P F + G + N T G + F D + + + +  
 Sbjct: 215 LKTPNVDG-----FRAYVRAFVHQAKPFYFGDNDTGWTDGDFDYLLREDSLTG 261

Query: 339 ILE 341  
 + E  
 15 Sbjct: 262 VRE 264

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 34

20 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 67> which encodes amino acid sequence <SEQ ID 68; NGS34>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -5.65  
 Possible cleavage site: 50  
 25 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 3.76 threshold: 0.0  
 30 PERIPHERAL Likelihood = 3.76  
 modified ALOM score: -1.25  
 Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2  
 35 ----- Final Results -----

bacterial cytoplasm --- Certainty= 0.310(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 40 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

45 >pir|H82649 hypothetical protein XF1674 XF1569 [imported] - Xylella fastidiosa  
 (strain 9a5c)  
 gb|AAF84378.1|AE003986\_8 (AE003986) hypothetical protein [Xylella fastidiosa]  
 gb|AAF84483.1|AE003993\_2 (AE003993) hypothetical protein [Xylella fastidiosa]  
 Length = 316

50 Score = 167 bits (424), Expect = 2e-40  
 Identities = 108/308 (35%), Positives = 152/308 (49%), Gaps = 30/308 (9%)

Query: 10 ETSVIRSLSSASLYMFTTRRMFYQRRGYVWQRANHHAPICNALERVFNGETKRLIINIPPR 69  
 E +VI++ A FTR F QR+ ++ HH I ++ V G K ++IN+PP  
 55 Sbjct: 10 EQAVIKARCEADHLFFTRYFFKQRQQLRFRVNWHHHVIAGVVDDVIAGRRKDVVINVPPG 69

Query: 70 YSKTEIAVVNFIAMGRVPDCEFIHASYSAAALAVNNSVQIRNLVQHEEYRAIFP-DLAL 128  
 SKTE+ +N +A + P F+H SYS LA+ NS R +VQ +EYRA++P ++A  
 Sbjct: 70 SSKTELVAINVMMARGLALNPFARFLHISYSDDLALLNSETAREIVQSDEYRALWPLEIAD 129

60 Query: 129 AGESGHHWKT-----AGGVMYXXXXXXXXXXXXXXXXXHHREGFGGCIIDDPHKADEARSE 183



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```

+S   W       AGGV Y               G+ G IIDD P K ++A S+
Sbjct: 130 DAKSKRWNVVVDGKKAGGV-YAVSLGGQVTGFRAGHMAPGWQGAI IIDDPLKVEDAYSK 188

Query: 184 VRRQNVIDWFQNTVESRKNSPDTP IILIMQRLHEKDLAGWLLDGGNGEEWEHLCLPAIQE 243
5      R      +TV+SRK SPDTP II+IMQRL + D G++ GG   WE + +PA+ +
Sbjct: 189 TGRSKANRKLVS TVKSRKASPDTP IIVIMQRLAQDDPTGFIQSGGFP GAWECIEIPALID 248

Query: 244 DG-----TALWPEKHDIETLRRMEQAAPYVFAGQYLQKPAPP 280
      D      + WP K + L +E   YVF+GQY Q+P+P
10 Sbjct: 249 DAYVSRLPEHVQGQVVRDAQDQDGRYSYWFYKEPLAELLALEATDRYVFSGQYQQRPSPL 308

Query: 281 DGGTFKPD 288
      GG K D
15 Sbjct: 309 GGGIIGD 316

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 35

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 69> which encodes amino acid sequence  
 20 <SEQ ID 70; NGS35>. Analysis of this protein sequence reveals the following:

```

GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -1.07
      Possible cleavage site: 40
25 >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
          calculated from 1
      ALOM: Finding transmembrane regions (Klein et al.)
          count: 0 value: 1.64 threshold: 0.0
          PERIPHERAL Likelihood = 1.64
30 modified ALOM score: -0.83
      Rule: cytoplasmic protein

*** Reasoning Step: 2
35 ----- Final Results -----

          bacterial cytoplasm --- Certainty= 0.020(Affirmative) < succ>

```

The protein has homology with the following sequences in the databases:

```

40 >ref|NP_047925.1| gp34 [Bacteriophage phi-C31]
    emb|CAA07104.1| (AJ006589) gp34 [Bacteriophage phi-C31]
        Length = 457

    Score = 59.7 bits (143), Expect = 1e-07
45 Identities = 68/272 (25%), Positives = 117/272 (43%), Gaps = 49/272 (18%)

Query: 226 GYSPVEQIIMTVNIALKRQVHALEYTAGSVPDALVGVPETWSADDIRRFQFYWDL LLSG 285
      G SP+   ++ +AL Q +   +++ G++P A+V VP T S + + R +E W   SG
50 Sbjct: 192 GCSPISYARESIGLALAAQKYGSKFFANGAMP GAVVEVPGTMSEGLARAREAWRAANS G 251

Query: 286 -----ETAQRRKMRFPV GELSRNFRETKQPLKDVYDEW LARVVCFAFSVEPTP 334
      E A+ K+   P E   F +T+Q + ++   AR+   F V P
Sbjct: 252 VDNAHRVALLTEGAKF SKVAMSPDEAQ--FLQTRQFQVPEI-----ARI-----FGVPPH- 299

55 Query: 335 FVAQVNRSAETS--REQLSDGMGSLKNWVKALIDDLARYMDMAA--YEFVWKGEESL 390
      ++   S + S   EQ+++ M SL+ W++ +   A + FV   + +
Sbjct: 300 LISDATNSTSWGSLAEQNI AFTMFSLRPWLRIEAGFNRL LFAETADRF R FVKFNLDEI 359

Query: 391 N---PREQAETIYAIYKNAGILTADEIRAELGKEPLP-GQG-----QPEPDK 432
      PKE+ E++++ GI + DE+RA   PLP G G   +PEP+
60 Sbjct: 360 KRGAPKERMELWSLGLONGIYSIDEVRAEDMTPLPDGLGEKYRVPLNLGEVGEEPEPEP 419

```

Query: 433 QDG----RKPEPPNQGAERLKGSESPMSDE 460  
 P E P++ E GK + + +E  
 Sbjct: 420 APAPPAIEPPAREPDEPEPEGKPDDEGATEE 451

A homolog (amino acids 641-700) was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS35 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 36

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 71> which encodes amino acid sequence <SEQ ID 72; NGS36>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): 4.3  
 Possible cleavage site: 26  
 >>> Seems to have a cleavable N-term signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 27  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 1.70 threshold: 0.0  
 PERIPHERAL Likelihood = 1.70  
 modified ALOM score: -0.84  
 Score for OM-PP discrimination: 0.02  
 Rule: outer membrane or periplasmic protein  
 Score for OM-PP discrimination: 0.02  
 Rule: outer membrane or periplasmic protein  
 \*\*\* Reasoning Step: 2  
 Outer membrane? Score: 0.00213559  
 Outer membrane? Score: 0.00213559  
 ----- Final Results -----  
 bacterial outer membrane --- Certainty= 0.232(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

>pir||D82437 TonB receptor-related protein VCA0625 [imported] - *Vibrio cholerae*  
 (group O1 strain N16961)  
 gb|AAF96526.1| (AE004392) TonB receptor-related protein [*Vibrio cholerae*]  
 Length = 784  
 Score = 103 bits (256), Expect = 2e-20  
 Identities = 104/427 (24%), Positives = 162/427 (37%), Gaps = 100/427 (23%)  
 Query: 31 NTEQQKELNTIVVHGKRS-ADQKGADVVYKNSNAYVGKEYLERYRVQSAGDVLKGLNG 89  
 NTEQ + T+ VHG+ DQ+ D L++ R + D+ G+  
 Sbjct: 57 NTEQAVD-ETVTVHGQSILTDQTRSD-----LDKVRGIANADIFSGITS 100  
 Query: 90 VYNNMTRTAGGAITPNIRGITGKGRIPVTIDGTEQTIDVMMNNYGVGDRNYLDPALFRSI 149  
 V + N GA+ IRG+ G+GR+P+ IDG+ Q+ GV DR Y+D L S+  
 Sbjct: 101 VQSNMHNHEAGALDIGIRGVQGEGRVPIFIDGSLQSTHTSRGYQGVSDRTYIDTDLSSL 160  
 Query: 150 AVEKSPALTRG--VKSGVGGAMSIRTIPEPSDIIPEGRNWGIEVKTEFSGNTVAQKNDLRQ 207  
 V K + VGG ++ T+ DII + + +G+ +K  
 Sbjct: 161 TVNKGATIESSPYASGAVGGVVNATLGIKDIKDDQAFGVVLK----- 204

Query: 208 FLGRDYRTLSPIGATADGVSGMPDVLTYGTGKPSPTALLLDEGIADTKFSGGKSHTNFKD 267  
 A A+ + PDV Y+ + LDE + F G  
 Sbjct: 205 -----ARANNHNRTPDVSGDYSEQGQ---YALDERGEHSAFKHG----- 240

5 Query: 268 DRQLMLSAAFKTDITDGLAAYSHRQKGNYYAGKRGYQSYLNNPI--YGADACYDQYPDKS 325  
 LML ++ + + + AYS R KGN++AGK+GY+ Y P+ G + + S  
 Sbjct: 241 --SLMLGLGYQAESFNTVLAYSRSKGNHFAKKGYEY--QEPVVGGQGEVVNTSFSFSDS 297

10 Query: 326 WREKDILCKSSASLVPMMAVLFPRGEEIMNSHTDTKILLKNNWYLPDNQKISLQYMDNK 385  
 W K S N +R H +L WY Y D K  
 Sbjct: 298 WLFK---LASDTGTAHNADFNYR-----HHAQKAGEVLMAYWYKSSDWEGNPFYPDGK 347

15 Query: 386 IGFGELNPLITAWILGFABEQSLNBFVQAPGIGTKIDSKTYKIGYEWKPNKKNWIDLQAD 445  
 + W LG A+ + TY Y ++P ++ W++L A+  
 Sbjct: 348 -----DRMPQWGLGTAKVN-----TYSANYYYQP-DHPWLNLAN 381

20 Query: 446 MWRVKTD 452  
 W + D  
 Sbjct: 382 FWYTRAD 388

Score = 94.7 bits (234), Expect = 5e-18  
 Identities = 80/290 (27%), Positives = 126/290 (42%), Gaps = 37/290 (12%)

25 Query: 929 SYDLADNHLRFARYARMSRFPSPLYELTAATGSGGLYGSETVAEYS-----LKPEKSTNWEV 984  
 +Y L + +LF + +R R PSLYE T S V Y+ +KPE++ N EV  
 Sbjct: 514 TYALTPTQLFLKSSRTYRMPSLYETTL-----SNEVFSYNPYNPIKPEQAWNNEV 564

30 Query: 985 GYNFNFAFHAKLRQGDRLRLTYYSNKIKNQIDTSN--EDGGMQ-----YDKAVSK 1033  
 G F + + + +L ++Y+ N IK+ I + GM + YDK  
 Sbjct: 565 GVQFMASNSVLQDDRLNLSVSYFRNSIKDFISGRLAKTPGMSEWQANFTFTNYDKLQLS 624

35 Query: 1034 GVELQSRLDSGRFFASFGGTYRLKHMVCDKGIAFKFDYLYLQRVPECLEGGFGLSRFFQSL 1093  
 G EL + + F T + +C A C GF +  
 Sbjct: 625 GWELGAHYQYAWLYTHFAATLYSETKICSVQQA-----QYAESDTCNSLGFAGLTPTRI 679

40 Query: 1094 QPKYSLTLDVGTRFFNEKLELGMRAIHHSKARRNYDKLIADGAGQVYARNGKPYGWHA 1153  
 PK +L L+VGT+FFN+ L+ G++ +HS + N +A A Y  
 Sbjct: 680 PPKQNLVNLVGTGKFFNDTLDGSKVSVYHSG--KSNPSDWLAGTAANPILEIPSDY----- 732

Query: 1154 TLLDAYARYRIGKHIDLNFSVTNLANRYLDPMSSTFVPGPGRTITFGIK 1203  
 +D Y++Y + + L F++ N+ +RY + P S +P PGRTIT G +  
 Sbjct: 733 -TIDLYSQYELNANTQLFFAINNVTDYQVRPGSVVSMPPDGRITITLGF 781

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
 45 useful antigens for vaccines or diagnostics.

### Example 37

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 73> which encodes amino acid sequence  
 <SEQ ID 74; NGS37>. Analysis of this protein sequence reveals the following:

50 GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): 4.47  
 Possible cleavage site: 21  
 >>> Seems to have a cleavable N-term signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 22

55 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 7.21 threshold: 0.0  
 PERIPHERAL Likelihood = 7.21  
 modified ALOM score: -1.94

60 Score for OM-PP discrimination: 16.42  
 Rule: outer membrane or periplasmic protein  
 Score for OM-PP discrimination: 16.42  
 Rule: outer membrane or periplasmic protein

## \*\*\* Reasoning Step: 2

Outer membrane? Score: 1.64214  
Outer membrane? Score: 1.64214

## ----- Final Results -----

bacterial outer membrane --- Certainty= 0.938(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

>sp|Q03155|AIDA\_ECOLI ADHESIN AIDA-I. PRECURSOR  
pir|S28634 adhesin AIDA-I precursor - Escherichia coli plasmid pIB6  
emb|CAA46156.1| (X65022) AIDA-I [Escherichia coli]  
Length = 1286

Score = 35.8 bits (81), Expect = 0.67  
Identities = 34/138 (24%), Positives = 62/138 (44%), Gaps = 16/138 (11%)

Query: 3 ASQLTLAVLLAAAFGSAYAVEVKGDDSSKGQLIQAESDFLPFGSGAADIKVSTGNGLSK 62  
A L + + + G+A+AV + G SS G + + E+ + G G ++ V++G ++  
Sbjct: 31 AKNTLLVLAVVSTIGNAFVNISGTVSS-GGTVSSGETQIVYSGRGNSNATVNSGG--TQ 87

Query: 63 SINLEAGPAQRIRNKYGNAPINGGNQNTNVNGAANSRYLQPGDINPIA--GWFSKTRLA- 119  
+N N + G+QN +GA S + G I ++ G S T L+  
Sbjct: 88 IVNNGGKTTATTVN-----SSGSQNVGTSGATISTIVNSGGIQRVSSGGVASATNLSG 140

Query: 120 ---QVWYEKRANNTVEVFS 134  
++ A+NT +FS

Sbjct: 141 GAQNIYNLGHASNTVIFS 158

The protein was expressed in *E.coli* as an insoluble 32.45kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## Example 38

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 75> which encodes amino acid sequence <SEQ ID 76; NGS38>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
Signal Score (-7.5): 0.34  
Possible cleavage site: 24  
>>> Seems to have a cleavable N-term signal seq.  
Amino Acid Composition of Predicted Mature Form:  
calculated from 25  
ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 3.98 threshold: 0.0  
PERIPHERAL Likelihood = 3.98  
modified ALOM score: -1.30  
Score for OM-PP discrimination: 2.87  
Rule: outer membrane or periplasmic protein  
Score for OM-PP discrimination: 2.87  
Rule: outer membrane or periplasmic protein

## \*\*\* Reasoning Step: 2

Outer membrane? Score: 0.287446  
Outer membrane? Score: 0.287446

## ----- Final Results -----

bacterial outer membrane --- Certainty= 0.607(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

```

>sp|Q03155|AIDA_ECOLI ADHESIN AIDA-I PRECURSOR
5  pir||S28634 adhesin AIDA-I precursor - Escherichia coli plasmid pIB6
   emb|CAA46156.1| (X65022) AIDA-I [Escherichia coli]
      Length = 1286

   Score = 35.8 bits (81), Expect = 0.67
   Identities = 34/138 (24%), Positives = 62/138 (44%), Gaps = 16/138 (11%)
10
Query: 3  ASQLTLAVLLAAAFGSAYAVEVKGDDSSKGLIQAESDFLPFGSGAADIKVSTGNGLSK 62
      A   L + + + G+A+AV + G SS G + + E+ + G G ++ V++G ++
Sbjct: 31 AKNTLLVLAVVSTIGNAFVNISGTVSS-GGTVSSGETQIVYSGRGNSNATVNSGG--TQ 87

15
Query: 63 SINLEAGPAQRIRNKYGNAPINGGNQNTNVNGAANSRYLQPGDINPIA--GWFSKTRLA- 119
      +N      N      + G+QN +GA S + G I ++ G S T L+
Sbjct: 88 IVNNGGKTTATTVN-----SSGSQNVGTSGATISTIVNSGGIQRVSSGGVASATNLSG 140

20
Query: 120 ---QVWYEKRANNTTEVFS 134
      ++      A+NT +FS
Sbjct: 141 GAQNIYNLGHASNTVIFS 158

>pir||G81213 conserved hypothetical protein NMB0313 [imported] - Neisseria
25  meningitidis (group B strain MD58)
   gb|AAF40758.1| (AE002388) conserved hypothetical protein [Neisseria meningitidis
      MC58]
      Length = 488

   Score = 84.3 bits (207), Expect = 3e-15
   Identities = 111/498 (22%), Positives = 185/498 (36%), Gaps = 35/498 (7%)
30

Query: 7  LLFLPLCTVCLAAPSNDAADERRRLLEDEGSRQTQQYRESGW--LDTEQARGEVEENDGYI 64
      +L LPL      S   A+E R D SR + E+ +D E+ G+V E +
Sbjct: 19 MLLLPLLA-----SAAYAEETPREPDLRSRPEFRLHEAEVKPIDREKVPGQVREKGV 72

35
Query: 65 SIGGEIYQVGDTAEELESATYHALNARQWHKVRQFAARYAKLPRHKPALIHLADALQKRD 124
      I GE      E L A+Y A+ + +R Y + + L A + +
Sbjct: 73 QIDGETLL--KNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKMLALYAQGILAAQA 130

40
Query: 125 EGDFAAGNSPQTALAEAPDNPRLLLEAGRFYAEDNQNKESAAAFEKVLKTDIPAEIRPI 184
      +G + A + ++ + A+PD P + + E+ QN+ +A F+++ ++P +
Sbjct: 131 DGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAAADQFDRLEAENLPPQIMEQ 190

45
Query: 185 VENYLSELGKRRRWGQISLGYGYNNSNVNQNGINQCVWEIAGMCLMERTLPAPTDSTFS 244
      VE Y L +R W      N+NQ Q      + T P D T
Sbjct: 191 VELYRKALRERDAWKVNGGFSVTREHNINQAPKRQ-----YGKWTFPKQVDGTAV 241

Query: 245 SYSATAEKTIVPLKGNHGVQVRGVLYGNRYTEKDKDSAAMPDYGYRNGSLYAGYAYADARS 304
      +Y AEK LK      G + G Y K      +      + G +AD R
50  Sbjct: 242 NYRLGAEEKWLSLKNWYTTAGGDVSGRVYPGNKK-----FNDMTAGVSGGIGFADRRK 294

Query: 305 SFSLLPYFEYDFRNRHRYRAWGADADWSRTLSPHWRINSHAGAKKTGYGGQSKTYFADF 364
      L + E      + GA ++R +P W+ S A + G ++ +D
55  Sbjct: 295 DAGLAVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSA---EWGRLEKNTRRARSND 351

Query: 365 KQYELGAGAEFSITLKSGLLVNFDAARKAYP-EKSSSSKEYTARLGAYRLFSGGTYLNAV 423
      ++      F + + D R+ P ++ + Y R A+ GG+ L+++
Sbjct: 352 THLQISNSLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRF-AWGQEWGSGSLSSL 410

60
Query: 424 LLY--RRSLYDAASFVSDNK--RRRDKQYIMAAAGFPQWNIGVYPELRFRTTIAHSNA 479
      L + Y+ F S K RRRDK+ +      + KG+ P L SN
Sbjct: 411 LRLGAARKHYEKPGFSGFGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSDN 470

Query: 480 VYYRYRQNEWLLGFKYRF 497
65  V+ Y +N + F F
Sbjct: 471 VFNEYEKNRAFVEFNKTF 488

```

-66-

```

>pir|[C81790 conserved hypothetical protein NMA2174 [imported] - Neisseria
      meningitidis (group A strain Z2491)
emb|CAB85386.1| (AL162758) conserved hypothetical protein [Neisseria
meningitidis
5      Z2491]
      Length = 490

Score = 84.0 bits (206), Expect = 4e-15
Identities = 111/498 (22%), Positives = 185/498 (36%), Gaps = 35/498 (7%)

10 Query: 7 LLFLPLCTVCLAAPSNDAADERRRLLEDEGSRQTQQYRESGW--LDTEQARGEVEENDGYI 64
      +L LPL S A+E R D SR + E+ +D E+ G+V E +
Sbjct: 21 MLLLPLLA-----SAAYAETPREPDLRSRPEFRLHEAEVKPIDREKVPQGVRKGVKVL 74

15 Query: 65 SIGGEIYQVGDTAEELSAIYHALNARQWHKVRQFAARYAKLPRHKPALIHLADALQKRD 124
      I GE E L A+Y A+ + +R Y + + L A + +
Sbjct: 75 QIDGETLL--KNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQODKMLALYAQGILAQ 132

20 Query: 125 EGDFAAGNSFQTALEAEFPDNPRLILLEAGRFYAEDNQNKESAAAFKVLKTDIPAE TRPI 184
      +G + A + ++ + A+PD P + + E+ QN+ +A F+++ ++P +
Sbjct: 133 DGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRLKAENLPPQIMEQ 192

25 Query: 185 VENYLSELGKRRRWHGQISLGYGYNVNVQNGINGQCVWEIAGMCLMERTLPAPT DSTFS 244
      VE Y L +R W N+NQ Q + T P D T
Sbjct: 193 VELYRKALRERDAWKVNGGFSVTREHNINQAPKRQ-----YGKWTFPKQVDGTAV 243

30 Query: 245 SYSATAEKTVP LKGNHGVQVRGVLYGNRYTEKDKDSAAMPDYGYRNGSLYAGYAYADARS 304
      +Y AEK LK G + G Y K + + G +AD R
Sbjct: 244 NYRLGAEEKWSLKNGWYTTAGGDVSGRVYPGNKK-----FNDMTAGVSGGIGFADRRK 296

35 Query: 305 SFSLLPYFEYDFRNHRHXYRAWGADADWSRTLSPHWRINSHAGAKRTGYGGQSKTYFADF 364
      L + E + GA ++R +P W+ S A + G ++ +D
Sbjct: 297 DAGLAVFHERRYGNDAYSYTNGARLYFNRWQTPKWQTLSSA---EWGRLKNTRRARSND 353

40 Query: 365 KQYELGAGAEFSITLKSGLLVNFDAARKAYP-EKSSSSKEYTARLGAYRLFSGGTYLNAV 423
      ++ F + + D R+ P ++ + Y R A+ GG+ L+++
Sbjct: 354 THLQISNSLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRF-AWGQEWGGSGLSSL 412

45 Query: 424 LLY--RRSLYDAASFVSDNK--RRRDKQYIMAAAGFPQWNIGVYPELRFRTIAHSNA 479
      L + Y+ F S K RRRDK+ + + KG+ P L SN
Sbjct: 413 LRLGAAKRHYEKPGFFSGFGKERRRDKELNTSLSLWHRALHFKGITPRLTSLSHRETRSDN 472

Query: 480 VYRYRQNEWLLGFKYRF 497
      V+ Y +N + F F
Sbjct: 473 VFNEYEKNRAFVEFNKTF 490

```

The protein was expressed in *E.coli* as an insoluble 52.03kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## 50 Example 39

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 77> which encodes amino acid sequence <SEQ ID 78; NGS39>. Analysis of this protein sequence reveals the following:

```

GvH: Examining signal sequence (von Heijne)
Signal Score (-7.5): -5.38
Possible cleavage site: 18
>>> Seems to have no N-terminal signal seq.
Amino Acid Composition of Predicted Mature Form:
      calculated from 1
ALOM: Finding transmembrane regions (Klein et al.)
count: 0 value: 7.16 threshold: 0.0
PERIPHERAL Likelihood = 7.16

```

-67-

modified ALOM score: -1.93  
Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

5

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.325(Affirmative) < succ>

10 The protein has homology with the following sequences in the databases:

>ref|NP\_052685.1| serine protease EspP [Escherichia coli]  
pir|T00317 probable serine proteinase espP, extracellular - Escherichia coli  
plasmid pO157  
pir|T42120 probable serine proteinase espP, extracellular - Escherichia coli  
plasmid pO157  
15 emb|CAA66144.1| (X97542) putative exoprotein-precursor [Escherichia coli]  
dbj|BAA31836.1| (AB011549) serine protease EspP [Escherichia coli]  
gb|AAC70088.1| (AF074613) putative exoprotein-precursor [Escherichia coli  
0157:H7]  
20 Length = 1300

Score = 58.9 bits (141), Expect = 2e-07  
Identities = 153/687 (22%), Positives = 248/687 (35%), Gaps = 106/687 (15%)

25 Query: 194 DLTVENKNTLSDA---EFGVYALNTSMVNLSSKDNNEVKSTQVGLYSQDGGSSINVD--- 247  
D +NT +DA Y N ++ +LS D E + + G + +V R  
Sbjct: 595 DYVAGMQNTEADAVKQNGNAYKTNNNAVSDLSQPDW-ETGTFRFGTLHLENSDFSVGRNAN 653

30 Query: 248 -----KDNIEGDAVALVGKGGSONIRAS-----RTNLISSKSLGIHAEQAAKIAITG 295  
K NI GD A + +NI R N++ S G E IT  
Sbjct: 654 VIGDIQASKSNITIGDTTAYIDLHAGKNITGDFGFRQNIVRGNSQG---ETLFTGGGITA 710

35 Query: 296 ASNTIHASNAAIRSLDKSEVKIDQITIDSNVANLARQDGSIH---LNYKDDTRITGATV 352  
+TI + A ++ + TI+ N A++ Q G ++ + +TG  
Sbjct: 711 EDSTIVIKDKAKALFSNYVYLNTKATIE-NGADVTTQSGMFSTSDISISGNLSMTGNPD 769

40 Query: 353 SDKGLVAIKPLNNTNIVADTIHYKGDVLAVNKGKVELDF-----TPNILLAGRLDNFSGLT 408  
D LN+ + + + ++A NK V D + +I+ + S L+  
Sbjct: 770 KDNKFEPSTYLNDAASYLLTDDSAR--LVAKNKASVVDIHSSTKSASIMFGHDESLSQLS 827

45 Query: 409 DSKHKNLFENYVANLDSKSAGEINFNLAKDAL----WTMTGQSWLDKLEGQGTIDFNDA 464  
D K L + D G +N A + W +TG S L L+ ++ + D+  
Sbjct: 828 DRTSKGLALGLLGGFDVSYRGSVNAPSASATMNTTWQLTGDSALKTLKSTNSMVFYFTDS 887

50 Query: 465 KTSGR--ALHIGELAGANK-FLMHLNKDGIHSDMLYVKKGTSTPQEVVVKNLSEVLDSMN 521  
+ + L + ELA +N + M N SD L VKK S ++ L + L  
Sbjct: 888 ANNKKFHTLTVDLATSNSAYAMRTNLS--ESDKLEVKKHLSGENNIL---LVDPLQKPT 942

55 Query: 522 YGERLRFATVTNSKNEFVNGKKYIDDTHLMEDALTVEYSAHNGXXXXXXXXXXSFNGSEM 581  
++L V+ K+ N K T D V  
Sbjct: 943 PEKQLNIELVSAPKDTNENVFKASKQTIGFSDVTFV----- 978

60 Query: 582 TAEKAGDDYVNKTYTDNRQNVYLKQATGNPSRNVKNINDMFDSTAHYAFT--LDTYAKR 639  
+ DD + T++ N K+AT N + S + AF ++ KR  
Sbjct: 979 ITTRETDDKI--TWSLTGYNTVANKEATR NAAA-----LPSVDYKAPLNEVNNLNKR 1028.

65 Query: 640 EGERAFSTLDKKEGDWIRLTHTRVIQSNAPFRHNNDFEIGYDRFSLNEQEKRRKWGISLD 699  
G+ ++ + G W R+ S F + ++G D+ K G+ L  
Sbjct: 1029 MGD--LRDINGEAGAWARIMSGTGSASGGFSDNYTHVQVGVDR-----KHLDGLDLF 1079

70 Query: 700 YGHGRTSLWNTFGKD-----KIRKYELALYNTTQYIDKEGDETYIDNVLKIGKLRNRVIA 755  
G T ++ D K + LY + + D YID + K N A  
Sbjct: 1080 TGFTVTHTDSSASADVFSGKTKSVGAGLYASAMF-----DSGAYIDLIGKYVHHDNEYTA 1134

75 Query: 756 RNHMQQLWGKGKYSNTLFSISTEYGRRKFLDDDKLWRITPQVQLQYSYLRTGYRI-DNG 814  
G G YS + E G R + +D W I PQ +L Y + G + D G  
Sbjct: 1135 -TFAGL--GTRDYSTHSWYAGAEAGYRYHVTEDA-W-IEPQAEVLVYGSVSGKQFAWKDQG 1189

Query: 815 INVNLSHA--NSLIGRLGLDVVRKFDG 839  
 +++++ N LIGR G+DV + F G  
 Sbjct: 1190 MHL SMKDKDYNPLIGRTGVDVGKSFSG 1216

Score = 36.6 bits (83), Expect = 1.2  
 Identities = 97/412 (23%), Positives = 164/412 (39%), Gaps = 83/412 (20%)

Query: 63 DNIVTMKSGDADADYVNNNSKVLTTETPYYSKRGSGNGIFAYGDKSLVKLIGENNIVK--SE 120  
 D V G + ++ SK Y + +G + A+ S V + +N + +E  
 Sbjct: 163 DKFVVETRGATEGADISLSKQQALERYGVNYRGEKKLIAFRAGSGVVSVKKNRITPFNE 222

Query: 121 ISEKSKALNGGFRHIGIYS-W---QNAKVE---LSAKSDN-----IVQGG 158  
 +S K + LNG F HI +S W N + + +++++ D+ +V G  
 Sbjct: 223 VSYKPEMLNGSFVHIDDWSGWLILTNQFDEFNNIASQGDGSGSALFVYDNQKKRWVAGT 282

Query: 159 IWGLYS----NNSSISLKGKNNVISNPKNVFAKKAKVDLTVENKNTLSDAEFGVYALN 214  
 +WG+Y+ N + K I N K N ++Y VD++ T+ + + +  
 Sbjct: 283 VWGIYNYANGKNHAAYSKWNQTTIDNLK-NKYSY---NVDMSGAQVATIENGK--LTGTG 336

Query: 215 TSMVNLSSKDNNEVKSTQVGLYSQ----DGGSINVDKDNIEGDAVALVGKG----GS 265  
 + ++ +KD + L S GG + D+K + GD G G GS  
 Sbjct: 337 SDTTDIKNKDLIFTGGGDILLKSSFDNGAGGLVFNDRKTYRVNGDDFTFKGAGVDTRNGS 396

Query: 266 Q---NIR-ASRTNL--ISSKSLGIHAEQAAK-----IAITGASNTIHASNAAIRSLDKS 313  
 NIR ++ NL I +L + Q + I GA T +N I S D  
 Sbjct: 397 TVEWNIRYDNKDNLHKIGDGLTDRKTKTQNTNLKTGEGLVILGAETKTF--NNIYTSGD-G 453

Query: 314 EVKIDGQITIDSNVAN---LARQDGSIHNLN-YKDDTRITGATVSDRGLV-----AIK 361  
 V+++ + + N A+ G++ LN Y AT D G V +I  
 Sbjct: 454 TVRLNAENALSGGEYNGIFFAKNGGTLDLNGYNQSFNKIAAT--DSGAVITNTSTKKSIL 511

Query: 362 PLNNTNIVADTIHYKG-----DVLAVNKGKVELDFTPNILLAGRLDNFSGLT 408  
 LNNT AD I++ DVL ++ K E ++L G +D + ++  
 Sbjct: 512 SLNNT---ADYIYHGNGINGNLVDLQHETKKE---NRRLILDGGVDTTNDIS 557

The protein was expressed in *E.coli* as an insoluble 95.92kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 40

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 79> which encodes amino acid sequence <SEQ ID 80; NGS40>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)

Signal Score (-7.5): -4.18

Possible cleavage site: 17

>>> Seems to have no N-terminal signal seq.

Amino Acid Composition of Predicted Mature Form:  
 calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)

count: 0 value: 7.05 threshold: 0.0

PERIPHERAL Likelihood = 7.05

modified ALOM score: -1.91

Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.108(Affirmative) < succ>



The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 41

- 5 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 81> which encodes amino acid sequence <SEQ ID 82; NGS41>. Analysis of this protein sequence reveals the following:

```

    GvH: Examining signal sequence (von Heijne)
          Signal Score (-7.5): -2.47
          Possible cleavage site: 17
10  >>> May be a lipoprotein
      Amino Acid Composition of Predicted Mature Form:
          calculated from 16
      ALOM: Finding transmembrane regions (Klein et al.)
          count: 0 value: 7.37 threshold: 0.0
15  PERIPHERAL Likelihood = 7.37
          modified ALOM score: -1.97
      Rule: inner or outer membrane protein
      Rule: inner or outer membrane protein

20  *** Reasoning Step: 2

      Lipoprotein?
      Inner membrane?

25  ----- Final Results -----

          bacterial outer membrane --- Certainty= 0.790(Affirmative) < succ>

```

The protein has no homology sequences in the databases.

- 30 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 42

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 83> which encodes amino acid sequence <SEQ ID 84; NGS42>. Analysis of this protein sequence reveals the following:

```

35  GvH: Examining signal sequence (von Heijne)
          Signal Score (-7.5): -5.2
          Possible cleavage site: 14
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
40  calculated from 1
      ALOM: Finding transmembrane regions (Klein et al.)
          count: 0 value: 6.58 threshold: 0.0
          PERIPHERAL Likelihood = 6.58
          modified ALOM score: -1.82
45  Rule: cytoplasmic protein

      *** Reasoning Step: 2

      ----- Final Results -----

50  bacterial cytoplasm --- Certainty= 0.514(Affirmative) < succ>

```

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 43

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 85> which encodes amino acid sequence

5 <SEQ ID 86; NGS43>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -4.34  
 Possible cleavage site: 39  
 >>> Seems to have no N-terminal signal seq.  
 10 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 2 value: -4.78 threshold: 0.0  
 INTEGRAL Likelihood = -4.78 Transmembrane 1881 -1897 (1876 -1898)  
 15 INTEGRAL Likelihood = -1.01 Transmembrane 1966 -1982 (1966 -1982)  
 PERIPHERAL Likelihood = 1.91  
 modified ALOM score: 1.46  
 Rule: cytoplasmic membrane protein  
 20 \*\*\* Reasoning Step: 2  
 ----- Final Results -----

25 bacterial inner membrane --- Certainty= 0.291(Affirmative) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 44

30 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 87> which encodes amino acid sequence  
 <SEQ ID 88; NGS44>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -3.49  
 Possible cleavage site: 58  
 35 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 1 value: -1.33 threshold: 0.0  
 40 INTEGRAL Likelihood = -1.33 Transmembrane 141 - 157 ( 140 - 157)  
 PERIPHERAL Likelihood = 2.54  
 modified ALOM score: 0.77  
 Rule: cytoplasmic membrane protein  
 45 \*\*\* Reasoning Step: 2  
 ----- Final Results -----

50 bacterial inner membrane --- Certainty= 0.153(Affirmative) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## Example 45

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 89> which encodes amino acid sequence <SEQ ID 90; NGS45>. Analysis of this protein sequence reveals the following:

```

5  GvH: Examining signal sequence (von Heijne)
    Signal Score (-7.5): -4.07
    Possible cleavage site: 46
    >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
    calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
    count: 0 value: 2.07 threshold: 0.0
    PERIPHERAL Likelihood = 2.07
    modified ALOM score: -0.91
    Rule: cytoplasmic protein
15  *** Reasoning Step: 2
    ----- Final Results -----
20  bacterial cytoplasm --- Certainty= 0.333(Affirmative) < succ>

```

The protein has homology with the following sequences in the databases:

```

25  >ref|NP_049512.1| putative portal protein [Bacteriophage 933W]
    ref|NP_050550.1| hypothetical protein [Bacteriophage VT2-Sa]
    gb|AAD25457.1|AF125520_52 (AF125520) putative portal protein [Bacteriophage
    933W]
    dbj|BAA84334.1| (AP000363) hypothetical protein [Bacteriophage VT2-Sa]
    dbj|BAA94158.1| (AP000422) portal protein [Escherichia coli O157:H7]
    Length = 714
30  Score = 314 bits (805), Expect = 2e-84
    Identities = 213/658 (32%), Positives = 327/658 (49%), Gaps = 22/658 (3%)
35  Query: 7  ETGVLDPKNGEPLTIG----EYRLFVGEMMNQPAWRAVADKEMDYADGRQLDNELLQKQR 62
    ET + KN T + + ++ +QP WR A+K Y DG QL E+LQ +
    Sbjct: 4  ETNTMATKNDNGATPRFSQRQLQALCSDIDSQPKWRDAANKACAYYDGDQLPPEVLQVLK 63
40  Query: 63 ELGLPPAVENLITPTLLSVQGYEATIRTDWRVTADGETGGRD-VADALNFKLNRAERQSR 121
    + G P + NLI PT+ V G EA RTD V +D + +A+A+N + A R
    Sbjct: 64 DRGQPMTIHNLIAPTVDGVLGMEAKTRTDLVMSDEPDDETEKLAEAINAEFADACRLGN 123
45  Query: 122 ADKACSDAFRGQIACGIGWVEVTRNPNPFEPYECGVIHRNAIHWDMKSYKYDLSARWL 181
    +KA SDA+ QI G+ WVEV RN +PF ++ + RN + WD S + DLSD RWL
    Sbjct: 124 MNKARSDAYAEQIKAGLSWVEVRRNSDPFGPEFKVSTVSRNEVFWDLWSREADLSDCRWL 183
50  Query: 182 IRRRWLLPERLAQFFPEYAGHFKAMGRGGSDDR-ISGEMLDGGGNTGLADAWGISGRNTV 240
    +RRRW+ + FP G + + DWR + G + L AW
    Sbjct: 184 MRRRWMDTDEAKATFP---GMAQVIDYAIIDWRGFVDTTVTEGQPSPLMSAWEEYQSWDR 240
55  Query: 241 SEEFWFNETTRELAFAEVWYRRWVTADCLRDKKTGRITVEFDGANPNHREMAANGAV-LFA 299
    + W R + + V+YR + + + GR V FD N A+G V +
    Sbjct: 241 QQNEWLQRRRRVLLQVVYYRTFERLPVI-ELSNGRVVAFDKNLMMQAVAVASGRVQVKV 299
60  Query: 300 ASVPRMRRFAFVVDLVVRDEPTPYPHQKFFYPVFFGFREDNTGIPYGYVRNMKYAQDNLN 359
    V R+R A+ VG + D P P FP VPF+G+R+D TG PYG + AQD +N
    Sbjct: 300 GRVSRIREAWFVGPFFHIVDRPCSAPQGMFPLVPFVGYRKDKTGEPYGLISRAIPAQDEVN 359
    Query: 360 STNSKLRWGLSAIRTVRTKGIVDMSDEQFRNRIARVDADIVLNKIEAAQPGAR--FDVSR 417
    'KL W L A R + + +SD I R D I LN + Q F V +
    Sbjct: 360 FRIKLTWLLQAKRVIMDEDATQLSDNDLMEQIERPDGIIKLNPRKNQKSVADVFRVEQ 419
    Query: 418 DFELSAQHWQMLQDSRATIRQISGITPSFMGNRGNATSGRQESIQVEQSNQSLGLVMDNF 477
    DF++++Q +Q++Q+S I+ G+ +F+G ATSG S VEQ +L + DN+
    Sbjct: 420 DFQVASQQFQVMQSEKLIQDTMGVYSAFLQDQSGATSGVAISNLVEQGATTLAEINDNY 479

```

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Query: 478 RQSRSLVGEILLAMIETDLGS-DEQTVVIEGDAVTOGRTVVINRPETDPVTGKAYLSNDL 536  
 ++ VG LLLA +++DL VVI D + +T+V+N E D L+ND+  
 Sbjet: 480 QFACQQVGRLLLAYLLDDLKRRNHAVVINRDDRRQRTIVLN-AEGD----NGELTNDI 534

Query: 537 QNIRLKVALEDVPSTNSYRSQQLGAMSEAVKSLPPEYQAAVLPPMVSLMDIPFKDKVIEK 596  
 + +AL V T ++++Q MSE ++ LPP+ QA VL V+L+D+P K + +E+  
 Sbjet: 535 SRLNTHIALAFVQOTPAFKAQLAORMSEVIQGLPPQVQAVVLDLWVNLDDVPQKQEFVER 594

Query: 597 IK-EVRVQETPEQI--EARIAQAVQDALAKSGNDIKRRELALKEQRTASEIKEIEARA 651  
 I+ + ++P+++ E + A Q AL + +++ RE+A + + ++ A A  
 Sbjet: 595 IRAALGTPKSPDEMTPEEQEVAQQQALQQQARLQMRMAGRVAKLEADAARAHAAA 652

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
 useful antigens for vaccines or diagnostics.

#### Example 46

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 91> which encodes amino acid sequence  
 <SEQ ID 92; NGS46>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -3.25  
 Possible cleavage site: 37  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1

ALOM: Finding transmembrane regions (Klein et al.).  
 count: 0 value: 4.77 threshold: 0.0  
 PERIPHERAL Likelihood = 4.77  
 modified ALOM score: -1.45  
 Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.281(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

>sp|P44184|YE10\_HAEIN HYPOTHETICAL PROTEIN HI1410  
 pir||B64028 hypothetical protein HI1410 - Haemophilus influenzae (strain Rd  
 KW20)  
 gb|AAC23058.1| (U32820) H. influenzae predicted coding region HI1410  
 [Haemophilus  
 influenzae Rd]  
 Length = 394

Score = 150 bits (379), Expect = 3e-35  
 Identities = 75/168 (44%), Positives = 114/168 (67%), Gaps = 2/168 (1%)

Query: 57 REIQKSMRDSVHRLKDKVAQLGLGHFYBITDFEIRGANGTLFVFSGLQSHTVDSIKSFE 116  
 REIQKS+ DSV ++L D++ L L F+++ +I G NG+ F F+GL+++ + SIKS  
 Sbjet: 3 REIQKSISDSVIQMLADQIEMLSLQAFDVQKTQIIGQNGSRFTFAGLKTN-ITSIKSMT 61

Query: 117 GIDIVWVEEGHGVSKKSWDVLPTIRKEGSEIWIITLNPDMETDETYRRFIAMPSEDTWLC 176  
 GID+VWVEEG VSK+SWD+L PTIR++GS+I ++ NP D+TY+RF+ P E  
 Sbjet: 62 GIDVWVEEGENVSKESWDILIPTIREDSQIIVSFNPKNILDDTYQRFVIHPERCKSV 121

Query: 177 EINWRDNPWFPEALNRERLKAQRSMNKEDYGNIEWGRPRMVSEGA VYR 224  
 +NW+DNP+FP+ L E ++ R + E Y +++EG P S+ A+ +  
 Sbjet: 122 LVNWQDNPFYFKEL-MEDMEQMRERDYELYRHVYEGEPVADSDLAIIK 168

>ref|NP\_050979.1| P18 [Bacteriophage APSE-1]

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gb|AAF03961.1|AF157835\_18 (AF157835) P18 [Bacteriophage APSE-1]  
Length = 469

Score = 117 bits (294), Expect = 2e-25  
Identities = 72/233 (30%), Positives = 110/233 (46%), Gaps = 13/233 (5%)

Query: 17 LFKPCRYKVMYXXXXXXXXXXXXXXXXXXXXXQRPRLRLCAREIQKSMRDSVHRLKDKVA 76  
+FKP R KV + R LC RE S+ DS H +L+ +V  
Sbjct: 1 MFKPKRIKVYFGGRGGMKTVSPAKIALITASMHKRRFLCLREFMNSIEDSGHAVLQAEVE 60

Query: 77 QLGLGHFYEITDFEIRGANGTLFVFSGLQSHTVDSIKSFEGIDIVWVEBGHGVSKKSWDV 136  
LGL + + I + I G N ++F + L + + SIKS D+ WVEE VS+KS D  
Sbjct: 61 TLGLQNRFRILNTYIEGINDSIFKYGQL-ARNIASIKSKHDFDVAWVEEAETVSEKSLDS 119

Query: 137 LPTPTIRKEGSEIWTILNPDMDTETYRRFIA-----MPSEDTWLCEINWRDNPW 185  
L PTIRK GSE+W + NP E Y+RF+ +D ++ ++++ DNPW  
Sbjct: 120 LIPTIRKPGSELWFSFNPAEEDGAVYKRFVKPYKELIDTQGYIEDDLVVGKVSYLDPNPW 179

Query: 186 FPEALNRERLKAQRSMNKEDYGNIEWGRPRMVSEGAVYRHEIQDAFHSGRVTL 238  
P L + K +R N + + +++ G E A + + E +A + L  
Sbjct: 180 LPAELKNDQAQMKRE-NYKKWRHVYGGCEDANYEDALIQPEWVEAIDAHIKL 231

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### 25 Example 47

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 93> which encodes amino acid sequence <SEQ ID 94; NGS47>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
Signal Score (-7.5): -4.87  
Possible cleavage site: 31  
>>> Seems to have no N-terminal signal seq.  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 4.88 threshold: 0.0  
PERIPHERAL Likelihood = 4.88  
modified ALOM score: -1.48  
Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.313(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

>ref|NP\_037739.1| Gp54 [Bacteriophage HK97]  
gb|AAF31132.1| (AF069529) Gp54 [Bacteriophage HK97]  
Length = 273

Score = 47.4 bits (111), Expect = 3e-04  
Identities = 33/123 (26%), Positives = 52/123 (41%), Gaps = 20/123 (16%)

Query: 242 NGGLSGKPKNANVPRRRKTHGVPLQEIADLYNEVLGGRLPSVQVLNDTRKRAIANRWCEM 301  
NGG G+ K P RRK + + + YN +G RLP +N+ RKR + +  
Sbjct: 160 NGGGDGQVK----PERRKAERIDYESFLNAYNTEVGDRLPHAVAVNEKRRRL-KKIIPQ 214

Query: 302 LGTAAPNGKVRFGDKETGLAWFAGFFRKVA---MNPFFWMGENQTGFVAGFDWIFKAGNFVK 359  
L T +G F + R PF+ G+N TG+ FD++ + +  
Sbjct: 215 LKTPNVDG-----FRAYVRAVFHQAKPFYFGDNDTGWTADFDYLLREDSLTG 261

Query: 360 ILE 362  
 + E  
 Sbjct: 262 VRE 264

- 5 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 48

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 95> which encodes amino acid sequence <SEQ ID 96; NGS48>. Analysis of this protein sequence reveals the following:

10 GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -6.85  
 Possible cleavage site: 15  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 15 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 7.16 threshold: 0.0  
 PERIPHERAL Likelihood = 7.16  
 modified ALOM score: -1.93  
 20 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 ----- Final Results -----  
 25 bacterial cytoplasm --- Certainty= 0.379(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

30 >dbj|BAA36059.1| (D90754) Outer membrane protein P.69 precursor [Escherichia coli]  
 Length = 762  
 Score = 64.7 bits (156), Expect = 1e-09  
 Identities = 79/292 (27%), Positives = 121/292 (41%), Gaps = 55/292 (18%)  
 35 Query: 3 NGARWTVTND SMLKELDLSEDAQVEFSDNNK----FVKVSVSKLRGDDGVFKMYGDIV-- 56  
 N + W VT++S L L LS V+F+ + F ++V L G+ F M D+V  
 Sbjct: 289 NNSVWNVTNSNLDTLALSHST-VDFASHGSTAGTFATLNVENLSGNS-TFIMRADVVGE 346  
 40 Query: 57 ----KGESDKLITRKSGEGTHIEYMDDAKAKTTGREYLKLVENKGNQEDNKASNKASYK 112  
 + D L S G H++ + TTG E L +V+ D AS AS +  
 Sbjct: 347 GNGVNNKGDLLNISGSSAGNHVLAIRNQSEATTGNEVLTVVKTT----DGAASFSASSQ 402  
 45 Query: 113 LNVRC TEQGGWCFALGESG-----ASKKVNISTDGKRDF-----YLYPD----- 151  
 + E GG+ + + ++G AS V T + PD  
 Sbjct: 403 V-----ELGGYLYDVRKNGTNWELIASGTVPPEPTPNPEPTPAPAQPPIVNPDPPTPEPAPT 457  
 Query: 152 ----TLTPGASSSVLFGEALYQLNAVSDETLVQRMGEIHADGMPQEDNNVWIKRVGKFGSG 208  
 T T A + L Y LN V + TL+QRMG++ +D N+W++ GG  
 50 Sbjct: 458 PKPTTTADAGGNYL--NVGYLLNYVENRTLMQRMGDLRNQ---SKDGNIWLRSYGGSLS 512  
 Query: 209 SRSDYRVGGYGNRYWGFAGGFNRTGFGDKWIHYKGLMLRHLQSSYASEDYVG 260  
 S ++ G+ Y G G ++ D Y GL ++ S++AS DY G  
 55 Sbjct: 513 FASG-KLSGFDMGYSIGIQQFGGDKR-LSDVMPLYVGL---YIGSTHASPDYSG 559

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

**Example 49**

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 97> which encodes amino acid sequence <SEQ ID 98; NGS49>. Analysis of this protein sequence reveals the following:

```

5   GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -8.37
      Possible cleavage site: 15
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 4.93 threshold: 0.0
      PERIPHERAL Likelihood = 4.93
      modified ALOM score: -1.49
15  Rule: cytoplasmic protein

      *** Reasoning Step: 2

      ----- Final Results -----

20      bacterial cytoplasm --- Certainty= 0.355(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

25  The protein has homology with the following sequences in the databases:

      gi|11282647|pir||H81959 patch repair protein (EC 3.1.-.-) NMA0429 [imported] -
      Neisseria meningitidis (group A strain Z2491)
      gi|7379179|emb|CAB83728.1| (AL162753) patch repair protein [Neisseria
30  meningitidis Z2491]
      Length = 140

      Score = 256 bits (628), Expect = 8e-68
      Identities = 131/140 (93%), Positives = 132/140 (93%)

35  Query: 1 MTDIPTPSKRSSFVMSKIHSKETKPEVLVRKFLFSQGFRYRKNDKRYAGKPDIVLPKYKTV 60
      MTDIFT SKRSFVM KIHSKETKPEVLVRKFLF QGFRYRKNDKRY GKPDIVL KYKTV
      Sbjct: 1 MTDIFTTSKRSSFVMLKIHSKETKPEVLVRKFLFFQGFRYRKNDKRYVGKPDIVLSKYKTV 60

40  Query: 61 VFIHGCFWHGHCNKGHIKSNMDFWLEKITKNRERDIKNETELEKIGFKVIVVWECELK 120
      VFIHGCFW+GHSCNKGHIKPSN DFWLEKITKN ERDIKNETELEKIGFKVIVVWECELK
      Sbjct: 61 VFIHGCFWYGHCNKGHIKPSNTDFWLEKITKN CERDIKNETELEKIGFKVIVVWECELK 120

      Query: 121 NKAICRERLNRLVEEIKDAV 140
      NKAICRERLNRLV EIKDAV
45  Sbjct: 121 NKAICRERLNRLVREIKDAV 140

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

**Example 50**

50 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 99> which encodes amino acid sequence <SEQ ID 100; NGS50>. Analysis of this protein sequence reveals the following:

```

      GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -6.6
      Possible cleavage site: 50
55  >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
      ALOM: Finding transmembrane regions (Klein et al.)

```

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count: 0 value: 7.80 threshold: 0.0  
 PERIPHERAL Likelihood = 7.80  
 modified ALOM score: -2.06  
 Rule: cytoplasmic protein

5

\*\*\* Reasoning Step: 2

----- Final Results -----

10

bacterial cytoplasm --- Certainty= 0.398(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

15 The protein has homology with the following sequences in the databases:

>gi|11352963|pir|G81959 conserved hypothetical protein NMA0428 [imported] -  
 Neisseria meningitidis (group A strain Z2491)  
 gi|7379178|emb|CAB83727.1| (AL162753) conserved hypothetical protein [Neisseria  
 meningitidis  
 Z2491]  
 Length = 548

20

Score = 371 bits (954), Expect = e-102  
 Identities = 189/197 (95%), Positives = 194/197 (97%)

25

Query: 1 VKGESGVDIENWKNKLPEKEREPVEVILNRLEDSELTNKEQAEVISALHSIPEYPYHW 60  
 VKGESGVDIE+WKNKLPEKEREPVEVILNRLEDSELTNKEQAEVISALHSIPEYPYHW  
 Sbjct: 350 VKGESGVDIEDWKNKLPEKEREPVEVILNRLEDSELTNKEQAEVISALHSIPEYPYHW 409

30

Query: 61 RHLHQDLHTACNDFYNEKKDYLSAAIEAVKVFEDKVQKQTGLHSIDGRELIEKAFGSKKS 120  
 RHLHQDLHTACNDFYNEKKDYLSAAIEAVKVFEDKVQKQTGLHSIDGRELIE+AFGSK S  
 Sbjct: 410 RHLHQDLHTACNDFYNEKKDYLSAAIEAVKVFEDKVQKQTGLHSIDGRELIEQAFGSKNS 469

35

Query: 121 MLLLTTNNKTQAEQNLEDGLEQLACGTWTGFRNPVQHELRLANLSPSIFNDKDALDLISLVS 180  
 +LLLTTNNKT+AEQNLEDGLEQLACGTWTGFRNPVQHELRLANLSPSIFNDKDALDLISLVS  
 Sbjct: 470 ILLLTTNNKTQAEQNLEDGLEQLACGTWTGFRNPVQHELRLANLSPSIFNDKDALDLISLVS 529

40

Query: 181 YLLRKVEQTKKRAKPTS 197  
 YLLRKVEQTKKR+K S  
 Sbjct: 530 YLLRKVEQTKKRKVVVS 546

>gi|10955124|ref|NP\_059780.1| ymh [Agrobacterium tumefaciens]  
 gi|5738274|gb|AAB91582.2| (AF242881) ymh [Agrobacterium tumefaciens]  
 Length = 266

45

Score = 58.7 bits (141), Expect = 5e-08  
 Identities = 40/127 (31%), Positives = 69/127 (53%), Gaps = 5/127 (3%)

50

Query: 61 RHLHQDLHTACNDFYNEKKDYLSAAIEAVKVFEDKVQKQTGLHSIDGRELIEKAFGSKKS 120  
 R +H D+ C + +Y A +EAVK DK++++TGL + DG L+++AF  
 Sbjct: 137 RGVHPDVLRFCEEL-LVDNYFHAVLEAVKSVADKIRQRTGL-TDDGAVLVDRAFGSDAP 194

55

Query: 121 MLLLTTNNKTQAEQNLEDGLEQLACGTWTGFRNPVQHELRLANLSPSIFNDKDALDLISLVS 180  
 ML + ++++E+ + G L GT++ FRN H R + S +DA DL S+ S  
 Sbjct: 195 MLAINELQSESEKGEQGFNSNLVKGTFSMFRNTTAHAPRIHWQMS---KEDAEDLFSMFS 251

Query: 181 YLLRKVE 187  
 + R+++

60

Sbjct: 252 LMHRRID 258

As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS50 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.



## Example 51

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 101> which encodes amino acid sequence <SEQ ID 102; NGS51>. Analysis of this protein sequence reveals the following:

```

5   GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): 0.14
      Possible cleavage site: 42
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
          calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 5.67 threshold: 0.0
      PERIPHERAL Likelihood = 5.67
      modified ALOM score: -1.63
15  Rule: cytoplasmic protein

      *** Reasoning Step: 2

      ----- Final Results -----

20      bacterial cytoplasm --- Certainty= 0.145(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

25  The protein has homology with the following sequences in the databases:

      >pir||G81959 conserved hypothetical protein NMA0428 [imported] - Neisseria
          meningitidis (group A strain Z2491)
      emb|CAC83727.1| (AL162753) conserved hypothetical protein [Neisseria
          meningitidis
30      Z2491]
          Length = 548

      Score = 532 bits (1371), Expect = e-150
      Identities = 272/285 (95%), Positives = 280/285 (97%)

35  Query: 1 MSEEKLMSPFEPTVIEHLGVKMYSHSTVPAIAELIANAYDACATEVEVRLFDKPEHKIVIK 60
      MSEEKLMSPFEPTVIEHLGVKMYSHSTVPAIAELIANAYDACATEVEVRLFDKPEHKIVIK
      Sbjct: 1 MSEEKLMSPFEPTVIEHLGVKMYSHSTVPAIAELIANAYDACATEVEVRLFDKPEHKIVIK 60

40  Query: 61 DNGIGMSFDEINDFYLRIGRNRREEKQASPCGRIPTGKKGLGKLALFRLGNKIEISTIQG 120
      DNGIGMSFDEINDFYLRIGRNRREEKQASPCGRIPTGKKGLGKLALF LGNKIEISTIQG
      Sbjct: 61 DNGIGMSFDEINDFYLRIGRNRREEKQASPCGRIPTGKKGLGKLALFGLGNKIEISTIQG 120

45  Query: 121 NERVTFITLDYAEIKKSERIYQPEFQKESVKEPTENGTTITLTELTKKQGYPLDNYVGHLS 180
      NERVTFITLDYAEI++S+ IYQPEF+KESV+ N E+GTTITLTELTKKQGYPLDNYV HLS
      Sbjct: 121 NERVTFITLDYAEIRRSKGIYQPEFRKESVESNIESGTTITLTELTKKQGYPLDNYVEHLS 180

      Query: 181 RLFDFFPAQDFKIKVSLNGSEPRIIDGNLKYNLVTPQFEWEYQDLATNISSLSSKFEQY EY 240
      RLFDFFPAQDFKIKVSLNGSEP+IIDGNLKY+LVTPQFEWEYQDLATNISSLSSKFEQY EY
50  Sbjct: 181 RLFDFFPAQDFKIKVSLNGSEPKIIDGNLKYDLVTPQFEWEYQDLATNISSLSSKFEQY EY 240

      Query: 241 SGLIQGKFITTEKPLKNNMKGITLFANGRMVMNPEFFTDSESSH F 285
      SGLIQGKFITTEKPLKNNMKGITLFANGRMVMNPEFFTDSESSH F
      Sbjct: 241 SGLIQGKFITTEKPLKNNMKGITLFANGRMVMNPEFFTDSESSH F 285

55  >emb|CAC22276.1| (AJ302030) putative heat shock protein [Listeria monocytogenes]
      Length = 181

      Score = 70.2 bits (171), Expect = 2e-11
60  Identities = 57/173 (32%), Positives = 90/173 (51%), Gaps = 10/173 (5%)

      Query: 1 MSEEKLMSPFEPTVIEHLGVKMYSHSTVPAIAELIANAYDACATEVEVRLFDKPEHKIVIK 60
      MSE++ + +P ++E LG +Y++ + ELIANAYDA A V V E+K++++
      Sbjct: 1 MSEKEYNLDDIDPRILELLGPHLYTNIYYILGELIANAYDADAKNVYVIDRIDEENKLIVE 60

```

Query: 61 DNGIGMSFD--BINDFYLRIGRNRREEKQASPC---GRIPTGKKGLGKLALFRLGNKIEI 115  
 D+G GMS++ ++ +F L + + R S R G+KG+GKLA + + I  
 Sbjct: 61 DDGSGMSYENKDVKNF-LSVAKESRTNAINSYTKLNNRRKMGKRGVGLASLSVSENVNI 119

5

Query: 116 STIQGNERTVFTLDYABI-KKSERIYQPEFQKESVKPNTENGTTITLTTELTKK 167  
 TI+ E+ F L I KK E I + +K +GT I +T T K  
 Sbjct: 120 KTIKDGEKSGFVLSRKVINKKLEAINEDTISFIKIK---NHGTAIEMTNPTYK 169

- 10 As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS51 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 52

- 15 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 103> which encodes amino acid sequence <SEQ ID 104; NGS52>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -3.5  
 Possible cleavage site: 49  
 20 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 7.64 threshold: 0.0  
 25 PERIPHERAL Likelihood = 7.64  
 modified ALOM score: -2.03  
 Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

30 ----- Final Results -----

bacterial cytoplasm --- Certainty= 0.213(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 35 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

2.1.1.73) NMA0427 [imported] - Neisseria meningitidis (group A strain Z2491)  
 40 gi|7379177|emb|CAB83726.1| (AL162753) modification methylase (cytosine-specific  
 DNA methylase)  
 [Neisseria meningitidis Z2491]  
 Length = 351

Score = 310 bits (794), Expect = 8e-84  
 Identities = 152/154 (98%), Positives = 153/154 (98%)

Query: 1 LGMENGFPKIMAGHQDETDFMHSCAGLS DINLKRLALIPKNGGNRLAFAHIPELQLECFI 60  
 LGMENGFPKI+AGHQDETDFMHSCAGLS DINLKRLALIPKNGGNRLAFAHIPELQLECFI  
 50 Sbjct: 198 LGMENGFPKIIAGHQDETDFMHSCAGLS DINLKRLALIPKNGGNRLAFAHIPELQLECFI 257

Query: 61 GKDNSFKDTFGRLWWDKPAPTITTKFFSISNGRFAHPEEDRALSLREGATLQSFPRNYVF 120  
 GKDNSFKDTFGRLWWDKPAPTITTKFFSISNGRFAHPEEDRALSLREGATLQSFPRNYVF  
 Sbjct: 258 GKDNSFKDTFGRLWWDKPAPTITTKFFSISNGRFAHPEEDRALSLREGATLQSFPRNYVF 317

55

Query: 121 KAGSRDKIARLIGNAVPPMYTEKIGRAIVDNIEC 154  
 KAGSRDKIARLIGNAVPPMY EKIGRAIVDNIEC  
 Sbjct: 318 KAGSRDKIARLIGNAVPPMYAEKIGRAIVDNIEC 351

>gi|127441|sp|P25265|MTD2\_HERAU MODIFICATION METHYLASE HGIDII (CYTOSINE-SPECIFIC METHYLTRANSFERASE  
 HGIDII) (M.HGIDII)  
 gi|538661|pir|JT0594 site-specific DNA-methyltransferase (cytosine-specific)  
 5 (EC 2.1.1.73) - Herpetosiphon aurantiacus  
 gi|48773|emb|CAA38941.1| (X55141) methyltransferase [Herpetosiphon aurantiacus]  
 Length = 354

10 Score = 95.6 bits (237), Expect = 3e-19  
 Identities = 62/142 (43%), Positives = 82/142 (57%), Gaps = 9/142 (6%)

Query: 12 AGHQDETFDMHSCAGLS DINLKR LALIPKNGGNRLAFAHIP-ELQLECFIGKD-NSFKDT 69  
 +G E D MH+ + L DINL+R+ G +A P EL EC + S+  
 15 Sbjct: 200 SGGHWEGD SMHAASRL EDINLRR IQHSVPGG-----TWADWPEELIAECHKKESGESYGSV 255

Query: 70 FGRLWWDKPAPTITTTKFFSISNGRFAHPPEEDRALSLREGATLQSFPRNYVFKAGSRDK-- 127  
 +GR+ WDK APTITT+ NGRF HPE+DRA+SLRE A LQ+FPR+Y F + K  
 Sbjct: 256 YGRMEWDK VAPTITTTQCNGYGNRFGHPEQDRAISLREAALLQTFFRSYQFAPEGQLKFK 315

20 Query: 128 -IARLIGNAVPPMYTEKIGRAI 148  
 ++R IGNAV P I ++I  
 Sbjct: 316 TVSRQIGNAVPVALGRVIAKSI 337

- 25 As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS52 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 53

- 30 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 105> which encodes amino acid sequence <SEQ ID 106; NGS53>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (~7.5): -7.56  
 Possible cleavage site: 31  
 35 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 5.36 threshold: 0.0  
 40 PERIPHERAL Likelihood = 5.36  
 modified ALOM score: -1.57  
 Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

45 ----- Final Results -----

50 bacterial cytoplasm --- Certainty= 0.189(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

55 >gi|11256915|pir|F81959 site-specific DNA-methyltransferase (cytosine-specific)  
 (EC2.1.1.73) NMA0427 [imported] - Neisseria meningitidis (group A strain Z2491)  
 gi|7379177|emb|CAB83726.1| (AL162753) modification methylase (cytosine-specific  
 DNA methylase)  
 [Neisseria meningitidis Z2491]  
 Length = 351

Score = 247 bits (606), Expect = 5e-65  
Identities = 124/149 (83%), Positives = 127/149 (85%)

5 Query: 1 LQPETLEKELGLKKNDDDLILIGCSPCYWSVIQTDKRKSEKSKSLLEFQRFVEYFNPG 60  
LQPETLEKELGLKKNDDDLILIGCSPCYWSVIQTDKRKSEKSKSLLEFQRFVEYFNPG  
Sbjct: 59 LQPETLEKELGLKKNDDDLILIGCSPCYWSVIQTDKRKSEKSKSLLEFQRFVEYFNPG 118

10 Query: 61 YVVVENVPGILSRMKESGLDNFIKLLLEKGFTVHFHNTADYGIPQSRKRFTLIANRIT 120  
YVVVENVPGILSRMKES LDNFIKLLLEKGFTVHFHNTADYGIPQSRKRFTLIANRIT  
Sbjct: 119 YVVVENVPGILSRMKESRLDNFIKLLLEKGFTVHFHNTADYGIPQSRKRFTLIANRIT 178

Query: 121 KKSQSSIRANGLRYAMFWEWKTAPFKL 149  
K+ L + FPK+  
15 Sbjct: 179 KEKLEPVKYSKRLTVRDVLGMENGFPKI 207

>gi|127441|sp|P25265|MTD2\_HERAU MODIFICATION METHYLASE HGIDII (CYTOSINE-SPECIFIC  
METHYLTRANSFERASE  
20 gi|538661|pir|JT0594 site-specific DNA-methyltransferase (cytosine-specific)  
(EC  
2.1.1.73) - Herpetosiphon aurantiacus  
gi|48773|emb|CAA38941.1| (X55141) methyltransferase [Herpetosiphon aurantiacus]  
25 Length = 354

Score = 71.9 bits (169), Expect = 4e-12  
Identities = 39/105 (37%), Positives = 57/105 (54%), Gaps = 1/105 (0%)

30 Query: 12 LKKNDDDLILIGCSPCYWSVIQTDKRKSEKSKSLLEFQRFVEYFNPGYVVVENVPGIL 71  
L N+ IL+GC+PCQ +S T K ++ LL EF R + P + +ENVP +  
Sbjct: 64 LYPNNQHKILVGCAPCQDFSQY-TKKSRTGKTWQLLTFESRLIREIEPDIISMENVPEVR 122

Query: 72 SRMKESGLDNFIKLLLEKGFTVHFHNTADYGIPQSRKRFTLIA 116  
+ + +NFI+ LE+ G+ V + + DYGIQ R R L A  
35 Sbjct: 123 TFNRGVFNFIQSLEQLGYHVSHSVHCPDYGIPQQRDLVLFA 167

As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS53 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

40 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 54

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 107> which encodes amino acid sequence <SEQ ID 108; NGS54>. Analysis of this protein sequence reveals the following:

45 GvH: Examining signal sequence (von Heijne)  
Signal Score (-7.5): -6.82  
Possible cleavage site: 50  
>>> Seems to have no N-terminal signal seq.  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
50 ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 6.89 threshold: 0.0  
PERIPHERAL Likelihood = 6.89  
modified ALOM score: -1.88  
Rule: cytoplasmic protein

55 \*\*\* Reasoning Step: 2

----- Final Results -----

60 bacterial cytoplasm --- Certainty= 0.253(Affirmative) < succ>

-81-

bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

5 The protein has homology with the following sequences in the databases:

gi|1074456|pir||D64155 hypothetical protein HI0597 - Haemophilus influenzae  
 (strain Rd KW20)  
 gi|1573586|gb|AAC22254.1| (U32741) conserved hypothetical protein [Haemophilus  
 influenzae Rd]  
 10 Length = 272

Score = 188 bits (459), Expect = 2e-47  
 Identities = 95/100 (95%), Positives = 97/100 (97%)

15 Query: 1 MNLFFRAMVSDLG GTLLTPEHLVGDLTIDTLRLVLEQKGVDIILATGRNHTDMSSILGKIG 60  
 MNLFFRAMVSDL GTLLTPEHLVGDLTIDTLR LEQKGVDIILATGRNHTD+SSILGKIG  
 Sbjct: 1 MNLFFRAMVSDLDG TLLTPEHLVGDLTIDTLRALEQKGVDIILATGRNHTDVSSILGKIG 60

20 Query: 61 AERAVMITSNGARVRDLQGNLLYSNSLPEELVLELYKTSY 100  
 AERAVMITSNGARVRDLQGNLLYSNSLPEELVLELYKT +  
 Sbjct: 61 AERAVMITSNGARVRDLQGNLLYSNSLPEELVLELYKTPF 100

A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS54 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

25 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 55

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 109> which encodes amino acid sequence <SEQ ID 110; NGS55>. Analysis of this protein sequence reveals the following:

30 GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -4.46  
 Possible cleavage site: 37  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 35 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 3.02 threshold: 0.0  
 PERIPHERAL Likelihood = 3.02  
 modified ALOM score: -1.10  
 40 Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

----- Final Results -----

45 bacterial cytoplasm --- Certainty= 0.311(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

50 The protein has homology with the following sequences in the databases:

aeruginosa (strain PAO1)  
 gi|9948791|gb|AAG06104.1|AE004699\_9 (AE004699) probable FMN oxidoreductase  
 [Pseudomonas aeruginosa]  
 55 Length = 411

Score = 279 bits (686), Expect = 2e-74  
 Identities = 157/375 (41%), Positives = 228/375 (59%), Gaps = 10/375 (2%)

Query: 1 MEEQLAQNDQ-PSEKLVRLYGAWAEGGAGVLVTGNVMVAESGKGSINDVLISDDRALEML 59  
 MEE +A Q PSE+L+RLY AWA+GGAG+L++GNVMV V++ DD LE  
 Sbjct: 24 MEENMADAAQAPSERLMRLYQAWADGGAGLLISGNVMVDSRAMTGPGGVLEDDAQLEKF 83

5 Query: 60 KKWAKARTQNDTLLIMQINHAGKQSPAVVNKTPLAPSAVPLV--GMNGFINPPRELSADE 117  
 ++WA+ +QINH G+Q A + + APSAVPL GM+ P+ +  
 Sbjct: 84 RRWARIGRSAGAQFWLQINHPGRQMQLNGQQAOWAPSAVPLELGGMSRHFATPKAMDEAM 143

10 Query: 118 INGLIQQFVQTAKIAEQAGFSGVQIYAVHGYLISQFLSPHHNRRQDQWGGSGLENRMRFIL 177  
 I +IQ+F ++A +AE+AGFSGV+I+A HGYL+SQFLSP NRR D WGGSGLENR R LL  
 Sbjct: 144 IAEVIQRFARSAGLAERAGFSGVEIHAAHGYLLSQFLSPLSNRRSDAWGGSGLENRRARLLL 203

15 Query: 178 ETYTAIRAAAGKDFLVGVKLNSADFOKGGFDESESVQVVQKLEMGIDFIEVSGGNYESP 237  
 E A+RA F V VKLNSADFO+GGF ++ +VV+ L +G+D +E+SGG+YE+P  
 Sbjct: 204 EIVRAVRAEVAPGFAVAVKLNSADFOKGGFSADDAREVVRMLDGLGVDLVELSGGSYEAP 263

20 Query: 238 QMLA-AKDS-TRKREAFFIDYAEKARAASQAPLIITGGFRSQTAMEDALSSGHLDLVGIA 295  
 M A+D T REA+F+++A RAA++ P+++TGG R + E L+SG +D+VGI  
 Sbjct: 264 AMQGEARDGRTLAREAYFVEFARDIRAAARMPVMVTGGIRRRPVAEQVLASG-VDMVGIG 322

25 Query: 296 RPFALVPDLANKMQNRTYQTVQADRIQTGVAFVDKKAGAMLEMNWYMTQMDLIGQKQSN 355  
 A+ P+L + Q I + +K ++ M Q+ + +G+ +N  
 Sbjct: 323 TALAIEPNLPRDWRAGKDSAPQLRPI-----TWRNKPLASLANMAAVKFLRLKLSRGRATN 378

Query: 356 PRIVGVESIAENFAG 370  
 P++ + ++ AG  
 Sbjct: 379 PRVSPLCALLAQAG 393

30 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 56

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 111> which encodes amino acid sequence <SEQ ID 1:12; NGS56>. Analysis of this protein sequence reveals the following:

35 GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -4.69  
 Possible cleavage site: 54  
 >>> Seems to have an uncleavable N-term signal seq  
 Amino Acid Composition of Predicted Mature Form:  
 40 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 4.29 threshold: 0.0  
 PERIPHERAL Likelihood = 4.29  
 modified ALOM score: -1.36

45 \*\*\* Reasoning Step: 2

----- Final Results -----

50 bacterial inner membrane --- Certainty= 0.042(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

55 The protein has homology with the following sequences in the databases:

>gi|7444004|pir||D70029 transcription regulator ArsR family homolog yvba -  
 Bacillus subtilis  
 gi|2635892|emb|CAB15384.1| (Z99121) similar to transcriptional regulator (ArsR  
 60 family)  
 [Bacillus subtilis]

Length = 90

Score = 51.3 bits (118), Expect = 3e-06  
Identities = 24/65 (36%), Positives = 42/65 (63%), Gaps = 1/65 (1%)

5

Query: 15 IFTVLSDENRHQILHVLWKHGRMNVNELTEHLHLSRPAVSHHLKIMLQAGAVAVEQVGKE 74  
+F +SD R +IL +L K G M ++ EH ++S+P++SHHL I+ QA ++ + G+  
Sbjct: 4 VFKAISDPTRRKILDLL-KGGDMTAGDIAEHFNISKPSISHHLNILKQAEVISDHRKQGF 62

10

Query: 75 RFYSI 79  
+YS+  
Sbjct: 63 IYYSI 67

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 57

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 113> which encodes amino acid sequence <SEQ ID 114; NGS57>. Analysis of this protein sequence reveals the following:

20 GvH: Examining signal sequence (von Heijne)  
Signal Score (-7.5): -2.57  
Possible cleavage site: 55  
>>> Seems to have no N-terminal signal seq.  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
25 ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 5.67 threshold: 0.0  
PERIPHERAL Likelihood = 5.67  
modified ALOM score: -1.63  
Rule: cytoplasmic protein  
30 \*\*\* Reasoning Step: 2  
----- Final Results -----  
35 bacterial cytoplasm --- Certainty= 0.160(Affirmative) < succ>  
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

40 The protein has homology with the following sequences in the databases:

>gi|10444407|gb|AAG17897.1|AF297971\_1 (AF297971) restriction endonuclease  
R.NgoMIII [Neisseria gonorrhoeae]  
Length = 213

45 Score = 319 bits (818), Expect = 1e-86  
Identities = 156/156 (100%), Positives = 156/156 (100%)

Query: 1 LYKQYADWNRLSYNAPIYVGKAVPGWRQARNSDNALNQSTELFHRLKEHSRSIAAVSDL 60  
LYKQYADWNRLSYNAPIYVGKAVPGWRQARNSDNALNQSTELFHRLKEHSRSIAAVSDL  
50 Sbjct: 58 LYKQYADWNRLSYNAPIYVGKAVPGWRQARNSDNALNQSTELFHRLKEHSRSIAAVSDL 117  
Query: 61 DPSPDFMCRFVIFEGAGSDMIGTIEAALIKLHKPLWNNSCVDGFGNHDPGKGRYEQAQSDWD 120  
DPSPDFMCRFVIFEGAGSDMIGTIEAALIKLHKPLWNNSCVDGFGNHDPGKGRYEQAQSDWD  
Sbjct: 118 DPSPDFMCRFVIFEGAGSDMIGTIEAALIKLHKPLWNNSCVDGFGNHDPGKGRYEQAQSDWD 177  
55 Query: 121 VLHSGRVWADRLNGIPNSYESILENINTHLEIKRK 156  
VLHSGRVWADRLNGIPNSYESILENINTHLEIKRK  
Sbjct: 178 VLHSGRVWADRLNGIPNSYESILENINTHLEIKRK 213

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 58

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 115> which encodes amino acid sequence <SEQ ID 116; NGS58>. Analysis of this protein sequence reveals the following:

5 GvH: Examining signal sequence (von Heijne)  
Signal Score (-7.5): -1.92  
Possible cleavage site: 16  
>>> Seems to have no N-terminal signal seq.  
10 Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 5.41 threshold: 0.0  
PERIPHERAL Likelihood = 5.41  
15 modified ALOM score: -1.58  
Rule: cytoplasmic protein  
\*\*\* Reasoning Step: 2  
20 ----- Final Results -----  
bacterial cytoplasm --- Certainty= 0.107(Affirmative) < succ>  
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
25 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

30 >gi|10444408|gb|AAG17898.1|AF297971\_2 (AF297971) DNA cytosine methyltransferase  
M.NgoMIII [Neisseria gonorrhoeae]  
Length = 377  
Score = 759 bits (1960), Expect = 0.0  
Identities = 377/377 (100%), Positives = 377/377 (100%)  
35 Query: 1 MKSLEIFSGAGGLAKGLELAGFQHASFIELNKDACNSLRSNFNPKLVIYQGDVADFDLSSQ 60  
MKSLEIFSGAGGLAKGLELAGFQHASFIELNKDACNSLRSNFNPKLVIYQGDVADFDLSSQ  
Sbjct: 1 MKSLEIFSGAGGLAKGLELAGFQHASFIELNKDACNSLRSNFNPKLVIYQGDVADFDLSSQ 60  
40 Query: 61 EGIEVIAGGPPCQPFSLGGKHLAHDERRDMFPHAVRYVEYYRPAKIFENVKGLLRKSFA 120  
EGIEVIAGGPPCQPFSLGGKHLAHDERRDMFPHAVRYVEYYRPAKIFENVKGLLRKSFA  
Sbjct: 61 EGIEVIAGGPPCQPFSLGGKHLAHDERRDMFPHAVRYVEYYRPAKIFENVKGLLRKSFA 120  
45 Query: 121 DYFEYILLRLTYPNLGILQNEWDKGHLTRLKEIEFNLYKGIKYKVSQLLNAADYGVPOK 180  
DYFEYILLRLTYPNLGILQNEWDKGHLTRLKEIEFNLYKGIKYKVSQLLNAADYGVPOK  
Sbjct: 121 DYFEYILLRLTYPNLGILQNEWDKGHLTRLKEIEFNLYKGIKYKVSQLLNAADYGVPOK 180  
50 Query: 181 RERVVIVGIRADLDIDWKFPKRTHSEDRLNWEKYVTGEYWEKHNEPKRFNKDIAEKLQKK 240  
RERVVIVGIRADLDIDWKFPKRTHSEDRLNWEKYVTGEYWEKHNEPKRFNKDIAEKLQKK  
Sbjct: 181 RERVVIVGIRADLDIDWKFPKRTHSEDRLNWEKYVTGEYWEKHNEPKRFNKDIAEKLQKK 240  
55 Query: 241 YGIFEPEKKPWQTVRDTLSDIPHLGNHKITGHEYRDGARIYPGHTGSGIDEPSKTIKAG 300  
YGIFEPEKKPWQTVRDTLSDIPHLGNHKITGHEYRDGARIYPGHTGSGIDEPSKTIKAG  
Sbjct: 241 YGIFEPEKKPWQTVRDTLSDIPHLGNHKITGHEYRDGARIYPGHTGSGIDEPSKTIKAG 300  
60 Query: 301 GHGVPGENMIRYDDGTVRYFTSYEAKLLQTFPEEFVISGAWGEAMRQIGNAVPVKLSEI 360  
GHGVPGENMIRYDDGTVRYFTSYEAKLLQTFPEEFVISGAWGEAMRQIGNAVPVKLSEI  
Sbjct: 301 GHGVPGENMIRYDDGTVRYFTSYEAKLLQTFPEEFVISGAWGEAMRQIGNAVPVKLSEI 360  
Query: 361 LGKHLMGVLSEKSSLHN 377  
LGKHLMGVLSEKSSLHN  
Sbjct: 361 LGKHLMGVLSEKSSLHN 377



Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 59

- 5 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 117> which encodes amino acid sequence <SEQ ID 118; NGS59>. Analysis of this protein sequence reveals the following:

```

    GvH: Examining signal sequence (von Heijne)
          Signal Score (-7.5): -3.82
          Possible cleavage site: 60
10  >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
          calculated from 1
    ALOM: Finding transmembrane regions (Klein et al.)
          count: 0 value: 2.86 threshold: 0.0
15  PERIPHERAL Likelihood = 2.86
          modified ALOM score: -1.07
    Rule: cytoplasmic protein

    *** Reasoning Step: 2

20  ----- Final Results -----

          bacterial cytoplasm --- Certainty= 0.197(Affirmative) < succ>
25  bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
          bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
          bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

30  >gi|11353338|pir|F81882 hypothetical protein NMA1155 [imported] - Neisseria
    meningitidis
          (group A strain Z2491)
    gi|7379848|emb|CAB84417.1| (AL162755) hypothetical protein NMA1155 [Neisseria
    meningitidis
35  Z2491]
    Length = 120

    Score = 131 bits (329), Expect = 2e-30
    Identities = 64/68 (94%), Positives = 67/68 (98%)

40  Query: 1 LSDISASRAAYMDVQKQYPFETVAVCVLPNHIHAIWTLPPDDADYSLRRRLIKTKFSAYS 60
    +S+ISASRAAYMDVQKQYPFETVAVCVLPNHIHAIWTLPPDDADYSLRRRLIKTKFSAYS
    Sbjct: 1 MSNISASRAAYMDVQKQYPFETVAVCVLPNHIHAIWTLPPDDADYSLRRRLIKTKFSAYS 60

    Query: 61 PHTKNLGA 68
45  P+TKNL A
    Sbjct: 61 PYTKNLSA 68

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### 50 Example 60

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 119> which encodes amino acid sequence <SEQ ID 120; NGS60>. Analysis of this protein sequence reveals the following:

```

55  GvH: Examining signal sequence (von Heijne)
          Signal Score (-7.5): -3.14
          Possible cleavage site: 16

```

-86-

>>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
     calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
     count: 0 value: 2.76 threshold: 0.0  
     PERIPHERAL Likelihood = 2.76  
     modified ALOM score: -1.05  
 Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.330(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

>gi|11281269|pir||D81804 hypothetical protein NMA1789 [imported] - Neisseria  
 meningitidis (group A strain Z2491)  
 gi|7380430|emb|CAB85016.1| (AL162757) hypothetical protein [Neisseria  
 meningitidis Z2491]  
     Length = 243

Score = 154 bits (389), Expect = 5e-37  
 Identities = 82/85 (96%), Positives = 82/85 (96%)

Query: 12 MNTKTELQKLL EEDISTLKETLIRVDALPPRYVRSIATPIVRRWLIDKQLNILAKEIGLT 71  
           MNTKTELQKLL EEDISTL ETLI DALPPRYVRSIATPIVRRWLIDKQLNILAKEIGLT  
 Sbjct: 1 MNTKTELQKLL EEDISTLTETLICADALPPRYVRSIATPIVRRWLIDKQLNILAKEIGLT 60

Query: 72 IELPILDTSLVFEKLS TLENKVN FY 96  
           IELPILDTSLVFEKLS TLENKVN FY

Sbjct: 61 IELPILDTSLVFEKLS TLENKVN FY 85

As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS60 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 61

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 121> which encodes amino acid sequence <SEQ ID 122; NGS61>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
     Signal Score (-7.5): -6.88  
     Possible cleavage site: 32

>>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
     calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)  
     count: 0 value: 5.52 threshold: 0.0  
     PERIPHERAL Likelihood = 5.52  
     modified ALOM score: -1.60  
 Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

----- Final Results -----

-87-

bacterial cytoplasm --- Certainty= 0.300(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

5

The protein has homology with the following sequences in the databases:

>gi|11281269|pir||D81804 hypothetical protein NMA1789 [imported] - Neisseria  
 meningitidis (group A strain Z2491)  
 gi|7380430|emb|CAB85016.1| (AL162757) hypothetical protein [Neisseria  
 meningitidis Z2491]  
 Length = 243

Score = 193 bits (491), Expect = 5e-49  
 Identities = 96/101 (95%), Positives = 97/101 (95%)

Query: 1 MAGGVYLGGKIISPIYHSSQEFSGEPIIYAETNIILCPAEKFLTLKRVFHNGNIFNMNQI 60  
 MAGGVYLGG+ IS IYHSSQEFSGEPIIYAE NIILCPAEKFLTLKRVFHNGNIFNMNQI  
 Sbjct: 86 MAGGVYLGGEFISSIYHSSQEFSGEPIIYAEPNIILCPAEKFLTLKRVFHNGNIFNMNQI 145

Query: 61 ITFLSNKQGGVRFDKNYDKYKTWQVAIEKAANFLKLGPNYN 101  
 ITFLSNKQGGV FDKNYDKYKTWQVAIEKAANFLKLGPNYN  
 Sbjct: 146 ITFLSNKQGGVHFDKNYDKYKTWQVAIEKAANFLKLGPNYN 186)

15

20

25

As a homolog (amino acids 1-96) was found in serogroup A *N.meningitidis* but not in serogroup B,  
 NGS61 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B  
*N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
 useful antigens for vaccines or diagnostics.

#### Example 62

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 123> which encodes amino acid sequence  
 <SEQ ID 124; NGS62>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -2.43  
 Possible cleavage site: 44  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 4.72 threshold: 0.0  
 PERIPHERAL Likelihood = 4.72  
 modified ALOM score: -1.44  
 Rule: cytoplasmic protein

35

40

45

\*\*\* Reasoning Step: 2

----- Final Results -----

50

bacterial cytoplasm --- Certainty= 0.324(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS62 protein and  
 nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 63

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 125> which encodes amino acid sequence <SEQ ID 126; NGS63>. Analysis of this protein sequence reveals the following:

```

5  GvH: Examining signal sequence (von Heijne)
    Signal Score (-7.5): 0.74
    Possible cleavage site: 24
10 >>> Seems to have a cleavable N-term signal seq.
    Amino Acid Composition of Predicted Mature Form:
        calculated from 25
    ALOM: Finding transmembrane regions (Klein et al.)
        count: 0 value: 10.72 threshold: 0.0
        PERIPHERAL Likelihood = 10.72
15 modified ALOM score: -2.64
    Score for OM-PP discrimination: -22.14
    Rule: outer membrane or periplasmic protein
    Score for OM-PP discrimination: -22.14
    Rule: outer membrane or periplasmic protein
20 *** Reasoning Step: 2

    Periplasmic space? Score: 2.21378
    Periplasmic space? Score: 2.21378
25 ----- Final Results -----

        bacterial periplasmic space --- Certainty= 0.931(Affirmative) < succ>
        bacterial outer membrane --- Certainty= 0.237(Affirmative) < succ>
30        bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>
        bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

35 >gi|11284146|pir||B81142 hypothetical protein NMB0912 [imported] - Neisseria
    meningitidis
        (group B strain MD58)
    gi|7226150|gb|AAF41320.1| (AE002443) hypothetical protein [Neisseria
    meningitidis MC58]
        Length = 208
40
    Score = 51.7 bits (119), Expect = 3e-06
    Identities = 30/72 (41%), Positives = 40/72 (54%)

45 Query: 5 LLKNWKPLLILSAIAFFAVSWQLDRAAQYRRGYGAAVSEVSERLKAAAVEHAEHARKSSA 64
    LLK WKP+ +L I +W DRA +YR G AA +E+S RLK +E A+ AR +
    Sbjct: 43 LLKYWKFPVGVLLLIIVLIFTAWHFDRAEKYRMGREAAAAEISNRLKDGYTEQAKQARSABQ 102

    Query: 65 AYQAQKAAREEK 76
        A A R+ K
50 Sbjct: 103 KAAAFERQTK 114

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 64

55 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 127> which encodes amino acid sequence <SEQ ID 128; NGS64>. Analysis of this protein sequence reveals the following:

-89-

McG: Examining signal sequence (McGeoch)  
 Length of UR: 0  
 Peak Value of UR: 2.99  
 Net Charge of CR: 4  
 5 Discriminant Score: 5.35  
 GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -2.53  
 Possible cleavage site: 33  
 >>> Seems to have an uncleavable N-term signal seq  
 10 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 3.23 threshold: 0.0  
 PERIPHERAL Likelihood = 3.23  
 15 modified ALOM score: -1.15  
 \*\*\* Reasoning Step: 2  
 ----- Final Results -----  
 20 bacterial inner membrane --- Certainty= 0.054(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 25 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 65

30 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 129> which encodes amino acid sequence <SEQ ID 130; NGS65>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -5.61  
 Possible cleavage site: 61  
 35 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 3.34 threshold: 0.0  
 40 PERIPHERAL Likelihood = 3.34  
 modified ALOM score: -1.17  
 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 45 ----- Final Results -----  
 bacterial cytoplasm --- Certainty= 0.236(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 50 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

>gi|1175791|sp|P44189|YE18\_HABIN HYPOTHETICAL PROTEIN HI1418  
 55 gi|1074769|pir|A64029 hypothetical protein HI1418 - Haemophilus influenzae  
 (strain Rd  
 KW20)  
 gi|1574254|gb|AAC23068.1| (U32821) H. influenzae predicted coding region HI1418  
 [Haemophilus  
 60 influenzae Rd]

Length = 201

Score = 104 bits (251), Expect = 1e-21

Identities = 58/119 (48%), Positives = 72/119 (59%), Gaps = 4/119 (3%)

5

Query: 51 LKMONTISVFSFKSQNVRTQI-LGAEFPWFCLGDVAEILQIQNAR---QLPLKDQGIQKSS 106  
+K Q S F+FK VR + E WFC DV IL N+R Q K G+ K  
Sbjct: 14 MKNQIQFSTFNFKDLPVRVILDPKGEFWFCGTDVCHILGYTNSRKALQDHCKQGGVTKRY 73

10

Query: 107 VATKKGNQELLFINEPNLYRVIFRSRKAEAVKFQDWIFEVVPQIRKTGGYQITPKTTA 165  
TK +QE+ FINEPNLYR+I +SRK EA F+ W+FEV+PQIRKTG YQ+ P+ A  
Sbjct: 74 TPTKSADQEMTFINEPNLYRLIIKSRKPEABPFEAWVFEVLPQIRKTGKYQLQPQOLA 132

15

>gi|11281012|pir||A81144 hypothetical protein NMB0900. [imported] - *Neisseria meningitidis*

(group B strain MD58)

gi|7226137|gb|AAF41308.1| (AB002442) hypothetical protein [*Neisseria meningitidis* MC58]

Length = 305

20

Score = 104 bits (249), Expect = 2e-21

Identities = 73/137 (53%), Positives = 93/137 (67%), Gaps = 2/137 (1%)

25

Query: 190 YSMIHQRFNVEAVEGIPADKLEAVAYVHALTLHTG-LAGEVPDREPLPAPQPALPISGN 248  
+S + +F E +PA++ PE ++ + + + G L GEV DREPLPAPQPALPISGN  
Sbjct: 164 WSAVKSFKGCSYKE-VPAEQFPEVLSVMGRVAVENGVLVYGEVLDREPLPAPQPALPISGN 222

30

Query: 249 ALADIAAMVYYGTRMIELGKDVSAPLKQLGCKQAVTMWTVWHETRSILKRSVAALVLRG 308  
AL D+A V YG I++G+DVS PLKQLGCKQAVTMWTVW ETRS LK + ALE L  
Sbjct: 223 ALYDLAVAVRYGAWAIQMGRLVSLPLKQLGCKQAVTMWTVWAEATRSRLKAAANALEALNA 282

35

Query: 309 YADKDASGRIACLEGI 325

+AD + + +I L I

Sbjct: 283 HADARHAAKIRPMLPEI 299

>gi|7460273|pir||T13267 hypothetical protein - *Lactococcus lactis* phage BK5-T

gi|928839|gb|AAA98590.1| (L44593) ORF266; putative [*Lactococcus* phage BK5-T]

Length = 266

40

Score = 75.9 bits (179), Expect = 6e-13

Identities = 42/111 (37%), Positives = 63/111 (55%), Gaps = 3/111 (2%)

45

Query: 55 NTISVFSFKSQNVRTQILGAEFPWFCLGDVAEILQIQNAR---QLPLKDQGIQKSSVATKK 111  
N + F+F + VRT ++ EPWF DVA + +N R + +KD+ ++S + T

Sbjct: 2 NELQNFNFNNLPVRTVLINDEPWFVGKDVAIAIGYKNFRDALKSHVKDKYKRESRITTPS 61

50

Query: 112 GNQELLFINEPNLYRVIFRSRKAEAVKFQDWIFEVVPQIRKTGGYQITPK 162

G Q + I+EP LY++ S+ A FQDW++EEV+P IRK G Y K

Sbjct: 62 GVQSVTVISEPGLYQLAGESKLPSAEPFQDWVYEEVLPITRKHGAYMTDAK 112

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 66

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 131> which encodes amino acid sequence <SEQ ID 132; NGS66>. Analysis of this protein sequence reveals the following:

55

GvH: Examining signal sequence (von Heijne)

Signal Score (-7.5): -3.12

Possible cleavage site: 53

>>> Seems to have no N-terminal signal seq.

60

Amino Acid Composition of Predicted Mature Form:

calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)

count: 0 value: 8.96 threshold: 0.0  
 PERIPHERAL Likelihood = 8.96  
 modified ALOM score: -2.29  
 Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.402(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 67

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 133> which encodes amino acid sequence <SEQ ID 134; NGS67>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): 5.71  
 Possible cleavage site: 22  
 >>> Seems to have a cleavable N-term signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 23  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 2.81 threshold: 0.0  
 PERIPHERAL Likelihood = 2.81  
 modified ALOM score: -1.06  
 Score for OM-PP discrimination: -32.34  
 Rule: outer membrane or periplasmic protein  
 Score for OM-PP discrimination: -32.34  
 Rule: outer membrane or periplasmic protein

\*\*\* Reasoning Step: 2

Periplasmic space? Score: 3.23391  
 Periplasmic space? Score: 3.23391

----- Final Results -----

bacterial periplasmic space --- Certainty= 0.928(Affirmative) < succ>  
 bacterial outer membrane --- Certainty= 0.199(Affirmative) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

>gi|7475078|pir|H69834 hypothetical protein yhjQ - Bacillus subtilis  
 gi|2226189|emb|CAA74479.1| (Y14081) hypothetical protein [Bacillus subtilis]  
 gi|2633396|emb|CAB12900.1| (Z99109) yhjQ [Bacillus subtilis]  
 Length = 108

Score = 32.9 bits (74), Expect = 2.1

Identities = 27/98 (27%), Positives = 44/98 (44%), Gaps = 4/98 (4%)

Query: 54 CLDAGQVCLTHCLSLLTQGDTSMSDCAVAVRQMLALCGAVHDLAAQNSPLTRDAARKVCLE 113  
 C+ A C T CL Q +S C R+ +C +SP ++ +C +  
 Sbjct: 15 CMKACNHCFTKCLEESVQ--HHLSCIRLDRECADICALAVKAMQTDSPFMKEICALCAD 72

-92-

Query: 114 ACKQCAKACKEHSAHAECKACYESCLDCIKECEKLAA 151  
 C+ C C +H H C+AC ++C C ++C +AA  
 Sbjct: 73 ICEACGTECGKHD--HDHCQACAKACFTCAEQCRSMAA 108

5 >gi|7479923|pir|T36241 hypothetical protein SCE39.31c - Streptomyces coelicolor  
 gi|4582392|emb|CAB40339.1| (AL049573) hypothetical protein [Streptomyces  
 coelicolor A3(2)]  
 Length = 136

10 Score = 30.9 bits (69), Expect = 7.7  
 Identities = 27/102 (26%), Positives = 43/102 (41%), Gaps = 6/102 (5%)

Query: 54 CLDAGQVCLTECLSLLTQGDTSMSDCAVAVRQMLALCGAVHDLAAQ----NSPLTRDAAK 109  
 C A C CLS T D ++ C +C A + ++ ++ +TR +

15 Sbjct: 34 CAQACTACADACLSEPTVAD--LTKCIRTDMDCADVCTATAAVLSRHTGYDANVTRAVLQ 91

Query: 110 VCLEACKQCAKACKEHSAHAECKACYESCLDCIKECEKLAA 151  
 C C C C H+ H C+ C E+C C + C++L A

20 Sbjct: 92 ACATVCAACGDECARHAGMHEHCRVCABACRSCEQACQBELLA 133

The protein was expressed in *E.coli* as a soluble 14.19kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 68

25 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 135> which encodes amino acid sequence <SEQ ID 136; NGS68>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -4.05  
 Possible cleavage site: 38

30 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 5.25 threshold: 0.0

35 PERIPHERAL Likelihood = 5.25  
 modified ALOM score: -1.55  
 Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

40 ----- Final Results -----

bacterial cytoplasm --- Certainty= 0.220(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 45 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

50 >gi|11353493|pir|A81795 hypothetical protein NMA2214 [imported] - Neisseria  
 meningitidis  
 (group A strain Z2491)  
 gi|7380833|emb|CAB85425.1| (AL162758) hypothetical protein [Neisseria  
 meningitidis Z2491]  
 Length = 208

55 Score = 263 bits (673), Expect = 3e-69  
 Identities = 140/145 (96%), Positives = 143/145 (98%)

60 Query: 1 LDWRGNKPLGAAELADLKPLYKDFMYWERGLHMYKASAVVPTGYVRVGNTAPLCGEDTQR 60  
 LDW+GNKPLGAAELADLKPLYKDFMYWERGLHMYKASAVVPTGYVRVGNTAPL GEDTQR



Sbjct: 44 LDWQGNKPLGAAELADLKPLYKDFMYWERGLHMYKASAVVPTGYVRVGNTAPLVGEDTQR 103  
 Query: 61 YASFWGDDGYDVYRQLRWRQIPEKQKAFKKAASKNTVMFAGREYGISKQNLSDVWDDFE 120  
 YASFWGDDGYDVYRQLRW+QIPEKQKAFKKAASK TVMFAGREYGISKQNLSDVWDDFE  
 5 Sbjct: 104 YASFWGDDGYDVYRQLRWQIPEKQKAFKKAASKNTVMFAGREYGISKQNLSDVWDDFE 163  
 Query: 121 DAMELKAFPCLSLFLTKWHKNLYE 145  
 DAMELKAFPCLSLFLTKWHKNLY+  
 10 Sbjct: 164 DAMELKAFPCLSLFLTKWHKNLYD 188  
 >gi|11280955|pir|B81219 hypothetical protein NMB0273 [imported] - Neisseria  
 meningitidis  
 (group B strain MD58)  
 15 gi|7225497|gb|AAF40727.1| (AE002383) hypothetical protein [Neisseria  
 meningitidis MC58]  
 Length = 141  
 Score = 216 bits (550), Expect = 5e-55  
 Identities = 117/121 (96%), Positives = 119/121 (97%)  
 20 Query: 25 MYWERGLHMYKASAVVPTGYVRVGNTAPLCGEDTQRYASFWGDDGYDVYRQLRWRQIPEKQ 84  
 MYWERGLHMYKASAVVPTGYVRVGNTAPL GEDTQRYASFWGDDGYDVYRQLRW+QIPEKQ  
 Sbjct: 1 MYWERGLHMYKASAVVPTGYVRVGNTAPLVGEDTQRYASFWGDDGYDVYRQLRWQIPEKQ 60  
 25 Query: 85 RKAFKKAASKNTVMFAGREYGISKQNLSDVWDDFEDAMELKAFPCLSLFLTKWHKNLY 144  
 RKAFKKAASK TVMFAGREYGISKQNLSDVWDDFEDAMELKAFPCLSLFLTKWHKNLY  
 Sbjct: 61 RKAFKKAASKNTVMFAGREYGISKQNLSDVWDDFEDAMELKAFPCLSLFLTKWHKNLY 120  
 Query: 145 E 145  
 30 +  
 Sbjct: 121 D 121

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### 35 Example 69

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 137> which encodes amino acid sequence <SEQ ID 138; NGS69>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -5.63  
 40 Possible cleavage site: 43  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 45 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 6.84 threshold: 0.0  
 PERIPHERAL Likelihood = 6.84  
 modified ALOM score: -1.87  
 Rule: cytoplasmic protein  
 50 \*\*\* Reasoning Step: 2  
 ----- Final Results -----  
 55 bacterial cytoplasm --- Certainty= 0.361(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

60 >gi|7464552|pir|C64707 hypothetical protein HP1499 - Helicobacter pylori (strain  
 26695)

-94-

gi|2314683|gb|AAD08545.1| (AE000648) *H. pylori* predicted coding region HP1499  
*Helicobacter pylori* 26695]  
 Length = 272

5 Score = 38.2 bits (88), Expect = 0.13  
 Identities = 34/123 (27%), Positives = 58/123 (46%), Gaps = 10/123 (8%)

Query: 3 EFKFIFGQDFGLSKKEAIRKVLKWLPSHLKFTLMVAQGIQG-----FHPKAVFWKNDKN 56  
 EF+ I G DF + ++IR +L ++ K + FHPK + N K  
 10 Sbjct: 54 EFETIVGLDFKMTDSKSIRFLDLNKTYYKLRFYCYGDKENNKTDIVFHPKIYMFNGK- 112

Query: 57 EYYALIGSSNLTHAAFNNSNYEAN-ILTRISEQDFIKVKSWADEI--AMKSIPVSEDWLEE 113  
 E ++IGS+NLT +N+E N I T+ + + + + I A +E++L+  
 Sbjct: 113 EKTSIIGSTNLTKGLENNFEVNTIFTEKKPLYTQLNATYNSIKYADSLFTPNEEYLQN 172

15 Query: 114 YQE 116  
 Y E  
 Sbjct: 173 YNE 175

20 A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS69 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 70

25 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 139> which encodes amino acid sequence <SEQ ID 140; NGS70>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -1.18  
 Possible cleavage site: 22  
 30 >>> Seems to have a cleavable N-term signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 23  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 4.19 threshold: 0.0  
 35 PERIPHERAL Likelihood = 4.19  
 modified ALOM score: -1.34  
 Score for OM-PP discrimination: -5.89  
 Rule: outer membrane or periplasmic protein  
 Score for OM-PP discrimination: -5.89  
 40 Rule: outer membrane or periplasmic protein

\*\*\* Reasoning Step: 2

Periplasmic space? Score: 0.588927  
 45 Periplasmic space? Score: 0.588927

----- Final Results -----

50 bacterial periplasmic space --- Certainty= 0.849(Affirmative) < succ>  
 bacterial outer membrane --- Certainty= 0.106(Affirmative) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

55 >gi|11353344|pir||A81886 hypothetical protein NMA1183 [imported] - *Neisseria meningitidis*  
 (group A strain Z2491)  
 gi|7379875|emb|CAB84445.1| (AL162755) hypothetical protein NMA1183 [*Neisseria meningitidis*]

Z24911  
Length = 74

Score = 58.7 bits (141), Expect = 2e-08  
Identities = 30/43 (69%), Positives = 32/43 (73%)  
Query: 62 IGGFGGVGGFGLKPALVYRNFRIIATNRPAATRARPQTIVA 104  
+G G+ G GGLKP LVY N IATNRPAATRA PR TTVA  
Sbjct: 32 MGNIDGIDGSGGLKPTLVYWNHCIIATNRPAATRAHPRHTTVA 74

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 71

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 141> which encodes amino acid sequence  
15 <SEQ ID 142; NGS71>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
Signal Score (-7.5): -1.98  
Possible cleavage site: 28  
>>> Seems to have a cleavable N-term signal seq.  
20 Amino Acid Composition of Predicted Mature Form:  
calculated from 29  
ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 5.04 threshold: 0.0  
PERIPHERAL Likelihood = 5.04  
25 modified ALOM score: -1.51  
Score for OM-PP discrimination: -9.17  
Rule: outer membrane or periplasmic protein  
Score for OM-PP discrimination: -9.17  
Rule: outer membrane or periplasmic protein  
30 \*\*\* Reasoning Step: 2  
Periplasmic space? Score: 0.916744  
Periplasmic space? Score: 0.916744  
35 ----- Final Results -----  
bacterial periplasmic space --- Certainty= 0.923(Affirmative) < succ>  
bacterial outer membrane --- Certainty= 0.146(Affirmative) < succ>  
40 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>  
bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
45 useful antigens for vaccines or diagnostics.

### Example 72

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 143> which encodes amino acid sequence  
<SEQ ID 144; NGS72>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
Signal Score (-7.5): -3.18  
Possible cleavage site: 42  
>>> Seems to have an uncleavable N-term signal seq  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
55 ALOM: Finding transmembrane regions (Klein et al.)

-96-

count: 4 value: -8.76 threshold: 0.0  
 INTEGRAL Likelihood = -8.76 Transmembrane 11 - 27 ( 8 - 37)  
 INTEGRAL Likelihood = -6.90 Transmembrane 80 - 96 ( 75 - 102)  
 INTEGRAL Likelihood = -2.39 Transmembrane 98 - 114 ( 98 - 114)  
 5 INTEGRAL Likelihood = -1.12 Transmembrane 47 - 63 ( 47 - 64)  
 PERIPHERAL Likelihood = 3.55  
 modified ALOM score: 2.25  
 Rule: cytoplasmic membrane protein

10 \*\*\* Reasoning Step: 2

----- Final Results -----

15 bacterial inner membrane --- Certainty= 0.450(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

20 >gi|11354095|pir||H81995 probable transmembrane transport protein NMA0047  
 [imported] - Neisseria meningitidis (group A strain Z2491)  
 gi|7378822|emb|CAB83364.1| (AL162752) putative transmembrane transport protein  
 [Neisseria meningitidis Z2491]  
 Length = 405

25 Score = 257 bits (658), Expect = 5e-68  
 Identities = 152/162 (93%), Positives = 154/162 (94%)

30 Query: 1 MTHTASKTPKLWAVIAAAAFILLITIGMRMTLGLFVQPVVNTTELNIAQFSLIITVFQLM 60  
 MTHTASKTPK W I AAAFILLITIGMRMTLGLFVQPVVNTTEL+IAQFSLII VFQLM  
 Sbjct: 1 MTHTASKTPKFWLTITAAAFILLITIGMRMTLGLFVQPVVNTTELSIAQFSLIIAVFQLM 60

Query: 61 WGVLPQLSGALADRFGAFRVLSGGALLVVCACLIASNIPTYWGLMIAVGLLLAFGTGSGG 120  
 WGV QPLSGALADRFGAFRVLSGGA+LLVVCACLIA NIPTYWGLMIAVGLLLAFGTGSGG  
 35 Sbjct: 61 WGVSQPLSGALADRFGAFRVLSGAVLLVVCACLIAPNIPTYWGLMIAVGLLLAFGTGSGG 120

Query: 121 FSIIMGQVAAQVPVTHKRGLASGLVNAGGSAGQFLFAPLVQGL 162  
 FSIIMGQVAAQVP HKRGLASGLVNAGGSAGQFLFAPLVQGL  
 Sbjct: 121 FSIIMGQVAAQVPAHKRGLASGLVNAGGSAGQFLFAPLVQGL 162

40 >gi|11351469|pir||F83484 probable MFS transporter PA1286 [imported] - Pseudomonas  
 aeruginosa  
 (strain PAO1)  
 gi|9947221|gb|AAG04675.1|AE004558\_4 (AE004558) probable MFS transporter  
 45 [Pseudomonas aeruginosa]  
 Length = 399

Score = 72.5 bits (177), Expect = 3e-12  
 Identities = 53/149 (35%), Positives = 81/149 (53%)

50 Query: 14 VIAAAAFILLITIGMRMTLGLFVQPVVNTTELNIAQFSLIITVFQLMWGVLPQLSGALAD 73  
 ++ + A IL +++G+R GLF+ P+ F+ I + L+WG+ QP +GALAD  
 Sbjct: 8 ILLSGALILALSGLVRHGFGLFLAPMSADFGWGREVFFAFAIALQNLVWGLAQPF+TGALAD 67

55 Query: 74 RFGAFRVLSGGALLVVCACLIASNIPTYWGLMIAVGLLLAFGTGSGGFSIIMGQVAAQVP 133  
 R+GA R + G LL ++ + GL ++ GLL+ G FS+I+G V VP  
 Sbjct: 68 RYGAARAVLVGGLLYALGLVLMGLSQSASGLSLSAGLLIGLGLSCTSF+SVILGAVGRAVP 127

60 Query: 134 THKRGLASGLVNAGGSAGQFLFAPLVQGL 162  
 +R +A G+ +A GS GQF P GL  
 Sbjct: 128 AEQRSMAMGISSAAGSFGQFAMLP+GTLGL 156

As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS72 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 73

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 145> which encodes amino acid sequence <SEQ ID 146; NGS73>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
Signal Score (-7.5): -4.26  
Possible cleavage site: 52  
>>> Seems to have no N-terminal signal seq.  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
ALOM: Finding transmembrane regions (Klein et al.)  
count: 3 value: -3.72 threshold: 0.0  
INTEGRAL Likelihood = -3.72 Transmembrane 172 - 188 ( 171 - 190)  
INTEGRAL Likelihood = -2.97 Transmembrane 119 - 135 ( 114 - 137)  
INTEGRAL Likelihood = -1.86 Transmembrane 209 - 225 ( 205 - 225)  
PERIPHERAL Likelihood = 4.88  
modified ALOM score: 1.24  
Rule: cytoplasmic membrane protein

\*\*\* Reasoning Step: 2

----- Final Results -----

bacterial inner membrane --- Certainty= 0.249(Affirmative) < succ>  
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

>gi|11354095|pir||H81995 probable transmembrane transport protein NMA0047  
[imported] - Neisseria meningitidis (group A strain Z2491)  
gi|7378822|emb|CAB83364.1| (AL162752) putative transmembrane transport protein  
[Neisseria meningitidis Z2491]  
Length = 405

Score = 222 bits (567), Expect = 3e-57

Identities = 116/123 (94%), Positives = 117/123 (94%), Gaps = 4/123 (3%)

Query: 103 QGLVVLPEVGWGTGTFYVWGAIALLLPVSWWLAGGNNNGNNAHTQHTQATHGQSLGEAV 162  
QGLVVLPEVGWGTGTFYVWGAIALL LPVSWWLA GGNNAHTQH QATHGQSLGEAV  
Sbjct: 160 QGLVVLPEVGWGTGTFYVWGAIALLLPVSWWLA----GGNNAHTQHAQATHGQSLGEAV 215

Query: 163 KTAFKTPSYILLHLSFFACGFHIAFLVTHLPTEVALCGLPATVASTSIAIIGLANIAGCV 222  
KTAFKTPSYILLHLSFFACGFHIAFLVTHLPTEVALCGLPATVASTSIAIIGLANIAGC+  
Sbjct: 216 KTAFKTPSYILLHLSFFACGFHIAFLVTHLPTEVALCGLPATVASTSIAIIGLANIAGCI 275

Query: 223 FSG 225  
FSG

Sbjct: 276 FSG 278

>gi|11351469|pir||F83484 probable MFS transporter PA1286 [imported] - Pseudomonas  
aeruginosa  
(strain PAO1)  
gi|9947221|gb|AAG04675.1|AE004558\_4 (AE004558) probable MFS transporter  
[Pseudomonas aeruginosa]  
Length = 399

Score = 54.4 bits (130), Expect = 1e-06

Identities = 37/115 (32%), Positives = 56/115 (48%), Gaps = 10/115 (8%)

Query: 111 VGWGTGTFYVWGAIALLILPVSWWLAGGNNGGNNAHTQHTQATHGQSLGEAVKTAFTKTPS 170  
 +GW+ G + LI+P++ + H QSLGEA++ A  
 Sbjet: 160 LGWSSALLALGLLVALIVPLAGLM-----KDRPLPPQGHEQSLGEALREACAHSG 209

5 Query: 171 YILLHLSFFACGFHIAFLVTHLPTEVALCGLPATVASTSIAIIGLANIAGCVFSG 225  
 + LL L FF CGF + F+ HLP + LPA V +T +A++GL N+ G +G  
 Sbjet: 210 FWLLALGFFVCGFQVVFIVGHLPAYLVDQHLPAQVGTTVLALVGLFNVFGTYIAG 264

As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS73 protein and  
 10 nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
 useful antigens for vaccines or diagnostics.

#### Example 74

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 147> which encodes amino acid sequence  
 15 <SEQ ID 148; NGS74>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): 0.41  
 Possible cleavage site: 30  
 >>> Seems to have no N-terminal signal seq.  
 20 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 2 value: -1.49 threshold: 0.0  
 INTEGRAL Likelihood = -1.49 Transmembrane 15 - 31 ( 15 - 31)  
 25 INTEGRAL Likelihood = -1.28 Transmembrane 83 - 99 ( 83 - 99)  
 PERIPHERAL Likelihood = 1.59  
 modified ALOM score: 0.80  
 Rule: cytoplasmic membrane protein

30 \*\*\* Reasoning Step: 2

----- Final Results -----

35 bacterial inner membrane --- Certainty= 0.160(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

40 >pir||H81995 probable transmembrane transport protein NMA0047 [imported] -  
 Neisseria meningitidis (group A strain Z2491)  
 emb|CAB83364.1| (AL162752) putative transmembrane transport protein [Neisseria  
 meningitidis Z2491]  
 Length = 405

45 Score = 148 bits (374), Expect = 2e-35  
 Identities = 97/106 (91%), Positives = 103/106 (96%)

50 Query: 1 MVLIYIFSPKTDLNFYIFAAALGFTWLATVPTAAVTGKLFGTRYLATLFLGLVMLTHQIG 60  
 M+LIYIFSPKTDLNFYIFAAALGFTWLATV PTA++TGKLFGTRYLATLFLGL ML+HQIG  
 Sbjet: 300 MILIYIFSPKTDLNFYIFAAALGFTWLATVPTASITGKLFGTRYLATLFLGLTMLSHQIG 359

Query: 61 GFLGSYIGGIVITQFGDYGWMWYADAVLAGTAALLVLPVREPRTAA 106  
 GFLGSYIGGIVITQFGDYGWMWYADA+LAGTAALL LP+REPRTAA  
 55 Sbjet: 360 GFLGSYIGGIVITQFGDYGWMWYADALLAGTAALLNLPVREPRTAA 405

>pir||F83484 probable MFS transporter PA1286 [imported] - Pseudomonas aeruginosa  
 (strain PA01)

-99-

gb|AAG04675.1|AE004558\_4 (AE004558) probable MFS transporter [Pseudomonas aeruginosa]

Length = 399

5 Score = 59.0 bits (142), Expect = 2e-08  
Identities = 40/101 (39%), Positives = 61/101 (59%)

Query: 1 MVLIIYIFSPKTDLNFYIFAAALGFTWLATVAPTAAVTGKLFQTRYLATLFGVLVMLTHQIG 60  
++++++ P + + Y F A+G WL+TV T LFG R L+ L G+V L HQ+G  
10 Sbjct: 286 VIVLFLWLPLSVYSAYAFGVAMGLLWLSTVPLTNGTVATLFGVRNLSMLGGIVFLFHQLG 345

Query: 61 GFLGSYIGGIVITQFGDYGWMWYADAVLAGTAALLVLPVRE 101  
FLG ++GG+V + G Y +W +L+ AALL FVRE  
15 Sbjct: 346 AFLGGWLGGVVYDRTGSYDLVWQLSILLSLLAALLNWPVRE 386

As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS74 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## 20 Example 75

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 149> which encodes amino acid sequence <SEQ ID 150; NGS75>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
Signal Score (~7.5): -5.2  
25 Possible cleavage site: 22  
>>> Seems to have no N-terminal signal seq.  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
ALOM: Finding transmembrane regions (Klein et al.)  
30 count: 0 value: 4.45 threshold: 0.0  
PERIPHERAL Likelihood = 4.45  
modified ALOM score: -1.39  
Rule: cytoplasmic protein

35 \*\*\* Reasoning Step: 2

----- Final Results -----

40 bacterial cytoplasm --- Certainty= 0.237(Affirmative) < succ>  
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

45 pir||S04419 type II site-specific deoxyribonuclease (EC 3.1.21.4) NgoPII -  
Neisseria gonorrhoeae  
emb|CAA36887.1| (X52661) NgoPII restriction and modification [N.gonorrhoeae]  
prf||1613419A NgoPII endonuclease [Neisseria gonorrhoeae]  
50 Length = 278

Score = 240 bits (614), Expect = 4e-63  
Identities = 128/129 (99%), Positives = 128/129 (99%)

55 Query: 1 MNIIDAIINLANNPVVGVNSHSQSNNRANQAGDALEEVKDLFSGSFNLTQRIARHAK 60  
MNIIDAIINLANNPVVGV SHSQSNNRANQAGDALEEVKDLFSGSFNLTQRIARHAK  
Sbjct: 1 MNIIDAIINLANNPVVGVESHQSNNRANQAGDALEEVKDLFSGSFNLTQRIARHAK 60

Query: 61 VFSYLGNNNSNPPDAMLNRNGDAIEVKKIESKDSALALNSSHPKSKLSVDDSMITKACKDAE 120  
VFSYLGNNNSNPPDAMLNRNGDAIEVKKIESKDSALALNSSHPKSKLSVDDSMITKACKDAE

-100-

Sbjct: 61 VFSYLGNNNSNPPDAMLRNGDAIEVKKIESKDSALALNSSHPKSKLSVDDSM LTKACKDAE 120

Query: 121 KWEEKDIY 129

KWEEKDIY

5 Sbjct: 121 KWEEKDIY 129

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 76

10 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 151> which encodes amino acid sequence <SEQ ID 152; NGS76>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)

Signal Score (-7.5): -1.73

Possible cleavage site: 13

15 >>> Seems to have no N-terminal signal seq.

Amino Acid Composition of Predicted Mature Form:  
calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)

count: 0 value: 9.39 threshold: 0.0

20 PERIPHERAL Likelihood = 9.39

modified ALOM score: -2.38

Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

25

----- Final Results -----

30 bacterial cytoplasm --- Certainty= 0.272(Affirmative) < succ>  
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

35 pir||S04419 type II site-specific deoxyribonuclease (EC 3.1.21.4) NgoPII -  
Neisseria gonorrhoeae  
emb|CAA36887.1| (X52661) NgoPII restriction and modification [N.gonorrhoeae]  
prf||1613419A NgoPII endonuclease [Neisseria gonorrhoeae]  
Length = 278

40 Score = 268 bits (687), Expect = 2e-71  
Identities = 136/136 (100%), Positives = 136/136 (100%)

45 Query: 1 LAMVYGIDYCADAE CYLKIKNQIKEGIGNIGGIQFAETKELGRVNRIDPLNITYLRVRGM 60  
LAMVYGIDYCADAE CYLKIKNQIKEGIGNIGGIQFAETKELGRVNRIDPLNITYLRVRGM  
Sbjct: 143 LAMVYGIDYCADAE CYLKIKNQIKEGIGNIGGIQFAETKELGRVNRIDPLNITYLRVRGM 202

Query: 61 WG IENPWFVFN YIYQRNMEKSFNFMAI INEDKWN SFNNTDKLLAIQDSKLAI SDIKIKNP 120  
WG IENPWFVFN YIYQRNMEKSFNFMAI INEDKWN SFNNTDKLLAIQDSKLAI SDIKIKNP  
50 Sbjct: 203 WG IENPWFVFN YIYQRNMEKSFNFMAI INEDKWN SFNNTDKLLAIQDSKLAI SDIKIKNP 262

Query: 121 NNPARLRNAKLITYHL 136  
NNPARLRNAKLITYHL

Sbjct: 263 NNPARLRNAKLITYHL 278

55 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.





## Example 77

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 153> which encodes amino acid sequence <SEQ ID 154; NGS77>. Analysis of this protein sequence reveals the following:

```

5   GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -4.51
      Possible cleavage site: 58
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
          calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 3.18 threshold: 0.0
      PERIPHERAL Likelihood = 3.18
      modified ALOM score: -1.14
15  Rule: cytoplasmic protein

      *** Reasoning Step: 2

      ----- Final Results -----

20      bacterial cytoplasm --- Certainty= 0.127(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

25  The protein has homology with the following sequences in the databases:

      >pir||CTNHP2 site-specific DNA-methyltransferase (cytosine-specific) (EC
          2.1.1.73) NgoPII - Neisseria gonorrhoeae
      emb|CAA30038.1| (X06965) NgoPII methylase (AA 1-341) [Neisseria gonorrhoeae]
      emb|CAA36888.1| (X52661) NgoPII restriction and modification [Neisseria
30  gonorrhoeae]
      gb|AAA17019.1| (L14564) cytosine methylase [Neisseria gonorrhoeae]
      prf||1613419B NgoPII methylase [Neisseria gonorrhoeae]
          Length = 341

35  Score = 682 bits (1761), Expect = 0.0
      Identities = 341/341 (100%), Positives = 341/341 (100%)

      Query: 1  MQNSSPTTYNPMKIIISLFSGCGGLDLGFEKAGFEIPAANEYDKTIWATFKANHPKTHLIE 60
      Sbjct: 1  MQNSSPTTYNPMKIIISLFSGCGGLDLGFEKAGFEIPAANEYDKTIWATFKANHPKTHLIE 60

      Query: 61  GDIRKIKEEDFPEEIDGIIGPPCQSWSEAGALRGIDDARGQLFFDYIRILKSKQPKFFL 120
      Sbjct: 61  GDIRKIKEEDFPEEIDGIIGPPCQSWSEAGALRGIDDARGQLFFDYIRILKSKQPKFFL 120

45  Query: 121  AENVSGMLANRHNGAVQNLLKMFDCGCGYDVTLTMANAKDYGVAQERKRVFYIGFRKDLEI 180
      Sbjct: 121  AENVSGMLANRHNGAVQNLLKMFDCGCGYDVTLTMANAKDYGVAQERKRVFYIGFRKDLEI 180

      Query: 181  KFSFPKGSTVEDKDKITLKDVIWDLQDTAVPSAPQNKTNPDVNNNEYFTGSPSPIFMSR 240
      Sbjct: 181  KFSFPKGSTVEDKDKITLKDVIWDLQDTAVPSAPQNKTNPDVNNNEYFTGSPSPIFMSR 240

50  Query: 241  NRVKAWDEQGFVQASGRQCQLHPQAPKMEKHGANDYRFAAGKETLYRRMTVREVARIQG 300
      Sbjct: 241  NRVKAWDEQGFVQASGRQCQLHPQAPKMEKHGANDYRFAAGKETLYRRMTVREVARIQG 300

55  Query: 301  FPDNFKFIYQNVNDAYKMIGNAVPVNLAYEIAAAIKKTLEI 341
      Sbjct: 301  FPDNFKFIYQNVNDAYKMIGNAVPVNLAYEIAAAIKKTLEI 341

60  Query: 301  FPDNFKFIYQNVNDAYKMIGNAVPVNLAYEIAAAIKKTLEI 341
      Sbjct: 301  FPDNFKFIYQNVNDAYKMIGNAVPVNLAYEIAAAIKKTLEI 341

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 78

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 155> which encodes amino acid sequence  
5 <SEQ ID 156; NGS78>. Analysis of this protein sequence reveals the following:

```

GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -8.33
      Possible cleavage site: 24
>>> Seems to have no N-terminal signal seq.
10 Amino Acid Composition of Predicted Mature Form:
      calculated from 1
      ALOM: Finding transmembrane regions (Klein et al.)
            count: 0 value: 2.17 threshold: 0.0
            PERIPHERAL Likelihood = 2.17
15 modified ALOM score: -0.93
      Rule: cytoplasmic protein

*** Reasoning Step: 2

20 ----- Final Results -----

            bacterial cytoplasm --- Certainty= 0.220(Affirmative) < succ>
            bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
            bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
25            bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

>pir||H82000 hypothetical protein NMA0089 [imported] - Neisseria meningitidis
      (group A strain Z2491)
30 emb|CAB83405.1| (AL162752) hypothetical protein NMA0089 [Neisseria meningitidis
      Z2491]
      Length = 226

      Score = 422 bits (1085), Expect = e-117
35      Identities = 217/228 (95%), Positives = 220/228 (96%), Gaps = 2/228 (0%)

      Query: 1 MERYKNAVRKDKAAELYLLNLSLSRELPHVVSIFEIVLRNKIDICFRQEFKDRNRLYDSI 60
                MERYKNAV KDKAAELYLLNLSLSRELPHVVSIFEIVLRNKIDIC +Q FKD N LY+SI
      Sbjct: 1 MERYKNAVGVKDKAAELYLLNLSLSRELPHVVSIFEIVLRNKIDICLQQAQFQDGNWLYNSI 60

40      Query: 61 QPQTNPALKYQGCFLRNGTKESAEILKVALSKIQNNSSGGKFDHNQLVAGLGFGFWRYLFA 120
                QPQTNPALKYQGCFLRNGTKESAEILKVALSKIQNNSSGGKFDHNQLVAGLGFGFWRYLFA
      Sbjct: 61 QPQTNPALKYQGCFLRNGTKESAEILKVALSKIQNNSSGGKFDHNQLVAGLGFGFWRYLFA 120

45      Query: 121 GSKDAQFDAAGKVLKVFPPKPKSTPSVQYNQKWIFRELSNINNFRNRLAHHEPICFSFK 180
                GSKDAQFDA GKVLKVFPPKPKSTPSVQ+QKWIFRELSNINNFRNRLAHHEPIC FK
      Sbjct: 121 GSKDAQFDATGKVLKVFPPKPKSTPSVQHNQKWIFRELSNINNFRNRLAHHEPIC--FK 178

      Query: 181 GAIKDTGYARNIHQSIFELLNYMDVDTASVFSHFSDQVIACDEIDKL 228
                GAIKDTGYARNIHQSIFELLNYMDVDTASVFSHFSDQVIACDEIDKL
50      Sbjct: 179 GAIKDTGYARNIHQSIFELLNYMDVDTASVFSHFSDQVIACDEIDKL 226

>ref|NP_053274.1| Hypothetical gene [Agrobacterium tumefaciens]
      dbj|BAA87659.1| (AB016260) Hypothetical gene [Agrobacterium tumefaciens]
55      Length = 380

      Score = 43.6 bits (102), Expect = 0.002
      Identities = 53/215 (24%), Positives = 86/215 (39%), Gaps = 42/215 (19%)

60      Query: 5 KNAVRKDKAAELYLLNLSLSRELPHVVSIFEIVLRNKIDICFRQEFKDRNRLYDSIQPQT 64
                K ++ A LYL N +++ + +++ E+ LRN +D F

```

Sbjct: 55 KGGNHEEYAMALYLYNARVAKAFLYPLNVAEVTLRNAVDGILVARFG----- 101

Query: 65 NPALKYQGCFLRNGTKESAEIKVALSKIQNNSGGKFDHNQLVAGLGFGFWRYLFAGGKD 124  
 A +Q R+ T L L K +G +Q+VA L F FW LF

5 Sbjct: 102 --ANWHQDATFRDQTLTGNGL--ATLDKAIQRAGAGAARDQIVATLTFDFWSNLFR---- 153

Query: 125 AQFDAAGKVLKVPKPKSTPSVQYNQKWIFRELSN----INNFRNRLAHHEPICFSFK 180  
 ++ + + + + P +Q+ + +B+ N IN FRNR+AHHEP+

10 Sbjct: 154 PEYGGGLWRRTTVNI-----AFPHLQHGESR--QEIQNLVKPINVFRNRVAHHEFVL---- 201

Query: 181 GAIKDTGYARNIHQSIFELLNMYMDVDTASVFSHPS 215  
 D +IH I L+ +TA+ H S

Sbjct: 202 ----DLNVT-DIHAKIVRLIELRCAETATWMKHHS 231

- 15 As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS78 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 79

- 20 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 157> which encodes amino acid sequence <SEQ ID 158; NGS79>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): 2.07  
 Possible cleavage site: 17

25 >>> Seems to have a cleavable N-term signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 18

ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 9.49 threshold: 0.0

30 PERIPHERAL Likelihood = 9.49  
 modified ALOM score: -2.40

Score for OM-PP discrimination: -11.72  
 Rule: outer membrane or periplasmic protein  
 Score for OM-PP discrimination: -11.72

35 Rule: outer membrane or periplasmic protein

\*\*\* Reasoning Step: 2

Periplasmic space? Score: 1.17242

40 Periplasmic space? Score: 1.17242

----- Final Results -----

45 bacterial periplasmic space --- Certainty= 0.932(Affirmative) < succ>  
 bacterial outer membrane --- Certainty= 0.240(Affirmative) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

- A homolog (amino acids 23-85) was found in serogroup A *N.meningitidis* but not in serogroup B, so
- 50 NGS79 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

**Example 80**

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 159> which encodes amino acid sequence <SEQ ID 160; NGS80>. Analysis of this protein sequence reveals the following:

```

5   GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -8.49
      Possible cleavage site: 57
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 4.98 threshold: 0.0
      PERIPHERAL Likelihood = 4.98
      modified ALOM score: -1.50
      Rule: cytoplasmic protein
15  *** Reasoning Step: 2

      ----- Final Results -----

20      bacterial cytoplasm --- Certainty= 0.428(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

25  The protein has homology with the following sequences in the databases:

      >pir||E81080 conserved hypothetical protein NMB1466 [imported] - Neisseria
      meningitidis (group B strain MD58)
      gb|AAF41823.1| (AE002496) conserved hypothetical protein [Neisseria meningitidis
      MC58]
30      Length = 243

      Score = 148 bits (375), Expect = 7e-35
      Identities = 82/189 (43%), Positives = 109/189 (57%)

35  Query: 120 VDRMFNMAGNHFARLGISGSGVHYWNARDFSEQAFHAEVGYRYRNSRLEWGFPRPFVKQNR 179
      + R N +HF GISG GVHYW+ +DFSEQ+ GY+ R+ +G PFV+QN
      Sbjct: 1 MSREINAGRHHFLYGGISGGGVHYWDNKDFSEQSLRLSFGYKNRSVTRSFQIVPFVEQN 60

40  Query: 180 LGNNRYTANTGIVLDYSRRLNEKWRSTQSFQYGRKQYHDEYLAKRYNSKTISVSGTFSYY 239
      LG +RY G D+S+RL+E+WR T + K Y ++ A RY+S T Y
      Sbjct: 61 LGGSRYNFVGGFNADFSQRLSERWRLTLNAGNMWKHYQEDRTAARYDSHMLAGATLMYS 120

      Query: 240 AMSAWQLYGGISGMFNDTVEKEQASRRYGVSLGTVKILDGGLGLKLGAGYTKRIFKAPAT 299
      A W LYGG + T E EQAS R G+ +G VK DGGLGL+ YT+R+F AP T
45  Sbjct: 121 APKDWLLYGGADWSHNITKEAEQASIRKGLRVGAVKTFDGGLGLRANLRYTRRMFDAPGT 180

      Query: 300 LIYNFTRRD 308
      ++Y F R+D
      Sbjct: 181 IVYRFFRKD 189

50  >gb|AAD11779.1| (AF118122) putative outer membrane protein OmpU [Neisseria
      meningitidis]
      Length = 488

55  Score = 72.1 bits (176), Expect = 7e-12
      Identities = 71/300 (23%), Positives = 128/300 (42%), Gaps = 17/300 (5%)

      Query: 3 EAADLYRELLSERPDLVYPRFDLGVMFLFEDKQYREALVQLHRAE-EVLPPDMRQLAREYI 61
      EA YREL++ +PD R L LF+++Q A Q R + E LPP + + Y
60  Sbjct: 136 RAISHYRELIAAQPDAPAVRMRLAAALFDNRQNEAAADQFDRLLKAENLPPQLMEQVELYR 195

      Query: 62 RQAEAVQAWHPSFNMNYEQTDNVNNAASLSDIVINGRKWIKSEDSLPKRANG--IRYELG 119
      + AW + + + N+N A + KW + PK+ +G + Y LG
      Sbjct: 196 KALRERDAWKVNGGFSVTREHNINQAPKRQY----GKW-----TFPKQVDGTAVNYRLG 246

```

Query: 120 VDRMPNMGHNFARLGISGSGVHYWNARDFSEQAFHAEVGYRYRNSRLEWGFPRPFVKQNR 179  
 ++ +++ + G SG Y + F++ G + + R + G F ++  
 5 Sbjct: 247 AEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGLAVFHERRT 306

Query: 180 LGNNRYTANTGIVLDYSRRLNEKWRSTQSFQYGRKQYHDEYLAKRYNSKTISVSGTFSYY 239  
 GN+ Y+ G L ++R KW++ S ++GR + R ++ + +S + +Y  
 10 Sbjct: 307 YGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLK---NTRRARSNDNTHLQISNSLVFY 363

Query: 240 AMSAWQLYGGISGMFD-NTVEKEQASRRYGVSLGTVKILDG-GLGLKLGAGYTKRIFKAP 297  
 + GG+ + N ++ RYG+ + G GL L G KR ++ P  
 10 Sbjct: 364 RNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAGWQEWGSGSLSSLLRLGAARKHYEKP 423

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
 15 useful antigens for vaccines or diagnostics.

### Example 81

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 161> which encodes amino acid sequence  
 <SEQ ID 162; NGS81>. Analysis of this protein sequence reveals the following:

20 GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -6.25  
 Possible cleavage site: 15  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 25 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 7.05 threshold: 0.0  
 PERIPHERAL Likelihood = 7.05  
 modified ALOM score: -1.91  
 Rule: cytoplasmic protein  
 30 \*\*\* Reasoning Step: 2  
 ----- Final Results -----  
 35 bacterial cytoplasm --- Certainty= 0.232(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

gi|10803654|ref|NP\_046052.1| putative ISH4 transposase [Halobacterium sp. NRC-1]  
 40 gi|7484109|pir|T08324 probable transposase H1306 - Halobacterium sp. (strain  
 NRC-1)  
 insertion sequence ISH4 plasmid pNRC100  
 gi|2822385|gb|AAC82891.1| (AF016485) putative ISH4 transposase [Halobacterium  
 sp. NRC-1]  
 45 gi|10580476|gb|AAG19350.1| (AE005029) Vng0918h [Halobacterium sp. NRC-1]  
 Length = 294  
 Score = 52.1 bits (124), Expect = 4e-06  
 Identities = 36/139 (25%), Positives = 63/139 (44%), Gaps = 7/139 (5%)  
 50 Query: 31 CPHCQSTHFVKNGKDCGNQRFLCRDCKKSFEVQTGTILYNTQKDIEVWEKYIHCMIK-KY 89  
 CP C++ ++ G QR+LC+DC ++F +QTGT+ ++ + W ++ I  
 Sbjct: 28 CPSCRAESVIRYGSYRVFQRYLCKDCDRTFNDQTGTVFEHSAVALRKWFLAVYTYIRLNT 87

Query: 90 PLRKCAEICKINLATAFTWRHKILDALQNMMEVELDGIVQADETYSTISYKGHHKKNFNL 149  
 55 +R+ ++ T + + L AL L+G V+ DE Y KG ++  
 Sbjct: 88 SIRQLDAEIDVSYKTVYRRVQRFLRALD--APRPHLEGPVEIDEFYVKAGLKGRRD--- 142

Query: 150 PRPAHKRGTRATKRGISKE 168  
 +P+ RG RG E  
 60 Sbjct: 143 -QPSRSRGLSTRGRGTYAE 160

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 82

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 163> which encodes amino acid sequence <SEQ ID 164; NGS82>. Analysis of this protein sequence reveals the following:

```

5  GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -4.66
      Possible cleavage site: 57
      >>> Seems to have no N-terminal signal seq.
10 Amino Acid Composition of Predicted Mature Form:
      calculated from 1
      ALOM: Finding transmembrane regions (Klein et al.)
            count: 1 value: -0.85 threshold: 0.0
            INTEGRAL Likelihood = -0.85 Transmembrane 76 - 92 ( 76 - 92)
15      PERIPHERAL Likelihood = 1.75
            modified ALOM score: 0.67
            Rule: cytoplasmic membrane protein

      *** Reasoning Step: 2
20      ----- Final Results -----

            bacterial inner membrane --- Certainty= 0.134(Affirmative) < succ>

25 The protein has homology with the following sequences in the databases:

      >gi|586070|sp|Q07605|T4BA_BACCO RESTRICTION ENZYME BCGI ALPHA SUBUNIT [INCLUDES:
      ADENINE-SPECIFIC
            METHYLTRANSFERASE ACTIVITY ]
      gi|1075788|pir||A53125 restriction enzyme BcgI alpha chain - Bacillus coagulans
30 gi|304140|gb|AA16626.1| (L17341) restriction endonuclease alpha subunit
      [Bacillus
            coagulans]
            Length = 637

35 Score = 91.4 bits (226), Expect = 1e-17
      Identities = 78/256 (30%), Positives = 123/256 (47%), Gaps = 42/256 (16%)

      Query: 1 MFALAASNILRGDGRKANLHQSSCFMTDFQDLIKNPKPETGLKRPNVGFLNPPYAQSKSD 60
            +F +A +NMILRGDGK+NL + +C F + I N G+ N +NPPY+Q+K+D
40 Sbjct: 394 LPTIATTNMILRGDGRKSNLIRDNCLT--FDNTIMN---GYGI---NKILMNPYPYSQARND 445

      Query: 61 AELH--ELYFVKEMLDMLAEGGTGIAIIPVSCVIAPSK----AKSEIVKYHRLKAVMSMP 114
            H EL F+++ L+ML GG AI+P S ++ ++ K +I+K H L+ V+++
45 Sbjct: 446 QTQHLSELSFIQQAELMLVVGKLCVVPQSTMVGKNRHDKARKKQILKQHTLETVITLN 505

      Query: 115 SELFYPVGTVTTCIVVFEAHKPHFQTVVIDPDTQBEISTKKACRKTWFGYWRDDGFETKH 174
            + F+ VG CIV+F+A H + ++ F + DDG KH
      Sbjct: 506 KDTFHGVGVNPCIVIFKAGIKHPEN-----KRVSFVNFEDDGHVVRKH 548

50 Query: 175 LGRIDLYDRWQGIKARWLEHYL-----NNEVHTGESVTAFVTDNDEWVAEAYLETDYSKI 229
            +G + G + EH L + + T V + D DEW+ Y D
      Sbjct: 549 VGLVG-----DGTEKGKREHLLAVLAGDEDDGTDLIVKTAIKDTDEWLHSFYFND-GIP 602

      Query: 230 TRADFEQVVREFALFQ 245
            + DF + V + FQ
55 Sbjct: 603 SEDDFYKTVANYLTFQ 618

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## Example 83

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 165> which encodes amino acid sequence <SEQ ID 166; NGS83>. Analysis of this protein sequence reveals the following:

```

5  GvH: Examining signal sequence (von Heijne)
    Signal Score (-7.5): -8.04
    Possible cleavage site: 43
    >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
    calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
    count: 1 value: -1.44 threshold: 0.0
    INTEGRAL Likelihood = -1.44 Transmembrane 55 - 71 ( 55 - 71)
    PERIPHERAL Likelihood = 4.03
    modified ALOM score: 0.79
15  Rule: cytoplasmic membrane protein

    *** Reasoning Step: 2

    ----- Final Results -----
20  bacterial inner membrane --- Certainty= 0.157(Affirmative) < succ>

```

The protein has homology with the following sequences in the databases:

```

25  >gi|586071|sp|Q07606|T4BB_BACCO RESTRICTION ENZYME BCGI BETA SUBUNIT
    gi|1075789|pir||B53125 restriction enzyme BcgI beta chain - Bacillus coagulans
    gi|304141|gb|AAA16627.1| (L17341) restriction endonuclease beta subunit
    [Bacillus coagulans]
    Length = 341

30  Score = 44.0 bits (103), Expect = 0.002
    Identities = 46/195 (23%), Positives = 79/195 (39%), Gaps = 23/195 (11%)

    Query: 4  LQEIFDVSYGSKLDLNKMSFNPTINFVGRSGKNNGVTASVDLLKNTKPYPAGLLTVALG 63
    + ++FDV G +D NK ++ R NG +D K K Y L ++G
35  Sbjct: 12 ISDLFDVVIGKTIDGKAQRNENGTPYITRKATRNGFEFMIDGKE-KLYSGKLPVITIG 70

    Query: 64 GSVLSTFLQNKPFYTAQNVAVLNPKTEMTEQOKLFYCAAFANAYRFSACGREANRT-LR 122
    F+Q F+T V + PK ++ L Y + NA + + N T L+
    Sbjct: 71 NETSKPFVQEFHFFTGTKVNICIPKLDLNRNH-LLYITMTIENATKMFYSYTYNSTRLK 129

40  Query: 123 QL--FVPSLDEIPSW-----VESVNLNPSAGVTEPKLKESLDLPVVRQSKR 166
    L +P E P W ++ ++ + GV++ + + L +
    Sbjct: 130 SLKILLPIKGEEPWDWYMTYISKILSNMEKNFDVQQNDGVSDLRSLKDLNLSW----SQFK 185

45  Query: 167 LDEIFTIQNGIAATK 181
    +DEIF+I +G+ TK
    Sbjct: 186 MDEIFSINSGVRLTK 200

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## Example 84

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 167> which encodes amino acid sequence <SEQ ID 168; NGS84>. Analysis of this protein sequence reveals the following:

```

55  Signal Score (-7.5): 3.15
    Possible cleavage site: 33
    >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
    calculated from 1

```



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ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 1.22 threshold: 0.0  
 PERIPHERAL Likelihood = 1.22  
 modified ALOM score: -0.74  
 5 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 ----- Final Results -----  
 10 bacterial cytoplasm --- Certainty= 0.072(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

15 >gi|2495432|sp|P55409|Y4DJ\_RHISN HYPOTHETICAL TRANSCRIPTIONAL REGULATOR Y4DJ  
 gi|7465604|pir||T02773 y4dJ protein - Rhizobium sp. plasmid pNGR234a  
 gi|2182353|gb|AAB91639.1| (AE000069) Y4dJ [Rhizobium sp. NGR234]  
 Length = 77  
 Score = 44.4 bits (104), Expect = 7e-04  
 20 Identities = 25/61 (40%), Positives = 36/61 (58%)  
 Query: 92 KAGGETFVSLRMKKGFTQSELATAAGLPQPYLSRIENSKQSLQDKTVQKLANALGVSPLE 151  
 K G F LR +KG TQ E+ +G Q YLS +E +++ T+ +LA ALGVS +E  
 Sbjct: 5 KLVGSNFARLRREKGLTQEEVEARSGFSQQYLSSLERGRNPVTITLYELAQAALGVSHVE 64  
 25 Query: 152 V 152  
 +  
 Sbjct: 65 L 65

30 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 85

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 169> which encodes amino acid sequence <SEQ ID 170; NGS85>. Analysis of this protein sequence reveals the following:

35 Signal Score (-7.5): -6.09  
 Possible cleavage site: 15  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 40 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 2.92 threshold: 0.0  
 PERIPHERAL Likelihood = 2.92  
 modified ALOM score: -1.08  
 Rule: cytoplasmic protein  
 45 \*\*\* Reasoning Step: 2  
 ----- Final Results -----  
 50 bacterial cytoplasm --- Certainty= 0.480(Affirmative) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

**Example 86**

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 171> which encodes amino acid sequence <SEQ ID 172; NGS86>. Analysis of this protein sequence reveals the following:

```

5   Signal Score (-7.5): -2.92
    Possible cleavage site: 21
    >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
        calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
    count: 1 value: -2.76 threshold: 0.0
    INTEGRAL Likelihood = -2.76 Transmembrane 179 - 195 ( 179 - 195)
    PERIPHERAL Likelihood = 2.17
    modified ALOM score: 1.05
15  Rule: cytoplasmic membrane protein

    *** Reasoning Step: 2

    ----- Final Results -----

20  bacterial inner membrane --- Certainty= 0.210(Affirmative) < succ>

```

The protein has homology with the following sequences in the databases:

```

25  >sp|Q05205|PPB_LYSEN ALKALINE PHOSPHATASE PRECURSOR (APASE)
    pir||A42467 alkaline phosphatase (EC 3.1.3.1) phoA precursor - Lysobacter
        enzymogenes
    emb|CAA39978.1| (X56656) alkaline phosphatase [Lysobacter enzymogenes]
        Length = 539

    Score = 37.5 bits (86), Expect = 0.40
    Identities = 28/82 (34%), Positives = 43/82 (52%), Gaps = 8/82 (9%)

30  Query: 189 VALGLQAYWDVAGANNNGATGQSPNIKTAQVPAKITRRNADGTTDTFGGGSARKSAAASVS 248
        V GL A W+V+ A + AQV +++ R+ GT D + G+A A AS S
    Sbjct: 458 VLRGLMA-WNVSSA-----AGKTLTGAQVKLQVSDRST-GTYDLYRAGAAWTEANASYS 509

35  Query: 249 GIEAGKKVTAVIPAVRGAVAYA 270
        G+ G K+ +V+P+ GA + A
    Sbjct: 510 GVSLGSKIGSVVPSATGAQSIA 531

```

40 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

**Example 87**

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 173> which encodes amino acid sequence <SEQ ID 174; NGS87>. Analysis of this protein sequence reveals the following:

```

45  Signal Score (-7.5): 0.18
    Possible cleavage site: 35
    >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
        calculated from 1
50  ALOM: Finding transmembrane regions (Klein et al.)
    count: 0 value: 1.70 threshold: 0.0
    PERIPHERAL Likelihood = 1.70
    modified ALOM score: -0.84
55  Rule: cytoplasmic protein

    *** Reasoning Step: 2

    ----- Final Results -----

```

bacterial cytoplasm --- Certainty= 0.138(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

5 >gi|12514207|gb|AAG55499.1|AE005289\_17 (AE005289) unknown protein encoded by  
cryptic prophage CP-933M  
[Escherichia coli O157:H7]  
gi|12514720|gb|AAG55907.1|AE005324\_10 (AE005324) unknown protein encoded by  
10 prophage CP-933N  
[Escherichia coli O157:H7]  
Length = 108

Score = 30.9 bits (69), Expect = 9.1  
Identities = 21/55 (38%), Positives = 28/55 (50%), Gaps = 3/55 (5%)

15 Query: 1 MAAPVSLLEEFKQIRIGVEHDDRDDFFLSVIDGVSAAAEAYIGRSLLAADYVGRYDG 55  
M A ++LEE K + V+HD DD + + +A AYI S D V R DG  
Sbjct: 1 MTALLTLEEIKAHLRVDHDADDDMLMDKVRQATAVLLAYIQGS---RDKVIREDG 52

20 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
useful antigens for vaccines or diagnostics.

### Example 88

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 175> which encodes amino acid sequence  
<SEQ ID 176; NGS88>. Analysis of this protein sequence reveals the following:

25 Signal Score (-7.5): -3.69  
Possible cleavage site: 43  
>>> Seems to have no N-terminal signal seq.  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
30 ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 6.05 threshold: 0.0  
PERIPHERAL Likelihood = 6.05  
modified ALOM score: -1.71  
Rule: cytoplasmic protein  
35 \*\*\* Reasoning Step: 2  
----- Final Results -----

40 bacterial cytoplasm --- Certainty= 0.227(Affirmative) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
useful antigens for vaccines or diagnostics.

### 45 Example 89

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 177> which encodes amino acid sequence  
<SEQ ID 178; NGS89>. Analysis of this protein sequence reveals the following:

50 Signal Score (-7.5): -4.77  
Possible cleavage site: 26  
>>> Seems to have no N-terminal signal seq.  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 1.38 threshold: 0.0

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PERIPHERAL Likelihood = 1.38  
 modified ALOM score: -0.78  
 Rule: cytoplasmic protein

5 \*\*\* Reasoning Step: 2

----- Final Results -----

10 bacterial cytoplasm --- Certainty= 0.284(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

>gi|9634142|ref|NP\_037684.1| gp24 [Enterobacteria phage HK022]  
 gi|6863134|gb|AAF30375.1|AF069308\_23 (AF069308) gp24 [Enterobacteria phage  
 15 HK022]

Length = 1183

Score = 44.9 bits (102), Expect = 0.006

Identities = 38/127 (29%), Positives = 64/127 (49%), Gaps = 11/127 (8%)

20 Query: 851 NKALRDKINLIDGNGAGSVNERVEAVRSTADGNAAVQTHARSI---NG-LEAQYTVK-- 904  
 NKA + +N + + ++ + +T +GN +A+ T+A++I NG L A Y +K  
 Sbjct: 989 NKASINSLNQTFSQYQATATQINGITATVNGNTSAITTAQAIANVNGDLSAMYNKVG 1048

25 Query: 905 VDANGK--VAGFGLATTPKNGTPESKFIVNADRFGI-GAAGKADVFPFVVDQKNRVGIN 961  
 V +NG+ AG G+ +S+ I ADRF + AAG + PFV+ Q + I  
 Sbjct: 1049 VSSNGQYYAAGMGIGVENTPSGMQSQVIFLADRFAVTTAAGNSVALPFVI--QNGQTFIR 1106

Query: 962 GELVVNG 968  
 + +G

30 Sbjct: 1107 ASFIQDG 1113

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 90

35 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 179> which encodes amino acid sequence <SEQ ID 180; NGS90>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -2.82

Possible cleavage site: 24

40 >>> Seems to have no N-terminal signal seq.

Amino Acid Composition of Predicted Mature Form:  
 calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)

count: 4 value: -9.66 threshold: 0.0

45 INTEGRAL Likelihood = -9.66 Transmembrane 321 - 337 ( 317 - 349)  
 INTEGRAL Likelihood = -6.48 Transmembrane 351 - 367 ( 340 - 371)  
 INTEGRAL Likelihood = -5.73 Transmembrane 907 - 923 ( 903 - 926)  
 INTEGRAL Likelihood = -0.00 Transmembrane 430 - 446 ( 430 - 446)  
 PERIPHERAL Likelihood = 2.17

modified ALOM score: 2.43

50 Rule: cytoplasmic membrane protein

\*\*\* Reasoning Step: 2

----- Final Results -----

55 bacterial inner membrane --- Certainty= 0.486(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

60 >gi|12514839|gb|AAG56002.1|AE005332\_9 (AE005332) putative tail component of  
 prophage CP-933X [Escherichia

-112-

coli 0157:H7]  
Length = 1026

Score = 111 bits (279), Expect = 3e-23  
Identities = 78/274 (28%), Positives = 146/274 (52%), Gaps = 10/274 (3%)

5 Query: 69 AAGNQAQQASEKVRAEVGKIGSGLSGLTKLLAGLATADFAKSVLDTADAMQSINSQVRQV 128  
AA + ++A ++ +++ +I + G+T AG A ++ AD S+N+++Q

10 Sbjct: 45 AAAREQRRALAEHSQLTEIRASAVGMTGAFAG---AFATGHLISLADEWSSVNARLKQA 101

Query: 129 TSSETEYLAVQQQLLDTANRTRASLESTANLYVSTSRALKDYGTYQOEILKFTAEANNAM 188  
+ S E+ + Q+ L+D + RT + A L+ ++ ++++YGY+ ++LK TEA + +

Sbjct: 102 SQSSDEFASSQKVLMDISQRTGTAFSDNAALFARSAASMREYGYSAADDVLKVTEAISTGL 161

15 Query: 189 TIGGVGAQQQAAALMQLSQALGSGVLQGEFKSISEAAPILLDTIAEYMGKSRDEIKKLG 248  
I G + + + Q SQAL GVL+G+EF S++E+ ++ +A MG +R ++K +

Sbjct: 162 KISGASTAEAGSVITQFSQALAQGVLRGEEFNSVNESGDRIVRALAAGMGVARKDLKAMA 221

20 Query: 249 SEGKLTADVIFKAISGASEKFGEQAAKMPVTMGQALT VFSNNWQSMVSKLLNDSGTMSGI 308  
+GKLTAD + A+ ++ A MP T+ ++T N + + V G +

Sbjct: 222 DDGKLTADKVVPAISQLGILRDEYAAMPETVSSSITKVENAFMAWV-----GGANEA 274

Query: 309 AAVIKLIADNLNLVVPPIVAGFAVAVAAVAPTLA 342  
+ V K ++ LN V + A AV A VA +A

25 Sbjct: 275 SGVTKTLSGMLNGVAGQIDNVATAVGALVAVGVA 308

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 91

30 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 181> which encodes amino acid sequence <SEQ ID 182; NGS91>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -0.63  
Possible cleavage site: 36  
>>> Seems to have no N-terminal signal seq.  
35 Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 0.16 threshold: 0.0  
PERIPHERAL Likelihood = 0.16  
40 modified ALOM score: -0.53  
Rule: cytoplasmic protein  
\*\*\* Reasoning Step: 2  
45 ----- Final Results -----  
bacterial cytoplasm --- Certainty= 0.250(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

50 (AF237934) putative integrase/recombinase  
[Pasteurella multocida]  
Length = 329

55 Score = 449 (206.9 bits), Expect = 4.4e-91, Sum P(2) = 4.4e-91  
Identities = 93/196 (47%), Positives = 129/196 (65%)

Query: 56 IFADLIRRYLSEVTPSKRGAREESYRIGRALKTPLAKVRLADLRPQDFADWRDQRLQEV 115  
IF D+I RY +EV+ +K+GAR E R+ R L+ ++ + + DLR +DF +W RL EVS

60 Sbjct: 55 IFRDVIERYQNEVSITKKGARNEIIRLNRFLRYDISNLYIRDRLRKEDFEWIRIRL TEVS 114

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Query: 116 PTVSGRELTTLSAVCEHAMKEWGLLRENVPVRKISKPKSRARTRRPTEQEIADICAALLY 175  
SV REL T+S+V A+ +WG + +P+ I KPK S R R +EQ+I I Y

Sbjct: 115 DASVRRELVTISSVLTTAINKWGYISRHPMTGIEKPKNSAERKERYSEQDIKTILETARY 174

5 Query: 176 RPNEKPKMAVQRVAVAVLFAIETAMRAGEICGLKWADVNMRRIAHLPTKNGDSRDVPL 235  
++ P QRVA+A+LFAIETAMRAGEI +KW +V + +RI HLP TKNG SRDVL

Sbjct: 175 CEDKLPITLKQRVAIAMLFIAIETAMRAGEIASIKWDNVFLEKRVHLPPTTKNGHSRDVPL 234

10 Query: 236 SLRAELIEQLRGIDD 251  
S RA LI +++ +++

Sbjct: 235 SQRAVALILKMKEVEN 250

Score = 248 (114.3 bits), Expect = 4.4e-91, Sum P(2) = 4.4e-91  
Identities = 48/76 (63%), Positives = 57/76 (75%)

15 Query: 254 VFSLDAKSLDVLFRARDNCGIQGLHFHDTREALTRLSKKVPVEVLAKISGHRDLRILL 313  
VF +SL FR + CG++ LHFHDTREALTRLSKKV V LAKISGHRDLRIL

Sbjct: 254 VFQTPBSLSTTFRVLKKECGLEHLHFHDTREALTRLSKKVDVMTLAKISGHRDLRILQ 313

20 Query: 314 NVYYRPDMADIAKMLD 329  
N YY P+M+++A +LD

Sbjct: 314 NTYYAPNMSEVANLLD 329

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
25 useful antigens for vaccines or diagnostics.

## Example 92

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 183> which encodes amino acid sequence  
<SEQ ID 184; NGS92>. Analysis of this protein sequence reveals the following:

30 Signal Score (-7.5): -7.85  
Possible cleavage site: 25  
>>> Seems to have an uncleavable N-term signal seq  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1.  
ALOM: Finding transmembrane regions (Klein et. al.)  
35 count: 1 value: -8.33 threshold: 0.0  
INTEGRAL Likelihood = -8.33 Transmembrane 6 - 22 ( 1 - 25)  
PERIPHERAL Likelihood = 5.99  
modified ALOM score: 2.17  
Rule: cytoplasmic membrane protein  
40 \*\*\* Reasoning Step: 2  
----- Final Results -----  
45 bacterial inner membrane --- Certainty= 0.433(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

>gi|9632051|ref|NP\_048840.1| A484L [Paramecium bursaria Chlorella virus 1]  
gi|7461623|pir|T17986 hypothetical protein A484L - Chlorella virus PBCV-1  
50 gi|1620155|gb|AAC96851.1| (U42580) A484L [Paramecium bursaria Chlorella virus 1]  
Length = 155

Score = 31.6 bits (70), Expect = 3.5  
Identities = 20/72 (27%), Positives = 36/72 (49%)  
55 Frame = +1

Query: 52 LQINLKMLEKRIDFLVENIDKYYQQYGSYPNNFDFISTKTDFTTESYCDFWDKNIAGYGN 231  
+ +NLKM I F +DKY +QY +Y N F T+ + + ++ + +I N

Sbjct: 23 IAVNLKMGVSIPF----VDKYSKQYPTYTKNALFHVTRFNNAVQKTFEYKNISIDTINN 78

60 Query: 232 CYFVKNDKDYTI 267

+ +++D Y I  
 Sbjct: 79 LFSIRDDVLYNI 90

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
 5 useful antigens for vaccines or diagnostics.

### Example 93

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 185> which encodes amino acid sequence  
 <SEQ ID 186; NGS93>. Analysis of this protein sequence reveals the following:

10 GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -5.08  
 Possible cleavage site: 14  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 15 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 0.79 threshold: 0.0  
 PERIPHERAL Likelihood = 0.79  
 modified ALOM score: -0.66  
 20 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 ----- Final Results -----  
 25 bacterial cytoplasm --- Certainty= 0.320(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

>gb|AAG22017.1|AF288038\_2 (AF288038) putative HsdR [Streptococcus thermophilus]  
 Length = 740  
 30 Score = 674 bits (1738), Expect = 0.0  
 Identities = 364/746 (48%), Positives = 489/746 (64%), Gaps = 40/746 (5%)  
 Query: 14 NENSrvKIPAVLHLMRLGYDYLsLKNANW---DRQTNIFFEIFVDSLcRINPDLPPDDAR 70  
 +E +RV+IPA HLMRLGY YL D +TNI IF + + N D  
 35 Sbjct: 8 SELTRVQIPAAFHLMRLGYTYLPHNGKEIMGRDPETNILISIFREQFLKFNNYATDLQVE 67  
 Query: 71 RLLADIRLELDNEDLGQKFYERLTNQSGGKKLIDFQNFNNFHVVTETPCINGDEAFRP 130  
 R L +I++ELD DLG+ FY R+ + SG +D++N +NN+PH+ E+ C NG + FRP  
 40 Sbjct: 68 RELNNIKIELDQNDLGAFYNRIVSDSG-PTYVDWENPENNTFHLALEVTCQNGGDEFERF 126  
 Query: 131 DIALLVNGMPLVFIEVKKPEN---NRGGIGEERERMGKRAKNPKFRRFINITQFMIFSNN 186  
 DI + +NG+PL +IEVK+PN K I E+ R R +N +FRRF NITQ + FS+N  
 45 Sbjct: 127 DIVIFINGLPLSYIEVKQPNNAIRDGKTAIQSEQSRTAVRFENRRFRFNITQLISFSDN 186  
 Query: 187 MEYDDGATEPAQGAfYASSACGKPFVFNyFREEHXXXXXXXXXXXXXXXXXVLQDNNLPV 246  
 + Y G + QG+FY S+A K FN F+EE + VL+D N  
 Sbjct: 187 LPYISGQGGQKQGSFYCSNAFSKTKFNAFKEEREELIYSIRSLGEEEBIDAVLKDVNRFA 246  
 50 Query: 247 IKHSPEFISNKSPTPTNRIILTSLLCRERLSFLLQHGLTYVK--ASQGLVQ--KHIMRYP 302  
 +K PEF +N+ P TP N ++SL ++RL FLL++GL YV+ + G +Q KH+MRYP  
 Sbjct: 247 LKSQPEFKTNQDPSTPCNTFISSLYQKKRLLFLLRYGLAYVEEHSKDGTLQKQHVMRYP 306  
 Query: 303 QLFATLAIEKHLANGGKKGVWHTQSGSKTALAYNTRYLTHYAKQGIVPKFYFIVDRL 362  
 Q FAT AIE + G +KGVWHTQSGSKTAL+Y+N RYLT+Y++KQGIVP+FYF+VDRL  
 55 Sbjct: 307 QFFATKAIEDAIGKGVKGVWHTQSGSKTALSYFNIRYLTNYFSKQGIVPQFYFVVDRL 366  
 Query: 363 DLLKQAQREFTARDLVVHTIDSREAFADIKSAQTLHNHAGKAEITVVNIQKFQDDPDVV 422  
 DL QA REFT R L V I+S Q L+ ++ VVNIQKF+D+ D+  
 60 Sbjct: 367 DLADQATREFTKRGLKVKRINS-----PQELNEKHDAYQVAVVNIQKFKNDSDLT 416

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Query: 423 ARNDYDLAIQRVYFLDEVHRSYNPKGSFLANLNQSDVNAVIGLTGTPLI-----GVTA- 476  
 + YDL Q +YF+DE HRSYN KGS+L NL +D NA+KI LTGTPLI G T  
 Sbjct: 417 DHSGYDLNRQNIYFIDEAHRSYNEKGSYLEPNLYNADKNAIKIALTGTPLITYKKDGKTKKE 476

5 Query: 477 GNVNTRLEFGDYIHKYYYNASIADGYTLRLIREEIGSRYKAQLQEQALAEIEKGSFDRK 536  
 + TR++FGDYIHKYYYN SI DG+TLRL+RE+I + YK LQ EI +G +  
 Sbjct: 477 SHATTRDIFGDYIHKYYYNQSIDDGFTLRLMREDIETSYKETLQTI--NEEILRGDLSKD 534

10 Query: 537 EIIYAHPHFVHPMLDYILDDFAKFRKTN-QDESLGAMVVCDSAEQARQL---FEHFQTASD 592  
 +I+AHP +V PMLD+IL+DF + R D+S+G M+VCDS++QAR++ E ++ +  
 Sbjct: 535 DIFAHPRYVSPMLDFILEDENRARDVVFDSDSIGGMIVCDSSKQAREIEKQLEERRSRGE 594

15 Query: 593 HNFTAALILHDVGTKEERDQWVKDFKAGKIDILFVYNMLLTGFDAPRLKKLYLGRLIKAH 652  
 N T+ALILHD G KE + V+ ++ GKID++ VY+MLLTGFDAPRLK+LYLGR IKAH  
 Sbjct: 595 TNITSALILHDEGDKEYKKDRVESYREGKIDLVIVYSMLLTGFDAPRLKRLYLGRKIKAH 654

20 Query: 653 NLLQTLTRVNRITYKSYRYGYVVDFAIEREFDKTNRAYWDELSNE-----LGDEIGS-YS 706  
 NLLQTLTRVNR YK Y++GYV+DFADI +EFDKTNRAY +EL+ E G+++ + +  
 Sbjct: 655 NLLQTLTRVNRPYKDYQPGYVIDFADISKEFDKTNRAYLEELNQEYDPKNTGEDOVENVFG 714

Query: 707 QLFKTAEBIEQEIADIKNALFDFDTE 732  
 LF +A+EI +++ + L ++ TE  
 Sbjct: 715 SLFVSADEISKQLEKSETILMNYPTTE 740

25 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 94

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 187> which encodes amino acid sequence <SEQ ID 188; NGS94>. Analysis of this protein sequence reveals the following:

30 Signal Score (-7.5): -3.19  
 Possible cleavage site: 35  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1

35 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 5.73 threshold: 0.0  
 PERIPHERAL Likelihood = 5.73  
 modified ALOM score: -1.65  
 Rule: cytoplasmic protein

40 \*\*\* Reasoning Step: 2

----- Final Results -----

45 bacterial cytoplasm --- Certainty= 0.302(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

50 >gi|10717100|gb|AAG22014.1|AF288037\_3 (AF288037) putative HsdS [Streptococcus thermophilus]  
 Length = 402

Score = 154 bits (389), Expect = 2e-36  
 Identities = 123/348 (35%), Positives = 168/348 (47%), Gaps = 48/348 (13%)

55 Query: 73 GKTA FVDILDDGEVAFGSTEFIVLRKNET--NPEFLYFPAISPDRKRAIECMGTSGR 130  
 GKT ++ DGE ++ IV +E+ +FLYYF + F G++ +  
 Sbjct: 74 GKT----VIFDGEDSYFQDSNIVWIENDESKVTNQFLYYFLQTNPFIT-----TNGSTIK 124

60 Query: 131 QRVNENALKTLELPIPEPQIQQSIAAVLSALDKKIALNKQINARLEEMAKTLYDYWFVQF 190  
 + N+N T +P Q Q I +L LDKKI +N QIN LE MAKTLYDYWFVQF  
 Sbjct: 125 RLYNDNLRDTKIPNVPSIQQQNQITDILGLDKKIQINNQNQINQELEAMAKTLYDYWFVQF 184



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Query: 191 DFPDANGKPYKSSGGDMVFDETLKREIPKGWGSIELQSCL---AKIPNTTKILNKDIXDF 247  
 DFPD NGKPYKSSGG MV++ LKREIP+GWG+ +L S L + N K N++ K +  
 Sbjct: 185 DFPDQNGKPYKSSGGKMVYNPELKREIPEGWGAELSSLLKIGKETTNPKKFPNEEFKYY 244  
 5  
 Query: 248 -----GKYPVVD-----QSQDFICGFTNDEKSILNPQDAHIIFGDHTRIVKLNVFOYA 295  
 G Y + +S F + S LNP +I+ + F  
 Sbjct: 245 SIPEFDTTGTYSLERGESIKSNKFKVEKNDLLVSKLNPWFNRVTYNLEENAIASTEF--- 301  
 10  
 Query: 296 RGADGTQVILSNERNMPNYLFYQIINQIDLSSY-----GYARHFK-----FLKEFKIIL 344  
 ++ R YQ+ + Y G + K + F+I  
 Sbjct: 302 -----IVWKTFRNFEKNFLYQVATGKEFIEYCTRFBATGTSNSHKRVSPDIMVGFQIPF 354  
 15  
 Query: 345 PSKDISQKYNEIANTFFVKVRNNLQNHHLTQLRDFLLPMLMNGQVSV 392  
 I QK+ EI ++ +V N +QN LTQLRD++LPMLMNGQV V  
 Sbjct: 355 EKTHI-QKGEIIDSIRTQVLQNNQNLQELTQLRDWILPMLMNGQVKV 401

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## 20 Example 95

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 189> which encodes amino acid sequence <SEQ ID 190; NGS95>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -6.12  
 Possible cleavage site: 19  
 25  
 >>> Seems to have an uncleavable N-term signal seq  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 30  
 count: 3 value: -10.51 threshold: 0.0  
 INTEGRAL Likelihood = -10.51 Transmembrane 112 - 128 ( 109 - 132)  
 INTEGRAL Likelihood = -4.46 Transmembrane 50 - 66 ( 46 - 70)  
 INTEGRAL Likelihood = -2.23 Transmembrane 7 - 23 ( 7 - 23)  
 PERIPHERAL Likelihood = 4.19  
 35  
 modified ALOM score: 2.60  
 Rule: cytoplasmic membrane protein  
 \*\*\* Reasoning Step: 2  
 40  
 ----- Final Results -----  
 bacterial inner membrane --- Certainty= 0.520(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

45 >pir||G69096 hypothetical protein MTH1717 - Methanobacterium thermoautotrophicum  
 (strain Delta H)  
 gb|AAB86189.1| (AE000928) unknown [Methanothermobacter thermautotrophicus]  
 Length = 557  
 50  
 Score = 35.4 bits (80), Expect = 0.50  
 Identities = 25/80 (31%), Positives = 47/80 (58%), Gaps = 5/80 (6%)  
 Query: 52 LLFYFLIPFIATATVLWL SKYLKDEFKQGEVKELEYVNDNFLPSYLG YFFVALSIPDNN 111  
 L+F+F+ P + TATVL + K + ++ F++ EV L + +PS++ ++ IP++  
 55 Sbjct: 92 LVFFFISPLLGTATVLVIYK-VARETFEREEVALLSAFLFSMVPSFVAR--TSVFIPESM 148  
 Query: 112 LFLLFVYGIIFLLVSCSKS 131  
 LL GI+++LV K+  
 60 Sbjct: 149 GLLL--TSGILYMLVKYLKT 166

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 96

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 191> which encodes amino acid sequence

5 <SEQ ID 192; NGS96>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -7.76  
 Possible cleavage site: 28  
 >>> Seems to have no N-terminal signal seq.  
 10 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 6.15 threshold: 0.0  
 PERIPHERAL Likelihood = 6.15  
 15 modified ALOM score: -1.73  
 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 20 ----- Final Results -----  
 bacterial cytoplasm --- Certainty= 0.362(Affirmative) < succ>

The protein has no homology with sequences in the databases.

25 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 97

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 193> which encodes amino acid sequence  
 <SEQ ID 194; NGS97>. Analysis of this protein sequence reveals the following:

30 GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -0.48  
 Possible cleavage site: 13  
 >>> Seems to have no N-terminal signal seq.  
 35 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 8.86 threshold: 0.0  
 PERIPHERAL Likelihood = 8.86  
 modified ALOM score: -2.27  
 40 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 ----- Final Results -----  
 45 bacterial cytoplasm --- Certainty= 0.127(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

50 >ref|NP\_052265.1| P2 J homolog; baseplate or base of tail fibre [Enterobacteria  
 phage  
 186]  
 gb|AAC34162.1| (U32222) P2 J homolog; baseplate or base of tail fibre  
 [Enterobacteria phage 186]  
 Length = 302

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Score = 112 bits (280), Expect = 3e-24  
 Identities = 65/151 (43%), Positives = 85/151 (56%), Gaps = 1/151 (0%)

```

5  Query: 1  MGNSRSLSQLPAPAAIBETDFEGIFARKKAALTALCPBSIRETVAQTLLESEPLTIDLQQ 60
      M   LS LP P  +EE DFE I A + A L +L PE  +E VA+TL LESEP+  LQ+
      Sbjct: 1  MATVDLSLLFPDVPDVEELDFETILAERIATLISLYPEDQQEAVARTLALESEPIVKLLQE 60

10 Query: 61  QAYQELLVRNRINEAVKANLLAYAQGSDDLHIAAQVGLSRKTIRXXXXXXXXXXXXEYET 120
      AY+E++ R R+NEA +A +LAYA+ SDLD++ A + + R +R          E E
      Sbjct: 61 NAYREVIWRQRVNEAARAGMLAYARDSLDNLGANFNVERLVVRPADDTTIPPTPAEMEL 120

      Query: 121 DDAFRARV-QAHPEKYAAGPRTAYEAHAIDA 150
      D FR R+ QA      AG  AYE H  A
15  Sbjct: 121 DADFRLRIQQAFEGMSVAGSTGAYEFHGRSA 151
  
```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 98

20 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 195> which encodes amino acid sequence <SEQ ID 196; NGS98>. Analysis of this protein sequence reveals the following:

```

      Signal Score (-7.5): -3.68
      Possible cleavage site: 33
      >>> Seems to have no N-terminal signal seq.
25  Amino Acid Composition of Predicted Mature Form:
      calculated from 1
      ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 4.61 threshold: 0.0
      PERIPHERAL Likelihood = 4.61
30  modified ALOM score: -1.42
      Rule: cytoplasmic protein

      *** Reasoning Step: 2

35  ----- Final Results -----

      bacterial cytoplasm --- Certainty= 0.182(Affirmative) < succ>
  
```

The protein has no homology with sequences in the databases.

40 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 99

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 197> which encodes amino acid sequence <SEQ ID 198; NGS99>. Analysis of this protein sequence reveals the following:

```

45  Signal Score (-7.5): -4.87
      Possible cleavage site: 19
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
50  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 4.93 threshold: 0.0
      PERIPHERAL Likelihood = 4.93
      modified ALOM score: -1.49
      Rule: cytoplasmic protein
55
  
```

\*\*\* Reasoning Step: 2

----- Final Results -----

5 bacterial cytoplasm --- Certainty= 0.189(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

10 >gi|10172952|dbj|BAB04058.1| (AP001508) BH0339-unknown conserved protein in  
others [Bacillus  
halodurans]  
Length = 283

Score = 83.7 bits (206), Expect = 1e-15

Identities = 59/156 (37%), Positives = 87/156 (54%), Gaps = 8/156 (5%)

15 Query: 10 VRGPFVQLAFAQSIDPIVPPEVSITRMAVTNEKDLEKERTMGRKYIVPYVVYRVHGFISAN 69  
VRGPFV + A SIDPI IT+ + D TMG K+ V + VY G I+  
Sbjct: 129 VRGFSIHTATSIDPIDIVSTQITKSVNSVTGDKRSSDTMGMKHRVDFGVYVFKGSINTQ 188

20 Query: 70 LAAKTGFSDDDLAKLWQALTLMEHDSRAAR--GEMAARKLVVFKHDSALGSQPAHKLFD 127  
LA KTGF+++D K+ +AL +FE+D S+AR G M K+ ++H S LG + K+  
Sbjct: 189 LAEKTGFTNEDAEEKIKRALITLTFENDSSSARPDGSMFVHKVYNWEHSSKLGQYSSAKVHR 248

25 Query: 128 AVKVERVNGESGTPASGFGDYKISVVSDDLNGVSVE 163  
++K+E ++ TP S F DY + + L+G+ VE  
Sbjct: 249 SLKIE---SKTDTPKS-FDDYAVELYE--LDGLGVE 278

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### 30 Example 100

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 199> which encodes amino acid sequence <SEQ ID 200; NGS100>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -3.03  
Possible cleavage site: 18  
35 >>> Seems to have no N-terminal signal seq.  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 6.63 threshold: 0.0  
40 PERIPHERAL Likelihood = 6.63  
modified ALOM score: -1.83  
Rule: cytoplasmic protein

45 \*\*\* Reasoning Step: 2

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.185(Affirmative) < succ>

50 The protein has homology with the following sequences in the databases:

>gi|1175791|sp|P44189|YE18\_HAEIN HYPOTHETICAL PROTEIN HI1418  
gi|1074769|pir|A64029 hypothetical protein HI1418 - Haemophilus influenzae  
(strain Rd  
KW20)  
55 gi|1574254|gb|AAC23068.1| (U32821) H. influenzae predicted coding region HI1418  
[Haemophilus  
influenzae Rd]  
Length = 201

60 Score = 144 bits (364), Expect = 1e-33

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Identities = 71/109 (65%), Positives = 79/109 (72%)

Query: 8 NFOQNSVTVADNKGELWFLANDVCEILGYTNPRRTVDLHCKSRGVTKRYTPTTSGEQEM 67  
 NF+ VR + D KGE WF DVC ILGYTN R+ + HCK GVTKRYTPT S +QEM  
 5 Sbjct: 24 NFKDLFVRVILDPKGEFWFCGTDVCHILGYTNSRKALQDHCKQGGVTKRYTPTKSADQEM 83

Query: 68 TYINEPNLYRLIIKSRKPAARAFEEVWVETVLPPIRKTGGCQVGPRTTA 116  
 T+INEPNLYRLIIKSRKP AE FE WV E VLP IRKTG Q+ P+ A  
 10 Sbjct: 84 TFINEPNLYRLIIKSRKPEAEFPAWVFEEVLPQIRKTGKYQLQPQOLA 132

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

**Example 101**

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 201> which encodes amino acid sequence  
 15 <SEQ ID 202; NGS101>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -1.23  
 Possible cleavage site: 47  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 20 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 3.55 threshold: 0.0  
 PERIPHERAL Likelihood = 3.55  
 modified ALOM score: -1.21  
 25 Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

----- Final Results -----

30 bacterial cytoplasm --- Certainty= 0.126(Affirmative) < succ>

The protein has homology with the following sequences in the databases:

35 >gi|9632520|ref|NP\_049514.1| hypothetical protein [Bacteriophage 933W]  
 gi|9633449|ref|NP\_050552.1| hypothetical protein [Bacteriophage VT2-Sa]  
 gi|4585431|gb|AAD25459.1|AF125520\_54 (AF125520) hypothetical protein  
 [Bacteriophage 933W]  
 gi|5881645|dbj|BAA84336.1| (AP000363) hypothetical protein [Bacteriophage VT2-  
 40 Sa]  
 gi|7649882|dbj|BAA94160.1| (AP000422) hypothetical protein [Escherichia coli  
 O157:H7]  
 Length = 404

Score = 177 bits (449), Expect = 3e-43  
 45 Identities = 130/425 (30%), Positives = 204/425 (47%), Gaps = 27/425 (6%)

Query: 7 TAYGDPQAMMKQAAGLFAMHMQRNSTLNRLAGKMPAGTA-GAEATLRKQTTQHMPVVRQC 65  
 T QA LF + S +N L + A A + KQT+ PVVR  
 50 Sbjct: 2 TTVTSAQANKLYQVALFTAANRNRSMVNILTEQQEAPKAVSPDKRSTKQTSAGAPVVRIT 61

Query: 66 DLTRMGDEIRFNLVNPVSALPIMGDNTAEGRGVGMSLSEAGLRVNQARFPVDGGGTMTN 125  
 DL + GDE+ F++++ +S P MGD EGRG +S ++ L++NQ R VD GG M+  
 Sbjct: 62 DLNKQAGDEVTFSSIMHKLSKRPTMGDERVEGRGEDLSHADFSLKINQGRHLVDAGGRMSQ 121

55 Query: 126 QRSPADYRALIRPAAQSLMDRYADQTLVHVMAGARGFHDNIEWGVPLAGDPKFNDYAVNP 185  
 QR+ + + R + + DQ +VH+AGARG + +P A P+F +N  
 Sbjct: 122 QRTKFNLAASARTLLGTYFNDLQDQCAIVHLAARGDFVADDTILPTAEHPEFKKIMIND 181

60 Query: 186 VKAPSKNRHFTASGDAVTGVGDNGGELKIASTDLFTMDTVDSMRTVLDQIPLPPPIVKFE 245  
 V P+ +RHF GD +I + D+F++ VD++ +D++ P V+  
 Sbjct: 182 VLPPTHDRHFFG-----GDATSFEQIEAADIFSIGLVDNLSLFIDEMAHPQLQPVRLS 233

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Query: 246 GDKAAGDSPLRVWLLSPAQYNRF---AADPKFRQLQASAIARASQANQNPLFLGDAGLWN 302  
 GD+ G+ P V ++P Q+N + + + Q+ A+ RA N +PLF G+ +W  
 Sbjct: 234 GDELHGEDFYVLYVTTPRQWWDWYTSTSGKDWNQMMVRAVNRAGFN-HPLFKGECAMWR 292

5 Query: 303 GFILVKMP-RPIRFYAGDEMYCADKFSSEBSGLKIPASFADKFAVDRSVILGGQAVLEA 361  
 ++ K PIRFY G ++ + + A +DR+++LG QA+ A  
 Sbjct: 293 NILVRKYAGMPIRFYQGSKVLVSENNLTATTK-----EVAAATNIDRAMLLGAQALANA 346

10 Query: 362 FANTGKHGGMPFFWSEKELDHGNRVETLVGTIRGVAKTRFAVDVGGGAKEITDYGVTVD 421  
 + G+ G F EK+ D NR E + I G+ K RF G ++ D+GV VD  
 Sbjct: 347 Y---GQKAGGHFNMVEKKTMDNRTETIAISWINGLKKIRFPEKSG----KMQDHGVIAVD 399

15 Query: 422 TVVPL 426  
 T V L  
 Sbjct: 400 TAVKL 404

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## 20 Example 102

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 203> which encodes amino acid sequence <SEQ ID 204; NGS102>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -6.09  
 Possible cleavage site: 15  
 25 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 2.92 threshold: 0.0  
 30 PERIPHERAL Likelihood = 2.92  
 modified ALOM score: -1.08  
 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 35 ----- Final Results -----  
 bacterial cytoplasm --- Certainty= 0.480 (Affirmative) < succ

40 The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## Example 103

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 205> which encodes amino acid sequence <SEQ ID 206; NGS103>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -1.29  
 Possible cleavage site: 34  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 50 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 1 value: -0.00 threshold: 0.0  
 INTEGRAL Likelihood = -0.00 Transmembrane 22 - 38 ( 22 - 38)  
 PERIPHERAL Likelihood = 4.88  
 55 modified ALOM score: 0.50

-122-

Rule: cytoplasmic membrane protein

\*\*\* Reasoning Step: 2

5 ----- Final Results -----

bacterial inner membrane --- Certainty= 0.100(Affirmative) &lt; succ&gt;

The protein has homology with the following sequences in the databases:

10 >gi|11277848|pir||E81145 replicative DNA helicase NMB0885 [imported] - Neisseria  
meningitidis (group B strain MD58)  
gi|7226124|gb|AAF41296.1| (AE002441) replicative DNA helicase [Neisseria  
meningitidis MC58]  
Length = 468

15 Score = 233 bits (594), Expect = 5e-60  
Identities = 158/456 (34%), Positives = 245/456 (53%), Gaps = 34/456 (7%)

20 Query: 15 SVGAEQNILGGILIEPTAIARCA-ILTPEKFYQAQHRIIFRALLDMAAANEPIDIITLND 73  
S+ AEQ++LGG+++E A R A +++ E FY+ +HR+IFR++ + + P D+IT+ +  
Sbjct: 23 SMEAEQSVLGGMLLENPAWDRIADVSGEDFYRHEHRLIFRSIAKLINESRPADVITVQE 82

25 Query: 74 KLEARGEAEENAGGLAYLIDLNQNTPSAKNISRYVGIVNDRFVERGLLKASAAIEKIAVSK 133  
L+ E E AGG YLI L QNTPSA NI RY IV +R + R L + I + A +  
Sbjct: 83 DLQRNEELEAAGGFYDLITLAQNTPSAANIRRYAEIVRERSIMRQLAEVGTETIARSAYNP 142

30 Query: 134 DGGTVAEKLSKAADLAAGKDAVKRETKTFGQTVEDLIGGLDKRLDGVR-----FG 185  
G + L +A +++ + + K +K + DL+ + +R+D + G  
Sbjct: 143 QGRDAGQLLDEAENKVFQIAESTAK--SKQGFLLEMPDLLKEVVQRIDMLYSRDNPDDEV TG 200

35 Query: 186 LPTGLMKLDGMTGGLPDGNLIVIAARPSMGKTVLAENIARFALKQKGK-AVHFQSYEMSAV 244  
+PTG + LD T GL G+LI++A RPSMGKT + NIA +G+ V S EM  
Sbjct: 201 VPTGFIDLDKKTSGLQPGDLIIIVAGRPSMGKTAFSINIAEHVAVEGRLPVAVFPMEMGGA 260

40 Query: 245 ELARRGMAAECNIPMQNLKLTGNLTQSDYANM-----PIYVSQAKWKFDVNCDDL 294  
+L R + + + LKTG L + + P+Y+ +  
Sbjct: 261 QLVMRMLGSVGRLDQSVLKTGRLEDEHWGRLEAVVKSLSAPVYIDETPGLTALELRARA 320

45 Query: 295 NVDELCLAKEKKLTTGLDLLVVDHLHIMPRAGRDE--VAELGNISRRLLKNLAELNTPV 352  
F K L L+V+D+L +M +GR + +ELG ISR LK LA EL P+  
Sbjct: 321 RRLARQFNK-----LGLIVIDYQLMAGSGRSDNRASELGEISRSLKALAKELQVPI 373

50 Query: 353 VLVAQLNRGNTKQADKRPNMADIRGSGAIEQDANIIMPHRESYYDGNENP--SIAELII 410  
+ ++QL+R + DKRP M+D+R SGAIEQDA++I+ +R+ YY+ ++P +AE II  
Sbjct: 374 IALSQLSRTVESRTDKRPMMSDLRESGAIEQDADLIMFMYRDEYYN-QDSFPMKGLAECII 432

55 Query: 411 AKNRDGE MGTVVCGWKGQFMKFEEEPDLAWQAPKHD 446  
K+R+G +G + W GQF KF+ + +A D  
Sbjct: 433 GKHRNGPVGKIFLTWTGQFTKFDNAAYIPEEKIED 468

60 >gi|11277846|pir||E81876 probable replicative DNA helicase (EC 3.6.1.-) NMA1105  
[imported] -  
Neisseria meningitidis (group A strain Z2491)  
gi|7379799|emb|CAB84367.1| (AL162755) putative replicative DNA helicase  
[Neisseria  
meningitidis Z2491]  
Length = 468

65 Score = 230 bits (588), Expect = 2e-59  
Identities = 158/456 (34%), Positives = 244/456 (52%), Gaps = 34/456 (7%)

Query: 15 SVGAEQNILGGILIEPTAIARCA-ILTPEKFYQAQHRIIFRALLDMAAANEPIDIITLND 73  
S+ AEQ++LGG+++E A R A +++ E FY+ +HR+IFR++ + + P D+IT+ +  
Sbjct: 23 SMEAEQSVLGGMLLENPAWDRIADVSGEDFYRHEHRLIFRSIAKLINESRPADVITVQE 82

Query: 74 KLEARGEAEENAGGLAYLIDLNQNTPSAKNISRYVGIVNDRFVERGLLKASAAIEKIAVSK 133  
L+ E E AGG YLI L QNTPSA NI RY IV +R + R L + I + A +

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Sbjct: 83 DLQRNEELEAAGGFYLLITLAQNTPSAANIRRYAEIVRERSIMRQLAEVGTIARSAYNP 142

Query: 134 DGGTVAEKLSKAADELAAGVGDVAVKRETKTFGQTVEDLIGGLDKRLDGVR-----FG 185  
 G + L + A +++ + + K +K + DL+ + +R+D + G

5 Sbjct: 143 QGRDAGQLLDEAENKVFQIAESTAK--SKQGFLEMPDLLKEVVQRIDMLYSRDNPDVETG 200

Query: 186 LPTGLMKLDGMTGGLPDGNLIVIAARPSMGKTVLAENIARFALKQGGK-AVHFQSYEMSAV 244  
 + TG + LD T GL G+LI++A RPSMGKT + NIA +GK V S EM

10 Sbjct: 201 VSTGFIDLDKKTSGQLPGDLIIVAGRPSMGKTAFSINIAEHVAVEGKLPVAVFSMEMGGA 260

Query: 245 ELARRGMAAECNIPMQNLKTGNLTQSDYANM-----PIYVSQAKEWKFDVNCDDL 294  
 +L R + + + LKTG L + + P+Y+ +

Sbjct: 261 QLVMRMLGSGVGRLDQSVLKTGRLEDEHWGRLEAVVKLSDAFVYIDETPGLTALELRARA 320

15 Query: 295 NVDELCEFLAKEKLLTGLDLLVVDHLHIMPRAGRDE--VAELGNISRRKLNLAELNTPV 352  
 F K L L+V+D+L +M +GR + +ELG ISR LK LA EL P+

Sbjct: 321 RRLARQFNK-----LGLIVIDYLQLMAGSGRSDNRASELGEISRLKALAKELQVPI 373

20 Query: 353 VLVAQLNRGNTKQADKRPNMADIRGSGAIEQDANIIIMPHRESYYDGNENP--SIAELII 410  
 + ++QL+R + DKRP M+D+R SGAIEQDA++I+ +R+ YY+ ++P +AE II

Sbjct: 374 IALSQLSRTVESRTDKRPMMSDLRESGAIEQDADLIMFYRDEYYN-QDSPMKGLAECII 432

Query: 411 AKNRDGMGTVVCGWKGQFMKFEEEPDLAWQAPKHD 446  
 K+R+G +G + W GQF KF+ + +A D

25 Sbjct: 433 GKHRNGPVGKIFLTWTGQFTKFDNAAYIPEEKIED 468

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 104

30 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 207> which encodes amino acid sequence <SEQ ID 208; NGS104>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -2.11  
 Possible cleavage site: 15  
 >>> Seems to have no N-terminal signal seq.

35 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 5.04 threshold: 0.0  
 PERIPHERAL Likelihood = 5.04  
 40 modified ALOM score: -1.51  
 Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

45 ----- Final Results -----  
 bacterial cytoplasm --- Certainty= 0.220(Affirmative) < succ

The protein has homology with the following sequences in the databases:

50 >gi|7515458|pir||T13296 hypothetical protein 8 - Streptococcus phage phi-01205  
 gi|2444088|gb|AAC79524.1| (U88974) ORF8 [Streptococcus thermophilus temperate  
 bacteriophage  
 01205]  
 Length = 157

55 Score = 62.1 bits (150), Expect = 3e-09  
 Identities = 53/161 (32%), Positives = 86/161 (52%), Gaps = 8/161 (4%)

Query: 5 TLYRCAADVQAGLDYFFDSETEREDTLEAV--IGQFEVKAQSVIAYIKNQEITEKMLEGH 62  
 TLY + + D ET + DTLEA+ +E K + + IK+ E + +

60 Sbjct: 3 TLYELTDQLLEIYNMVDVDET-KLDTLEAIDWTTDYENKVEGYVKVIKSLEADIEARKNE 61



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Query: 63 IRQMTGKLKAAKARNQSLKDYLRNMQAAGITEIKADDGTFKASFRKSEAVVILDEAQIP 122  
 +++ G K+ +++ LK LA +M G T + D FK FRKSEAVV+ +E ++P  
 5 Sbjct: 62 KKRLDGLNKSDQSKIDKLKTALAVSMAETGQTRV--DTTLFKVGFVKSEAVVV-NEEKLP 118

Query: 123 AEFMREAVKTEPDKTAIRKAIESGRQVAGAKIEGRKNLQIR 163  
 E+ K PDK +++ ++SG+ + GA +E R+NL IR  
 Sbjct: 119 KEYQIATYK--PDKKTLKELLKSGKHIEGATLEERRNLNIR 157

- 10 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 105

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 209> which encodes amino acid sequence <SEQ ID 210; NGS105>. Analysis of this protein sequence reveals the following:

- 15 Signal Score (-7.5): -5.52  
 Possible cleavage site: 31  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1
- 20 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 2.60 threshold: 0.0  
 PERIPHERAL Likelihood = 2.60  
 modified ALOM score: -1.02  
 Rule: cytoplasmic protein
- 25 \*\*\* Reasoning Step: 2
- Final Results -----
- 30 bacterial cytoplasm --- Certainty= 0.135(Affirmative) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### 35 Example 106

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 211> which encodes amino acid sequence <SEQ ID 212; NGS106>. Analysis of this protein sequence reveals the following:

- Signal Score (-7.5): 4.8  
 Possible cleavage site: 26
- 40 >>> Seems to have a cleavable N-term signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 27
- ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 7.80 threshold: 0.0
- 45 PERIPHERAL Likelihood = 7.80  
 modified ALOM score: -2.06  
 Score for OM-PP discrimination: 4.38  
 Rule: outer membrane or periplasmic protein  
 Score for OM-PP discrimination: 4.38
- 50 Rule: outer membrane or periplasmic protein
- \*\*\* Reasoning Step: 2
- Outer membrane? Score: 0.437687
- 55 Outer membrane? Score: 0.437687

## ----- Final Results -----

bacterial outer membrane --- Certainty= 0.768(Affirmative) < succ>

5

The protein has no homology with sequences in the databases, although it is similar to HMW1 from *Haemophilus influenzae*.

The protein was expressed in *E.coli* as an insoluble 43.56kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

10

## Example 107

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 213> which encodes amino acid sequence <SEQ ID 214; NGS107>. Analysis of this protein sequence reveals the following:

Signal Score (-7.5): -3.83  
Possible cleavage site: 51  
>>> Seems to have no N-terminal signal seq.  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 4.61 threshold: 0.0  
PERIPHERAL Likelihood = 4.61  
modified ALOM score: -1.42  
Rule: cytoplasmic protein

15

20

25

\*\*\* Reasoning Step: 2

## ----- Final Results -----

bacterial cytoplasm --- Certainty= 0.146(Affirmative) < succ>

30

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## Example 108

35 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 215> which encodes amino acid sequence <SEQ ID 216; NGS108>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
Signal Score (-7.5): -6.14  
Possible cleavage site: 19  
>>> Seems to have no N-terminal signal seq.  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 8.43 threshold: 0.0  
PERIPHERAL Likelihood = 8.43  
modified ALOM score: -2.19  
Rule: cytoplasmic protein

40

45

\*\*\* Reasoning Step: 2

50

## ----- Final Results -----

-126-

bacterial cytoplasm --- Certainty= 0.574(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

5

The protein has homology with the following sequences in the databases:

>pir||G81977 probable lipoprotein NMA0586 [imported] - Neisseria meningitidis  
 (group A strain Z2491)  
 emb|CAB83877.1| (AL162753) putative lipoprotein [Neisseria meningitidis Z2491]  
 Length = 280

Score = 52.9 bits (126), Expect = 5e-06  
 Identities = 43/134 (32%), Positives = 63/134 (46%), Gaps = 23/134 (17%)

15 Query: 174 LGDIRGVATDEDKLPKAGSFQYEGRAFGNGVLSKESLDNHNGVFRYTIDFDRRKSGSGSI 233  
 +GDI G T DKLP+ G Y G AFG D+ +G YTIDF ++G G I  
 Sbjct: 156 IGDIAGEHTSFDKLPEGGRATYRGTAFGS-----DDASGKLTYTIDFAAKQGHGKI 206

20 Query: 234 EGMEQYQYKIKLEEA AIERIPYRESGSSSLGLKDRVSYFGVNEGVMAMLEKDNEIKKYHLGIF 293  
 E ++ ++ ++ AA + P ++ + + ++L E Y LGIF  
 Sbjct: 207 EHLKS-PELNVDLAASDIKPKKRHAVI-----SGSVLYNQAEGKSYSLGIF 252

Query: 294 GEAANEVAGAVSQE 307  
 G A EVAG+ E  
 25 Sbjct: 253 GGQAQEVAGSAEVE 266

>pir||D81032 hypothetical protein NMB1870 [imported] - Neisseria meningitidis  
 (group B strain MD58)  
 gb|AAF42204.1| (AE002537) hypothetical protein [Neisseria meningitidis MC58]  
 Length = 320

Score = 50.6 bits (120), Expect = 3e-05  
 Identities = 50/168 (29%), Positives = 76/168 (44%), Gaps = 28/168 (16%)

35 Query: 136 VYEQPYSVVRGYFGYSRKDGNPIEGDGQNPEEIPFDLYLGDIRGVATDEDKLPKAGSFQY 195  
 VY+Q +S + + +D E G+ + F +GDI G T DKLP+ G Y  
 Sbjct: 163 VYKQSHSALTAFQTEQIQDS---EHSKGMVAKRQFR--IGDIAGEHTSFDKLPEGGRATY 217

40 Query: 196 EGRAFGNGVLSKESLDNHNGVFRYTIDFDRRKSGSGSIEGMEQYQYKIKLEEA AIERIPYR 255  
 G AFG D+ G YTIDF ++G+G IE ++ ++ ++ AA + P  
 Sbjct: 218 RGTAFGS-----DDAGGKLTYTIDFAAKQGNKIEHLKS-PELNVDLAADIKPDG 267

Query: 256 ESGSSSLGLKDRVSYFGVNEGVMAMLEKDNEIKKYHLGIFGEAANEVAGA 303  
 + + + ++L E Y LGIF A EVAG+  
 45 Sbjct: 268 KRHAVI-----SGSVLYNQAEGKSYSLGIFGGKAQEVAGS 302

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 109

50 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 217> which encodes amino acid sequence <SEQ ID 218; NGS109>. Analysis of this protein sequence reveals the following:

GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -5.39  
 Possible cleavage site: 25  
 55 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 7.00 threshold: 0.0  
 60 PERIPHERAL Likelihood = 7.00  
 modified ALOM score: -1.90

-127-

Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

5 ----- Final Results -----

10 bacterial cytoplasm --- Certainty= 0.353(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology with the following sequences in the databases:

15 >pir||A82012 hypothetical protein NMA0179 [imported] - Neisseria meningitidis  
 (group A strain Z2491)  
 emb|CAB83494.1| (AL162752) hypothetical protein NMA0179 [Neisseria meningitidis  
 Z2491]  
 Length = 97

20 Score = 183 bits (464), Expect = 1e-45  
 Identities = 92/97 (94%), Positives = 95/97 (97%)

25 Query: 44 MKANDKLNKQIDVLQKQSAATHNEAYIEMNTLLYRHREVVSIHNRKADYAEKGKRIALF 103  
 MK NDKLNKQIDVLQKQSAATHNEAYIEMNTLLYRHREVVSIHNRKADYAEKGKEIALF  
 Sbjct: 1 MKTNDKLNKQIDVLQKQSAATHNEAYIEMNTLLYRHREVVSVHNRKADYAEKGKEIALF 60

Query: 104 PRGLNGITKLPAAVLLPERPYHFDKMEVLYIFSRIIPR 140  
 PRGLNGITKLPAAVLLPERPYHFDKMEVL+IFS IPR  
 Sbjct: 61 PRGLNGITKLPAAVLLPERPYHFDKMEVLHIFSWIPR 97

30 As a homolog was found in serogroup A *N.meningitidis* but not in serogroup B, NGS109 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## Example 110

35 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 219> which encodes amino acid sequence <SEQ ID 220; NGS110>. Analysis of this protein sequence reveals the following:

40 GvH: Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -2.76  
 Possible cleavage site: 41  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 1 value: -0.00 threshold: 0.0  
 45 INTEGRAL Likelihood = -0.00 Transmembrane 88 - 104 ( 88 - 104)  
 PERIPHERAL Likelihood = 7.69  
 modified ALOM score: 0.50  
 Rule: cytoplasmic membrane protein

50 \*\*\* Reasoning Step: 2

----- Final Results -----

55 bacterial inner membrane --- Certainty= 0.100(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology with sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 111

- 5 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 221> which encodes amino acid sequence <SEQ ID 222; NGS111>. Analysis of this protein sequence reveals the following:

```

GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -5.89
      Possible cleavage site: 21
10 >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
          calculated from 1
      ALOM: Finding transmembrane regions (Klein et al.)
          count: 0 value: 2.44 threshold: 0.0
15 PERIPHERAL Likelihood = 2.44
          modified ALOM score: -0.99
      Rule: cytoplasmic protein

      *** Reasoning Step: 2
20 ----- Final Results -----

          bacterial cytoplasm --- Certainty= 0.293(Affirmative) < succ>
          bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
25          bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
          bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology with the following sequences in the databases:

```

30 >gb|AAC45840.1| (AF001598) restriction endonuclease [Neisseria gonorrhoeae]
      Length = 374

      Score = 539 bits (1390), Expect = e-152
      Identities = 285/285 (100%), Positives = 285/285 (100%)

35 Query: 1 MGFIEPFLSSYTPLSRDYVQARTNRKRQTLLSKIVYTHSGFQRSVTENSNIQINFLIKT 60
      MGFIEPFLSSYTPLSRDYVQARTNRKRQTLLSKIVYTHSGFQRSVTENSNIQINFLIKT
      Sbjct: 90 MGFIEPFLSSYTPLSRDYVQARTNRKRQTLLSKIVYTHSGFQRSVTENSNIQINFLIKT 149

40 Query: 61 LVEHPQGKLNKKEIAAMMLVDLKTFOQDYLTETELNDYFQGGIESGFIERKYNQISYLWN 120
      LVEHPQGKLNKKEIAAMMLVDLKTFOQDYLTETELNDYFQGGIESGFIERKYNQISYLWN
      Sbjct: 150 LVEHPQGKLNKKEIAAMMLVDLKTFOQDYLTETELNDYFQGGIESGFIERKYNQISYLWN 209

45 Query: 121 LLDKLLDLKRVGDDLYFAEDAQRIFGNLDEITVRKRDPLYHRLYKNQLQEESSEHYGNVK 180
      LLDKLLDLKRVGDDLYFAEDAQRIFGNLDEITVRKRDPLYHRLYKNQLQEESSEHYGNVK
      Sbjct: 210 LLDKLLDLKRVGDDLYFAEDAQRIFGNLDEITVRKRDPLYHRLYKNQLQEESSEHYGNVK 269

50 Query: 181 CMLEKLAYPVLIAASHIKPFILSDDTEAYDPNNGLLLSRTLDSLFDLKYISFDDEGNMVKS 240
      CMLEKLAYPVLIAASHIKPFILSDDTEAYDPNNGLLLSRTLDSLFDLKYISFDDEGNMVKS
      Sbjct: 270 CMLEKLAYPVLIAASHIKPFILSDDTEAYDPNNGLLLSRTLDSLFDLKYISFDDEGNMVKS 329

      Query: 241 KRLSDDVWRRWCDVKLDNNLLNDRKRSYLAYHRELMLQEDQEFHI 285
      KRLSDDVWRRWCDVKLDNNLLNDRKRSYLAYHRELMLQEDQEFHI
      Sbjct: 330 KRLSDDVWRRWCDVKLDNNLLNDRKRSYLAYHRELMLQEDQEFHI 374

```

- 55 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## Example 112

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 223> which encodes amino acid sequence <SEQ ID 224; NGS112>. Analysis of this protein sequence reveals the following:

```

5   GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -9.08
      Possible cleavage site: 54
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 1 value: -1.22 threshold: 0.0
      INTEGRAL Likelihood = -1.22 Transmembrane 160 - 176 ( 160 - 177)
      PERIPHERAL Likelihood = 0.58
      modified ALOM score: 0.74
15  Rule: cytoplasmic membrane protein

      *** Reasoning Step: 2

      ----- Final Results -----

20      bacterial inner membrane --- Certainty= 0.149(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

25  The protein has homology to the following sequences in the databases:

      ^ **gbp_12644572 gi|12644572|sp|Q50973|T2B1_NEIGO TYPE II RESTRICTION
      ENZYME NGOBI (ENDONUCLEASE NGOBI) (R.NGOBI) (R.NGOI)
      gb|AAB03207.2| (U42459) NgoI restriction endonuclease R.NgoI [N.gonorrhoeae]
30      Length = 350

      Score = 694 bits (1791), Expect = 0.0
      Identities = 349/350 (99%), Positives = 349/350 (99%)

35  Query: 1 MTLEEQQAKEALDGIKKSRVHLYKPIQIAEILYHDCIKQLDFLNLDTYRNQSKRWDE 60
      MTLEEQQAKEALDGIKKSRVHLYKPIQIAEILYHDCIKQLDFLNLDTYRNQSKRWDE
      Sbjct: 1 MTLEEQQAKEALDGIKKSRVHLYKPIQIAEILYHDCIKQLDFLNLDTYRNQSKRWDE 60

40  Query: 61 ICRRFLGRISTSSAKFQDNLFKNAIPPEKLAVLGTNLNRSDDGGVESYIYKQFFNRFSQM 120
      ICRRFLGRISTSSAKFQDNLFKNAIPPEKLAVLGTNLNRSDDGGVESYIYKQFFNRFSQM
      Sbjct: 61 ICRRFLGRISTSSAKFQDNLFKNAIPPEKLAVLGTNLNRSDDGGVESYIYKQFFNRFSQM 120

      Query: 121 SEALAYVGNTDRYSFQLSEFLNLFWLEPGLKRSIDKIYEIVVYALFDALVSELGITVSID 180
      SE LAYVGNTDRYSFQLSEFLNLFWLEPGLKRSIDKIYEIVVYALFDALVSELGITVSID
45  Sbjct: 121 SERLAYVGNTDRYSFQLSEFLNLFWLEPGLKRSIDKIYEIVVYALFDALVSELGITVSID 180

      Query: 181 FPKENLFLWEEYQDFAEKIITMPKNEHLKLPKIHVRVGTNAADRGLDMWSNFGGLAIQVK 240
      FPKENLFLWEEYQDFAEKIITMPKNEHLKLPKIHVRVGTNAADRGLDMWSNFGGLAIQVK
      Sbjct: 181 FPKENLFLWEEYQDFAEKIITMPKNEHLKLPKIHVRVGTNAADRGLDMWSNFGGLAIQVK 240

50  Query: 241 HLSLDEELAEDIVSSISADRVIVCKKAEQSVIVSLLTQIGWKSRIQNIIVTEDDLISWYE 300
      HLSLDEELAEDIVSSISADRVIVCKKAEQSVIVSLLTQIGWKSRIQNIIVTEDDLISWYE
      Sbjct: 241 HLSLDEELAEDIVSSISADRVIVCKKAEQSVIVSLLTQIGWKSRIQNIIVTEDDLISWYE 300

55  Query: 301 KALRGQYPIAEALLENIKTEIMREFFAVNEANEFLDFAQNRGYDITVTHF 350
      KALRGQYPIAEALLENIKTEIMREFFAVNEANEFLDFAQNRGYDITVTHF
      Sbjct: 301 KALRGQYPIAEALLENIKTEIMREFFAVNEANEFLDFAQNRGYDITVTHF 350

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

**Example 113**

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 225> which encodes amino acid sequence <SEQ ID 226; NGS113>. Analysis of this protein sequence reveals the following:

```

5   GvH Examining signal sequence (von Heijne)
      Signal Score (~7.5): -1.7
      Possible cleavage site: 43
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
          calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 4   value: -9.77 threshold: 0.0
      INTEGRAL   Likelihood = -9.77   Transmembrane 187 - 203 ( 183 - 208)
      INTEGRAL   Likelihood = -7.22   Transmembrane 25 - 41 ( 19 - 46)
      INTEGRAL   Likelihood = -4.14   Transmembrane 139 - 155 ( 138 - 155)
15  INTEGRAL   Likelihood = -2.87   Transmembrane 86 - 102 ( 85 - 102)
      PERIPHERAL Likelihood = 1.27
      modified ALOM score: 2.45
      Rule: cytoplasmic membrane protein

20  *** Reasoning Step: 2

      ----- Final Results -----

25  bacterial inner membrane --- Certainty= 0.491(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology to the following sequences in the databases:

```

30  ^ **gbp_15902668 gi|15902668|ref|NP_358218.1| \ (NC_003098) ABC
      transporter membrane-spanning permease - glutamine
      transport [Streptococcus pneumoniae R6]
      gb|AAK99428.1| (AE008440) ABC transporter membrane-spanning permease - glutamine
      transport [Streptococcus pneumoniae R6]
35  Length = 226

      Score = 218 bits (556), Expect = 7e-56
      Identities = 113/218 (51%), Positives = 155/218 (70%)

40  Query: 1  MNWPYLIDAVPKFADA AKLTLELSVYGVVLSLLFGLPVAVVTAYRIRPFYALARAYIELS 60
      M+W +.. +P + A LTL ++V+G++ S L GL V+++ YRI +A AYIELS
      Sbjct: 1  MDWSIVEQYLPYQKAFFLT LHI AVWGILGSFLLGLIVSII RH YRIPVLAQVATAYIELS 60

      Query: 61 RNTPLLIQLFFLYYGLPKMGIKWDGFTCGVIALVFLGASYMAEAVRAGILAVPKQVQVAG 120
      RNTPLLIQLFFLY+GLP++GI C + LVFLG SYMAE+ R+G+ A+ + Q G
45  Sbjct: 61 RNTPLLIQLFFLYFGLPRIGIVLSSEVCATLGLVFLGGSYMAESFRSGLEAISQTQQEIG 120

      Query: 121 KAIGLSRFQVFRYVELPQVWAVVPAIGANILFLMKETSVVSTVGIAELLFVTKDVIGMD 180
      AIGL+ QVFRYV LPQ AVA+P+ AN++FL+KETSV S V +A+L++V KD+IG+
50  Sbjct: 121 LAIGLTPLQVFRYVVL PQA TAV ALPSP SANVIFLIKETSVFSAVALADLMYVAKDLIGLY 180

      Query: 181 YKTNEALFLLFAAYLIILLPVSL LAR IENRVRSAKYG 218
      Y+T+ AL +L AYLI+LLP+SL+ IE R+R A +G
      Sbjct: 181 YETDIALAMLVVAYLIMLLPISLVFSWIERRIRHAGFG 218
55

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

**Example 114**

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 227> which encodes amino acid sequence <SEQ ID 228; NGS114>. Analysis of this protein sequence reveals the following:

```

5   GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -0.46
      Possible cleavage site: 17
      >>> Seems to have a cleavable N-term signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 18
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 3   value: -5.36 threshold: 0.0
      INTEGRAL   Likelihood = -5.36   Transmembrane 50 - 66 ( 47 - 67)
      INTEGRAL   Likelihood = -4.83   Transmembrane 183 - 199 ( 176 - 200)
      INTEGRAL   Likelihood = -1.81   Transmembrane 72 - 88 ( 72 - 88)
15  PERIPHERAL Likelihood = 0.26
      modified ALOM score: 1.57
      Rule: cytoplasmic membrane protein

      *** Reasoning Step: 2

20  ----- Final Results -----

      bacterial inner membrane --- Certainty= 0.314(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
25  bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology to the following sequences in the databases:

```

30  ^ **gbp_15902667 gi|15902667|ref|NP_358217.1| \ (NC_003098) ABC
      transporter membrane-spanning permease - glutamine
      transport [Streptococcus pneumoniae R6]
      gb|AAK99427.1| (AE008440) ABC transporter membrane-spanning permease - glutamine
      transport [Streptococcus pneumoniae R6]
      Length = 225

35  Score = 218 bits (555), Expect = 9e-56
      Identities = 111/206 (53%), Positives = 151/206 (72%)

40  Query: 3  EGLLLTAQISLISVAASCVLGTLFGLVLRSRNRLVRFVGRFYLETIRIVPILVWLFGLYF 62
      +GL +T IS++SV S + GT+ G+++ S +R++RF+ R YLE IRI+P LV LF +YF
      Sbjct: 20 QQLGVTIGISILSVLLSMMFGTVMGIIMTSHSRIIRFLTRLYLEFIRIMPQLVLLFIVYF 79

      Query: 63 GLSVWTGIHIGGFVVCVWFSLWGVAEMGDLVRGALESIEKHQVESGLAPGLSRGQVFR 122
      GL+ I+I G + VF+LWG AEMGDLVRGA+ S+ KHQ ESG A GL+ Q++
45  Sbjct: 80 GLARNFNINISGETSAITVFTLWGTAEMGDLVRGAITSLPKHQFESGQALGLTNVQLYYH 139

      Query: 123 IELPQSIRRVLPGAVNLFTRMIKTSSLAWLIGVIEVVKVGQQIENSLLTQPNASFVWYG 182
      I +PQ +RR+LP A+NL TRMIKT+SL LIGV+EV KVGQQII+++ LT P ASFW+YG
50  Sbjct: 140 IIIPQVLRLLPQAINLVTRMIKTTSLVVLIGVVEVTKVGQQIIDSNRLTIPTASFWTYG 199

      Query: 183 LIFMLYFFCCWPLSLLAAKLEQKWEH 208
      I +LYF C+P+S L+ LE+ W +
      Sbjct: 200 TILVLYFAVCYPISKLSHLEKHWRN 225

```

55 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

**Example 115**

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 229> which encodes amino acid sequence <SEQ ID 230; NGS115>. Analysis of this protein sequence reveals the following:



-132-

GvH Examining signal sequence (von Heijne).  
 Signal Score (-7.5): -0.639999  
 Possible cleavage site: 38  
 >>> May be a lipoprotein  
 5 Amino Acid Composition of Predicted Mature Form:  
 calculated from 23  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 5.25 threshold: 0.0  
 PERIPHERAL Likelihood = 5.25  
 10 modified ALOM score: -1.55  
 Rule: inner or outer membrane protein  
 Rule: inner or outer membrane protein  
 \*\*\* Reasoning Step: 2  
 15 Lipoprotein?  
 Inner membrane?  
 ----- Final Results -----  
 20 bacterial outer membrane --- Certainty= 0.790(Affirmative) < succ>  
 bacterial inner membrane --- Certainty= 0.700(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>  
 25 The protein has homology to the following sequences in the databases:  
 ^ \*\*gbp\_4588485 gi|4588485|gb|AAD26123.1| \ (AF109148) antigenic protein  
 [Actinobacillus pleuropneumoniae]  
 Length = 278  
 30 Score = 407 bits (1045), Expect = e-112  
 Identities = 212/282 (75%), Positives = 242/282 (85%), Gaps = 7/282 (2%)  
 35 Query: 1 MKLNAKLKALLASAAIAVGLTACGGSGDAQSSQSSGAA-TVAAIKEKGVIRIGVFGDKP 59  
 MKL+ LK LLA+A A LTAC +A ++QSS A +VA IKEKGVIRIGVFGDKP  
 Sbjct: 1 MKLSTTLKTLTATAITAFALTACD-----NANNAQSSSTAKDSVAQIKEKGVIRIGVFGDKP 56  
 40 Query: 60 PFGYVDANGKNQGF DVEIAKDLAKDLLGSPDKVEFVLTEAANRVEYVRSQKVDLILANFT 119  
 PFGYVDANGK+QGF DVEIAK++A DLLGS DKVEFVLTEAANRVEY++S KVDLILANFT  
 Sbjct: 57 PFGYVDANGKSQGF DVEIAKEIANDLLGSSDKVEFVLTEAANRVEYLRNKRVDLILANFT 116  
 45 Query: 120 QTPERAFAVDFA PVMKVALGVVSPKNKPITDMAQLKDQTLVKNKGT TADAFFTKSHPEV 179  
 +TPERA E VDFA PVM VALGVVSPK + I+D+ QL+ +TLLVKNKGT TADA+FTK+HPE+  
 Sbjct: 117 KTPERAFAVDFAAPYMNVALGVVSPKVRLLISDLKQLEGKTLVKNKGT TADAYFTKNHPEI 176  
 50 Query: 180 KLLKFDQNTETFDALKDGRGVALAHDNALWAWAKENPNFEVAIGNLGPAEFIAPAVQKG 239  
 LLLKFDQNTETFDALKDGRGVALAHDNAL+WAWAKENP F+VAIG++GPAE IAPAVQKG  
 Sbjct: 177 NLLKFDQNTETFDALKDGRGVALAHDNALVWAWAKENPTFDVAIGSVGPABQIAPAVQKG 236  
 Query: 240 NADLLNWVNGEIAAMKKDGRLLKAAYEKTLFPVYGEKVKEAL 281  
 N LL+ +N EIA K +G+LKAAYEKTLPVYG+ KPE L  
 Sbjct: 237 NQALLDVINKIEAEFKTNGKLLKAAYEKTLVPVYGD--KPELL 276

55 The protein was expressed in *E.coli* as a soluble 28.16kDa His-fusion product, lacking its leader peptide  
 and its poly-glycine sequence (GGGSG), and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
 useful antigens for vaccines or diagnostics.

#### Example 116

60 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 231> which encodes amino acid sequence  
 <SEQ ID 232; NGS116>. Analysis of this protein sequence reveals the following:

-133-

5      GVH Examining signal sequence (von Heijne)  
       Signal Score (-7.5): -7.13  
       Possible cleavage site: 61  
     >>> Seems to have no N-terminal signal seq.  
 5      Amino Acid Composition of Predicted Mature Form:  
       calculated from 1  
     ALOM: Finding transmembrane regions (Klein et al.)  
       count: 1   value: -1.86 threshold: 0.0  
       INTEGRAL   Likelihood = -1.86   Transmembrane   51 - 67 ( 51 - 67)  
 10      PERIPHERAL Likelihood = 1.54  
       modified ALOM score: 0.87  
     Rule: cytoplasmic membrane protein  
  
     \*\*\* Reasoning Step: 2  
 15      ----- Final Results -----

20           bacterial inner membrane --- Certainty= 0.174(Affirmative) < succ>  
           bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
           bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
           bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology to sequences in the databases.

25      Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
       useful antigens for vaccines or diagnostics.

#### Example 117

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 233> which encodes amino acid sequence  
 <SEQ ID 234; NGS117>. Analysis of this protein sequence reveals the following:

30      GVH Examining signal sequence (von Heijne)  
       Signal Score (-7.5): 0.25  
       Possible cleavage site: 40  
     >>> Seems to have a cleavable N-term signal seq.  
     Amino Acid Composition of Predicted Mature Form:  
       calculated from 41  
 35      ALOM: Finding transmembrane regions (Klein et al.)  
       count: 2   value: -4.57 threshold: 0.0  
       INTEGRAL   Likelihood = -4.57   Transmembrane   100 - 116 ( 99 - 118)  
       INTEGRAL   Likelihood = -1.59   Transmembrane   54 - 70 ( 54 - 70)  
       PERIPHERAL Likelihood = 0.53  
 40      modified ALOM score: 1.41  
     Rule: cytoplasmic membrane protein  
  
     \*\*\* Reasoning Step: 2  
 45      ----- Final Results -----

50           bacterial inner membrane --- Certainty= 0.283(Affirmative) < succ>  
           bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
           bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
           bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

55      ^ \*\*gbp\_15793413 gi|15793413|ref|NP\_283235.1| \ (NC\_003116) putative  
       integral membrane protein [Neisseria meningitidis Z2491]  
     pir||C81957 probable integral membrane protein NMA0408 [imported] - Neisseria  
       meningitidis (group A strain Z2491)  
     emb|CAB83707.1| (AL162753) putative integral membrane protein [Neisseria  
       meningitidis Z2491]  
       Length = 550  
 60

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Score = 1115 bits (2885), Expect = 0.0  
 Identities = 539/550 (98%), Positives = 545/550 (99%)

```

5  Query: 1  MVAYAFLEFLFVTAALVLLIVRSHYRWTFYFFASALFVFLAGGMLMLTAQWQRALNFASVWFV 60
    Sbjct: 1  MVAYFLFLFVTAALVLIIRSHYRWTFYFFASALFVFLAGGMLMLTAQWQRALNFASVWFV 60

    Query: 61 VLILFHRLKIHYYKQPLLIISDFLLIADWRNWETLFHYKEAVIGMAGLLALAGYAVFGWSG 120
    Sbjct: 61 VLILFHRLKIHYYKQPLLIISDFLLIADWRNWETLFHYKEAVIGMAGLLALAAAYAVFGWSG 120

    Query: 121 ADSLGMPWRWAGAVLFAAAFVSVRHFSKHGPAVKTWLDSLDDGRDVFNLNPMSCRAVFF 180
    Sbjct: 121 ADSLDVFWRWAGAVLFAAAFVSMRHFSKHGPAVKTWLDSLDDGRDVFNLNPMSCRAVFF 180

15  Query: 181 QVPVFECDGEAFARQMPSETRPYGMSDEKPDIVVTLMESTLDPHCDFDFAAAKIPDLKMFG 240
    Sbjct: 181 QVPVFECDGEAFARQMPSETRPCGMSDEKPDIVVTLMESTLDPHCDFDFAAAKIPDLKMFG 240

    Query: 241 RQEDTVFSSPLRVHTFGGATWKSEFAFLAGVPSTDFGALASGVFYSVPHLQTGFVRNLR 300
    Sbjct: 241 RQEDTVFSSPLRVHTFGGATWKSEFAFLAGVPSTDFGALASGVFYSVPHLQTGFVRNLR 300

    Query: 301 EHGYPFCVALSPFTKGNYNAAAYDHFNFNLMPQPDLYGYPAPMGKNLWHISSEEMMQYAR 360
25  Sbjct: 301 EHGYPFCVALSPFTKGNYNAAAYDHFNFNLMPQPDLYGYPAPMGKNLWHISSEEMMQYAR 360

    Query: 361 MILEKRHPDLENVRQPMFVYVLTMKHEGFPYRTDTDNVFDLADPDLNAKTVSALNDYIGRI 420
    Sbjct: 361 MILEKRHPDLENVRQPMFVYVLTMKHEGFPYRTDTDNVFDLADPDLNAKTVSALNDYIGRI 420

30  Query: 421 ADLDKAVESFDRLYHERGKPFVFGYFGDHQVPFEGVSVRKKWDYAQPDYVTQFAVRSNIA 480
    Sbjct: 421 ADLDKAVESFDRLYHERGKPFVFGYFGDHQVPFEGVSVRKKWDYAQPDYVTQFAVRSNIA 480

    Query: 481 GGFVQRQDFDLAFAGGVLMEAAAGLEAKDGFMRANMAMRGLCGGGLEDPCPNRELVGNYRN 540
35  Sbjct: 481 GGFVQRQDFDLAFAGGVLMEAAAGLEAKDGFMRANMAMRGLCGGGLEDPCPNELVGNYRN 540

    Query: 541 YLYDVLKIA 550
40  Sbjct: 541 YLYDVLKIA 550
  
```

45 A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS117 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 118

50 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 235> which encodes amino acid sequence <SEQ ID 236; NGS118>. Analysis of this protein sequence reveals the following:

```

    GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): 0.59
      Possible cleavage site: 19
    >>> May be a lipoprotein
55  Amino Acid Composition of Predicted Mature Form:
      calculated from 22
    ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 8.33 threshold: 0.0
      PERIPHERAL Likelihood = 8.33
60  modified ALOM score: -2.17
  
```

-135-

Rule: inner or outer membrane protein  
 Rule: inner or outer membrane protein

\*\*\* Reasoning Step: 2

Lipoprotein?  
 Inner membrane?

----- Final Results -----

bacterial outer membrane --- Certainty= 0.790(Affirmative) < succ>  
 bacterial inner membrane --- Certainty= 0.700(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology to sequences in the databases.

The protein was expressed in *E.coli* as a soluble 12.98kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## Example 119

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 237> which encodes amino acid sequence <SEQ ID 238; NGS119>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -4.75  
 Possible cleavage site: 47  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 7.69 threshold: 0.0  
 PERIPHERAL Likelihood = 7.69  
 modified ALOM score: -2.04  
 Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

----- Final Results -----

bacterial cytoplasm --- Certainty= 0.213(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

^ \*\*gbp\_2625122 gi|2625122|gb|AAB86635.1| \ (AF031495) putative  
 hemoglobin receptor component precursor HpuA [Neisseria gonorrhoeae]  
 Length = 360

Score = 668 bits (1724), Expect = 0.0  
 Identities = 331/331 (100%), Positives = 331/331 (100%)

Query: 1 VSIPTATPLPAGEVTLSSDNGNIENINTAGAGSASDAPSRSRRLDAAAPQNTSGISIRQR 60  
 VSIPTATPLPAGEVTLSSDNGNIENINTAGAGSASDAPSRSRRLDAAAPQNTSGISIRQR  
 Sbjct: 30 VSIPTATPLPAGEVTLSSDNGNIENINTAGAGSASDAPSRSRRLDAAAPQNTSGISIRQR 89

Query: 61 EVEKDYFGYKSKETSIFIKTPGGAQYALSSYADPITVSYSSPDFKIPDRHAGQRLADGSR 120  
 EVEKDYFGYKSKETSIFIKTPGGAQYALSSYADPITVSYSSPDFKIPDRHAGQRLADGSR  
 Sbjct: 90 EVEKDYFGYKSKETSIFIKTPGGAQYALSSYADPITVSYSSPDFKIPDRHAGQRLADGSR 149

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Query: 121 IFICCSDSGATSYAEITKQDYMKGAWIGPNGEIDLFAGGFPVGKTPPPAFSYGSSTPET 180  
 IFICCSDSGATSYAEITKQDYMKGAWIGPNGEIDLFAGGFPVGKTPPPAFSYGSSTPET  
 5 Sbjct: 150 IFICCSDSGATSYAEITKQDYMKGAWIGPNGEIDLFAGGFPVGKTPPPAFSYGSSTPET 209

Query: 181 ALSKKGKITYQVWGIRVRNGQFVTSSYTPPKSGSYGTLANTPVLSTFITSNFNSNTLAGKI 240  
 ALSKKGKITYQVWGIRVRNGQFVTSSYTPPKSGSYGTLANTPVLSTFITSNFNSNTLAGKI  
 Sbjct: 210 ALSKKGKITYQVWGIRVRNGQFVTSSYTPPKSGSYGTLANTPVLSTFITSNFNSNTLAGKI 269

10 Query: 241 LGNSDYGPDVDIQNATITGPTFSGDATSGGKSGKLEGGKFFGKFASTRSSEVSIGGKITFD 300  
 LGNSDYGPDVDIQNATITGPTFSGDATSGGKSGKLEGGKFFGKFASTRSSEVSIGGKITFD  
 Sbjct: 270 LGNSDYGPDVDIQNATITGPTFSGDATSGGKSGKLEGGKFFGKFASTRSSEVSIGGKITFD 329

Query: 301 GDRSLDTVFGGVSYEKKLDDTSQDTNHLTKQ 331  
 15 GDRSLDTVFGGVSYEKKLDDTSQDTNHLTKQ  
 Sbjct: 330 GDRSLDTVFGGVSYEKKLDDTSQDTNHLTKQ 360

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## 20 Example 120

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 239> which encodes amino acid sequence <SEQ ID 240; NGS120>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -7.24  
 25 Possible cleavage site: 38  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 30 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 6.42 threshold: 0.0  
 PERIPHERAL Likelihood = 6.42  
 modified ALOM score: -1.78  
 Rule: cytoplasmic protein

35 \*\*\* Reasoning Step: 2

----- Final Results -----

40 bacterial cytoplasm --- Certainty= 0.280(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

45 ^ \*\*gsa\_AAR91313 *N. gonorrhoeae* glycosyltransferase LgtC  
 |WO9610086-A1|09-JUL-1996  
 Length = 306

Score = 535 bits (1379), Expect = e-151  
 50 Identities = 252/253 (99%), Positives = 252/253 (99%)

Query: 8 GGGNIRFIDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLVLDTDVLVRDGLKP 67  
 GGGNIRFIDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLVLDTDVLVRDGLKP  
 Sbjct: 54 GGGNIRFIDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLVLDTDVLVRDGLKP 113

55 Query: 68 LWDTDLGGNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIKMSC 127  
 LWDTDLGGNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIKMSC  
 Sbjct: 114 LWDTDLGGNWVGACIDLFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIKMSC 173

60 Query: 128 EWVEQYKDVMQYQDQDILNGLFKGGVCYANSRNFNMPNTNYAFMANGFASRHTDPLYLDRT 187  
 EWVEQYKDVMQYQDQDILNGLFKGGVCYANSRNFNMPNTNYAFMANGFASRHTDPLYLDRT

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Sbjct: 174 EWVEQYKDVMQYQDQDILNGLFKGGVCYANSRNFMPNTNYAFMANGFASRHTDPLYLDRT 233  
 Query: 188 NTAMPVAVSHYCGSAKPWHRDCTVWGAERFTELAGSLTTPPEWRGKLAVPPTKRLQRW 247  
 NTAMPVAVSHYCGSAKPWHRDCTVWGAERFTELAGSLTTPPEWRGKLAVPPTK MLQRW  
 5 Sbjct: 234 NTAMPVAVSHYCGSAKPWHRDCTVWGAERFTELAGSLTTPPEWRGKLAVPPTKMLQRW 293  
 Query: 248 RKKLSARFLRKIY 260  
 RKKLSARFLRKIY  
 10 Sbjct: 294 RKKLSARFLRKIY 306

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 121

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 241> which encodes amino acid sequence  
 15 <SEQ ID 242; NGS121>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -6.22  
 Possible cleavage site: 37  
 >>> Seems to have no N-terminal signal seq.  
 20 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 3.23 threshold: 0.0  
 PERIPHERAL Likelihood = 3.23  
 25 modified ALOM score: -1.15  
 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 30 ----- Final Results -----  
 bacterial cytoplasm --- Certainty= 0.402(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 35 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

^ \*\*gbp\_15281345 gi|15281345|dbj|BAB63435.1| \ (AB058945) DNA adenine  
 methylase M.Ssu4109IB [Streptococcus suis]  
 40 Length = 271  
 Score = 269 bits (687), Expect = 4e-71  
 Identities = 127/211 (60%), Positives = 158/211 (74%), Gaps = 1/211 (0%)  
 45 Query: 1 MIFADPPYFLSNDGFSCQNGQMVSVNKGNWDKSKGMAADLEFYEEWLRLCYALLKPNGTI 60  
 MIFADPPYFLSN G S GQ+VSV+KG+WDK + EF +W+RL +LKPNGTI  
 Sbjct: 44 MIFADPPYFLSNGGISNSGGQVVSVDKGDWDKVNLSLEEKHEFNRRKWIRLAKNVLPNGTI 103  
 Query: 61 WVCGETFHNIYILIGYLMQTVGYHILNNITWEKPNPPNLSRFFTHSTETILWAKK-NKKA 119  
 50 W+ G+FHNIY +G ++ G+ ILNNITW+K NP PNLSR+FTHTSTETILWA+K +KKA  
 Sbjct: 104 WISGSFHNIYSVGMALQEGEFKILNNITWQKTNPAPNLSCRYFTHSTETILWARKDDKKA 163  
 Query: 120 KHTFHYEMMKAQNNKGQMKCVWTFAPPNKTEKTFGKHPTQKPLPLLERCILSASNIGDLI 179  
 +H ++YE+MK N+GQMK VW K+EK GKHPTQKP LLER IL+++ GD I  
 55 Sbjct: 164 RHYYNYELMKELNDGKQMKDVVVGGLTKKSEKWAGKHPTQKPEYLLERIILASTREGDYI 223  
 Query: 180 FDPFMGSGTTGVAALKHGRRFCGCELEEDFL 210  
 DPF+GSGTTGV A + GR+F G + E D+L  
 60 Sbjct: 224 LDPFVGSCTTGVAKRLGRKFIGIDAERDYL 254

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 122

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 243> which encodes amino acid sequence  
5 <SEQ ID 244; NGS122>. Analysis of this protein sequence reveals the following:

```

    GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -2.55
      Possible cleavage site: 23
    >>> May be a lipoprotein
10  Amino Acid Composition of Predicted Mature Form:
      calculated from 15
    ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 11.46 threshold: 0.0
      PERIPHERAL Likelihood = 11.46
15  modified ALOM score: -2.79
    Rule: inner or outer membrane protein
    Rule: inner or outer membrane protein

    *** Reasoning Step: 2
20  Lipoprotein?
    Inner membrane?

    ----- Final Results -----
25  bacterial outer membrane --- Certainty= 0.790(Affirmative) < succ>
      bacterial inner membrane --- Certainty= 0.700(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>
30
```

The protein has no homology to sequences in the databases:

The protein was expressed in *E.coli* as an insoluble 14.85kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### 35 Example 123

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 245> which encodes amino acid sequence  
<SEQ ID 246; NGS123>. Analysis of this protein sequence reveals the following:

```

    GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -5.65
      Possible cleavage site: 20
40  >>> Seems to have no N-terminal signal seq.
    Amino Acid Composition of Predicted Mature Form:
      calculated from 1
    ALOM: Finding transmembrane regions (Klein et al.)
45  count: 0 value: 4.24 threshold: 0.0
      PERIPHERAL Likelihood = 4.24
      modified ALOM score: -1.35
    Rule: cytoplasmic protein

    *** Reasoning Step: 2
50  ----- Final Results -----

      bacterial cytoplasm --- Certainty= 0.404(Affirmative) < succ>

```

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bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

5 The protein has no homology to the sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 124

10 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 247> which encodes amino acid sequence <SEQ ID 248; NGS124>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -5  
 Possible cleavage site: 18  
 >>> Seems to have no N-terminal signal seq.  
 15 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 1 value: -1.59 threshold: 0.0  
 INTEGRAL Likelihood = -1.59 Transmembrane 289 - 305 ( 289 - 305)  
 20 PERIPHERAL Likelihood = 3.76  
 modified ALOM score: 0.82  
 Rule: cytoplasmic membrane protein  
 \*\*\* Reasoning Step: 2  
 25 ----- Final Results -----  
 bacterial inner membrane --- Certainty= 0.164(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 30 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

35 ^ \*\*gbp\_1617515 gi|1617515|gb|AAC82509.1| \ (U65994) pilin gene inverting  
 protein homolog PivNG [Neisseria gonorrhoeae]  
 Length = 320  
 Score = 614 bits (1584), Expect = e-175  
 Identities = 311/320 (97%), Positives = 316/320 (98%)  
 40 Query: 1 MRNTVGLDISKLTFTDATAMVGKTEHSAKFDNDSKGLDQFSDRLKSLGYQNLHICMEATGS 60  
 MRN VGLDISKLTFA+AMVGKTEHSAKFDNDSKGLDQFSDRLKSLG QNLHICMEATG+  
 Sbjct: 1 MRNAVGLDISKLTFTNASAMVGKTEHSAKFDNDSKGLDQFSDRLKSLGCQNLHICMEATGN 60  
 45 Query: 61 YYEEVADYFAQYYSVYVVNPLKISKYAESRFKRTKTDKQDAKLIQYCRSAQESLVKRQ 120  
 YYEEVADYFAQYYSVYVVNPLKISKYAESRFKRTKTDKQDAKLIQYCR A+ESELVKRQ  
 Sbjct: 61 YYEEVADYFAQYYSVYVVNPLKISKYAESRFKRTKTDKQDAKLIQYCR LAKESLVKRQ 120  
 50 Query: 121 KPTDEQYRLSRMTAAYAQIKSECAAMKNRHHAAKDEEAAKAYAEI IKAMNEQLEVLKEKI 180  
 KPTDEQYRL RMTAAYAQIKSECAAMKNRHHAAKDEEAAKAYA+I IKAMNEQLEVLKEKI  
 Sbjct: 121 KPTDEQYRLLRMTAAYAQIKSECAAMKNRHHAAKDEEAAKAYAQI IKAMNEQLEVLKEKI 180  
 55 Query: 181 KEQTEKPNCKEGVKRLETIPAIGRMTAAVLFHHLTSSKFETSNKFAAFAGLSPQQKESGT 240  
 KEQTEKPNCKEGVKRLETIPAIGRMTAAVLFHHLTSSKFETSNKFAAFAGLSPQQKESGT  
 Sbjct: 181 KEQTEKPNCKEGVKRLETIPAIGRMTAAVLFHHLTSSKFETSNKFAAFAGLSPQQKESGT 240  
 Query: 241 SVRGKGKLTGFGNRKLRVLFMPAMVAYRIRAFPDFIKRLEEKKKPKKVIIAALMRKLAV 300  
 SVRGKGKLTGFGNRKLRVLFMPAMVAYRIRAFPDFIKRLEEKKKPKKVIIAALMRKLAV  
 Sbjct: 241 SVRGKGKLTGFGNRKLRVLFMPAMVAYRIRAFPDFIKRLEEKKKPKKVIIAALMRKLAV 300  
 60



Query: 301 IAYHVHKKGGDYDPSRYKSA 320  
 IAYHVHKKGGDYDPSRYKSA  
 Sbjct: 301 IAYHVHKKGGDYDPSRYKSA 320

- 5 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 125

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 249> which encodes amino acid sequence <SEQ ID 250; NGS127>. Analysis of this protein sequence reveals the following:

10 GvH Examining signal sequence (von Heijne)  
 Signal Score (~7.5): -5.8  
 Possible cleavage site: 52  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 15 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 1.70 threshold: 0.0  
 PERIPHERAL Likelihood = 1.70  
 modified ALOM score: -0.84  
 20 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 ----- Final Results -----  
 25 bacterial cytoplasm --- Certainty= 0.383(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>  
 30

The protein has homology to the following sequences in the databases:

^ \*\*gbp\_1076012 gi|1076012|pir|B55225 stress-sensitive restriction  
 system protein 2 - Corynebacterium glutamicum (ATCC 13032)  
 gb|AAC00044.1| (U13922) This orf may encode a typeI or typeIII restriction  
 35 endonuclease which is stress-sensitive and  
 ATP-dependent. It contains a typical ATP binding region  
 (Walker motif) [Corynebacterium glutamicum]  
 Length = 632  
 40 Score = 298 bits (764), Expect = 2e-79  
 Identities = 199/633 (31%), Positives = 321/633 (50%), Gaps = 32/633 (5%)  
 Query: 2 LRTYLNQLTP-PELADSVKNTVDGFMEKLSQTEPKIA-QNVLLLGNVQSGKTAQVLGVLS 59  
 L Y+ L+ +L + V TVD F + I+ Q VLL G+VQSGKT+ +LG+++  
 45 Sbjct: 7 LNNYITSLSDNADLREKVTATVDAFRHTVMDDFDYISDQQVLLYGDVQSGKTSMLGIIA 66  
 Query: 60 ALADDGDHKVFLYLTDSVDLQDQTVKRKANLKNFIVLSEADDRSFMEVMKAENP--IL 117  
 D H + + LT+ + L QT R + +V F K+ P +  
 50 Sbjct: 67 DCLDSTPHTIVI-LTSPNTRLVQQTYDRVAQAFPDTLVCDRDGYNDFRANQKSLTPRKSI 125  
 Query: 118 VVIKKNARVLKRWRNLFASQSSSLKGYPLVIVDDEADAASLNTNSDKPAKDASTINKLLND 177  
 VV+ K VL W +F +L G+P++I+DDEADA SLNT ++ D STIN L  
 Sbjct: 126 VVVGKIPAVLGNWLRVFNDSGALSGHPVLIIDDEADATSLNTEKVNQ--SDVSTINEQLTS 183  
 55 Query: 178 IKNSCCQSLFIQLTATPQSLLLQHEESDWQPEFIHFFEAGEKYIGGNFVFSPPS-YIVR 236  
 I++ +++Q+T TPQ++LLQ ++S+W E + F GE YIGG FS+ + Y+  
 Sbjct: 184 IRDLATGCIYLQVTGTPQAVLLQSDSNWAAEHVLFHAPGESYIGGQLFFSELNNPYLRL 243  
 Query: 237 FIDSELDDMKDESGEIAEGAKQALLSFLITCAEFALCDKANCNFALHPSYKIQDHQAFSK 296  
 F +++ D+ S A+ ++L+T A F L ++ C +HPS+ H+ F++  
 60 Sbjct: 244 FANTQFDEDSRFS-----DAITYTYLLTAALFKLRGESLCTMLIHPSHTASSHRDFAQ 295

Query: 297 KIQAFNLNDLVQAVNNGEDLAGSFKESYLDLQTKPDIIHFDEIYEKLTALLENKQISTLV 356  
 + + L + + +F+ +Y L +T ++ +I L + ++ I +  
 Sbjct: 296 EARLQLTFAFERFYEPM-IQHNFRAYEQLAQTDNLPLRKILNLGGMEDDFSIIH--I 352  
 5  
 Query: 357 VNSQTET-DFDLEKGFNIIIGGNVIGRGLTIPKLQTVYYSRTAKKPNADTFWQHSRIFGY 415  
 VNS T + D G+NII+GGN +GRGLT LQTV+Y R +K+P ADT WQH+R+FGY  
 Sbjct: 353 VNSDNPTVEEDWADGYNIIVGGNSLGRGLTFNNLQTVFYVRESKRPQADTLWQHARMFGY 412  
 10  
 Query: 416 DRDKSLRLRYIPFDVYFFVQLNQANNLIIGQAKNSG--GNIQVIYPKNINPTRKNVLKF 473  
 R K +R+++P + F ++ N I Q + +I+VI + PTR NVL  
 Sbjct: 413 KRHKDTMRVFMPTIAQTFQEVYLGNEAIKNQLDHGTHINDIRVILGDGVAPTRANVLDK 472  
 15  
 Query: 474 DSINQIVGGVNYFPLHPNEDNLSEINKILPSILKDEIQSDLYQIDIEDLFLVLDKLGRYV 533  
 + + GGVNYF P N+ ++K L + L + I + + +L+  
 Sbjct: 473 RKGVNLGGVNYFAADPRIKNVEALDKKLLAYLDKHGEDS--TIGMRAITILNAF--TVD 529  
 20  
 Query: 534 PDDWNKEKFIAGVEALKAQRPSFKTYVLIKTGRKLSRATGTMLSEDDRKLGEKYPNDLFL 593  
 P+D + F A + + +P ++++T RK+++ TG +LS D+ L L  
 Sbjct: 530 PNDLDLATFKAALLDFERNQPHLTARMVLRNKRKNVQGTGALLSPTDQALSRAEVAHPLL 589  
 Query: 594 TLYQVVGKDKG-----WQGDVFWLPNIKLP 619  
 LY++ G D W W+PNIKLP  
 Sbjct: 590 ILYRIEGVNDAAAQRGEPTWSSDPIWVWPNIKLP 622  
 25

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 126

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 251> which encodes amino acid sequence  
 30 <SEQ ID 252; NGS128>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -4.98  
 Possible cleavage site: 20  
 >>> Seems to have no N-terminal signal seq.  
 35 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 7.37 threshold: 0.0  
 PERIPHERAL Likelihood = 7.37  
 40 modified ALOM score: -1.97  
 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 45 ----- Final Results -----  
 bacterial cytoplasm --- Certainty= 0.225(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 50 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

^ \*\*gbp\_11387195 gi|11387195|sp|Q50976|T2F7\_NEIGO TYPE II RESTRICTION  
 ENZYME NGOFVII (ENDONUCLEASE NGOFVII) (R.NGOFVII)  
 55 (R.NGOVII)  
 pir||T10166 restriction endonuclease (EC 3.1.21.-) NgoVII - N.gonorrhoeae  
 gb|AAA86271.1| (U43736) R.NgoVII [Neisseria gonorrhoeae]  
 Length = 326  
 60 Score = 651 bits (1679), Expect = 0.0  
 Identities = 317/326 (97%), Positives = 320/326 (97%)

Query: 1 MNTVFSNIAKITEKSLNAVWMDLFKSADEVLMATGYVSNDAVVELHKILELNDHIQKI 60  
 MNTVFSNIAKITEKSLNAVWMDLFKSADEVLMATGYVSNDAVVELHKILELNDHIQKI  
 Sbjct: 1 MNTVFSNIAKITEKSLNAVWMDLFKSADEVLMATGYVSNDAVVELHKILELNDHIQKI 60  
 5  
 Query: 61 DLLVGMHYLEGFSLQYDSLCKLNDFLRHEKRGAVYVSPFVKFHGKMSFKNYQKINGLI 120  
 DLLVGMHYLEGFSLQYDSLCKLNDFLRHEKRGAVYVSPFVKFHGKMSFKNYQKINGLI  
 Sbjct: 61 DLLVGMHYLEGFSLQYDSLCKLNDFLRHEKRGAVYVSPFVKFHGKMSFKNYQKINGLI 120  
 10  
 Query: 121 GSANLTCFWDSTERTYETMLHLNGKPAQILQADIQSTIHLGKNIQEVERPSKPIEHNSH 180  
 GSANLTCFWDSTERTYETMLHLNGKPAQILQADIQSTIHLGKNIQEVERPSKPIEHNSH  
 Sbjct: 121 GSANLTCFWDSTERTYETMLHLNGKPAQILQADIQSTIHLGKNIQEVERPSKPIEHNSH 180  
 15  
 Query: 181 LENC LGVQKIAPEQIRQLFAQTSEYHFSIPAKTEEKS NLNVFFGEGRRDKRGFVKPRPWY 240  
 LENC LGVQKIAPEQIRQLFAQTSEYHFSIPAKTEEKS NLNVFFGEGRRDKRGFVKPRPWY  
 Sbjct: 181 LENC LGVQKIAPEQIRQLFAQTSEYHFSIPAKTEEKS NLNVFFGEGRRDKRGFVKPRPWY 240  
 20  
 Query: 241 EVELIVSKDITSQEGYPVLKSFTVITDDGWQFQCKTSGDY SKNFRSENDLKT LGKWKIGR 300  
 EVELIVSKDITSQEGYPVLKSFTVITDDGWQFQCKTSGDY SK + +LKT LGKWKIGR  
 Sbjct: 241 EVELIVSKDITSQEGYPVLKSFTVITDDGWQFQCKTSGDY SKTSTQKMN LKT LGKWKIGR 300  
 Query: 301 LESHGCLQNN EKITHETLREYGN DHF 326  
 LESHGCLQNN EKITHETLREYGN+ F  
 Sbjct: 301 LESHGCLQNN EKITHETLREYGN ESF 326  
 25

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 127

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 253> which encodes amino acid sequence <SEQ ID 254; NGS129>. Analysis of this protein sequence reveals the following:

30 GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -5.5  
 Possible cleavage site: 48  
 >>> Seems to have no N-terminal signal seq.  
 35 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 10.03 threshold: 0.0  
 PERIPHERAL Likelihood = 10.03  
 40 modified ALOM score: -2.51  
 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 45 ----- Final Results -----  
 bacterial cytoplasm --- Certainty= 0.545(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 50 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

55 ^ \*\*gbp\_15804186 gi|15804186|ref|NP\_290225.1| \ (NC\_002655)  
 DNA-damage-inducible protein [Escherichia coli O157:H7  
 EDL933]  
 ref|NP\_312547.1| (NC\_002695) DNA-damage-inducible protein [Escherichia coli  
 O157:H7]  
 gb|AAG58789.1|AE005591\_13 (AE005591) DNA-damage-inducible protein [Escherichia  
 coli O157:H7  
 60 EDL933]

dbj|BAB37943.1| (AP002566) DNA-damage-inducible protein [Escherichia coli O157:H7]

Length = 278

5 Score = 340 bits (872), Expect = 2e-92  
Identities = 161/266 (60%), Positives = 197/266 (73%)

Query: 1 MTENNAPENAKHIDETGNEYWSARTLQQILEYSEWRNFQRAIDKAITACETSGNDKNHH 60  
M + FE +H G E+WSAR L +L+Y +WRNFQ+ + +A ACE S + H  
10 Sbjct: 5 MNEHHQPFEIRHYGTEGQEFWSARELAPLLDYRDWRNFQKVLARATQACEASNQAASDH 64

Query: 61 FVETNMIALGKGGQREVADYRLSRYACYLIVQNGDPSKSVIAAGQTYFAVQARRQELQD 120  
FVET KM+ LG G QRE+ D LSRACYL+VQNGDP+K VIAAGQTYFA+Q RRQEL D  
15 Sbjct: 65 FVETTKMVLGSGAQRELEVDHLSRYACYLVVQNGDPAKPVIAAGQTYFAIQTRRQELAD 124

Query: 121 EAAFRSLGEDKQRLLLRRQLREHNTDLAAAKDAGVEKPFVEYAVFQNHGYRGLYGGLDQK 180  
+ AF+ L ED++RL LR +L+EHN L AA+ A V ++A+FQNHGY+GLYGGLD++  
15 Sbjct: 125 DEAFKQLREDEKRLFLRNELKEHNKQLVEAAQQAAVATATDFAIFQNHGYQGGLYGGLDQK 184

Query: 181 GIHSRKLKKSQRILDHMHNAEPANLFRATQTEKLRRKNIQKQTQANRVHFEVQKVR 240  
IH KGLKKSQ+ILDHM ++E AANLFRATQTEKL+R + K QAN HF+VG KVR  
20 Sbjct: 185 AIHQLKGLKKSQKILDHMGSTELAANLFRATQTEKLKRDGVNSKQQANTTHFDVGSKVR 244

Query: 241 QTIEELGGIMPENQPVPEKSIKQLEN 266  
QTI+ELGG MPE P P+ SIKQLEN  
25 Sbjct: 245 QTIQELGGTMPEELPTPQVSIKQLEN 270

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### 30 Example 128

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 255> which encodes amino acid sequence <SEQ ID 256; NGS130>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
Signal Score (-7.5): -3.68  
35 Possible cleavage site: 14  
>>> Seems to have an uncleavable N-term signal seq  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)  
count: 3 value: -3.45 threshold: 0.0  
40 INTEGRAL Likelihood = -3.45 Transmembrane 68 - 84 ( 68 - 92)  
INTEGRAL Likelihood = -1.59 Transmembrane 10 - 26 ( 10 - 26)  
INTEGRAL Likelihood = -1.44 Transmembrane 46 - 62 ( 45 - 62)  
PERIPHERAL Likelihood = 1.48  
45 modified ALOM score: 1.19  
Rule: cytoplasmic membrane protein

\*\*\* Reasoning Step: 2

50 ----- Final Results -----

bacterial inner membrane --- Certainty= 0.238(Affirmative) < succ>  
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
55 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

60 ^ \*\*gbp\_17988861 gi|17988861|ref|NP\_541494.1| \ (NC\_003318) hypothetical  
protein [Brucella melitensis]  
gb|AAL53758.1| (AB009687) hypothetical protein [Brucella melitensis]  
Length = 99

-144-

Score = 108 bits (270), Expect = 3e-23  
 Identities = 59/91 (64%), Positives = 69/91 (74%)

5 Query: 11 LLFSCMLAVTCPTRLIGFFALNRNRLSRRRAQTVMEAAPGCVLISVIAPYFVSDKPHELIA 70  
 L M +VT TR+ G+ LRNRTL S RA VMEAAPGCVLISVIAP FVSDKP LIA  
 Sbjct: 8 LTLAMASVTYLTRIGGYVLLRNRLSNRAMAVMEAAPGCVLISVIAPDFVSDKPANLIA 67

10 Query: 71 IALTAFAACRF SMLPTVLIGVGSSGSGISGWL 101  
 +A+T FAA RFSML TVLIG+G++ I +L+  
 Sbjct: 68 LAVTVFAATRF SMLPTVLIGMGAASICRYLI 98

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### 15 Example 129

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 257> which encodes amino acid sequence <SEQ ID 258; NGS131>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -1.65  
 Possible cleavage site: 43  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1

20 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 7.05 threshold: 0.0  
 PERIPHERAL Likelihood = 7.05  
 modified ALOM score: -1.91  
 Rule: cytoplasmic protein

25 \*\*\* Reasoning Step: 2

30 ----- Final Results -----

35 bacterial cytoplasm --- Certainty= 0.152(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

40 ^ \*\*gbp\_16760390 gi|16760390|ref|NP\_456007.1| \ (NC\_003198) hypothetical  
 protein [Salmonella enterica subsp. enterica serovar  
 Typhi]  
 emb|CAD01841.1| (AL627270) hypothetical protein [Salmonella enterica subsp.  
 enterica serovar Typhi]  
 45 Length = 227

Score = 104 bits (259), Expect = 2e-21  
 Identities = 68/221 (30%), Positives = 115/221 (51%), Gaps = 11/221 (4%)

50 Query: 2 DKEKVL D K I K K L A L G R S V N E H E A A Q A L R Q A Q A L M E K Y K V N A E D I A L S K V S E Q R A D -- R K 59  
 D++K ++K+K K L A L S N H E A A A L R + A + L M + + + D I A + S + E +  
 Sbjct: 3 D Q D K H I E K L K K L L A L A A S G N P H E A A L A L R R A R K L M D V H G I T H S D I A M S D I D E T I S H Y W P T 62

55 Query: 60 M A F K L A G W Q W G V A N M I A D I F G C K S Y Q R G K T --- M M F Y G I G N R A E T S A Y A F D V V Y R Q I S A D 116  
 + + + G + N + I + F G S T + F Y G R A + A Y + V + R Q +  
 Sbjct: 63 G S L R P P R Y M L G L M N I I R E A F G V N S I I H P G T Y P G V G F Y G N R E R A A L A A Y T W E V L A R Q L K K A 122

Query: 117 R R K F L K T - C R A G K P S H R T Y L A D R F C G G W I A S A W E T V K K F E M S D E E K A I M D G Y K K E Y P D M 175  
 R + + + + + K + R T D + F G W + + + + F + + D + E + + M + + + Y P  
 60 Sbjct: 123 R Q Q Y I S A Q N K R I K T A T R T S R G D Q F A E G W V L A V I S E I Q S F A L T D D E R E L M Q Q W L E H K Y P Q T 182

Query: 176 AEARTRDAKSSILQGSMEYEALTRGMESGKQVKLHYAVNG 216  
 R R S G Y G G+ V+LH V+G  
 Sbjct: 183 QTTRARKPGRS-RNGDASRY-----AGFREGQNVRLHRPVS 218

- 5 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 130

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 259> which encodes amino acid sequence <SEQ ID 260; NGS132>. Analysis of this protein sequence reveals the following:

10 GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -4.06  
 Possible cleavage site: 30  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 15 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 2.49 threshold: 0.0  
 PERIPHERAL Likelihood = 2.49  
 modified ALOM score: -1.00  
 20 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 ----- Final Results -----  
 25 bacterial cytoplasm --- Certainty= 0.075(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>  
 30

The protein has no homology to sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 131

- 35 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 261> which encodes amino acid sequence <SEQ ID 262; NGS133>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): 1.64  
 Possible cleavage site: 53  
 40 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 3.82 threshold: 0.0  
 45 PERIPHERAL Likelihood = 3.82  
 modified ALOM score: -1.26  
 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 50 ----- Final Results -----  
 bacterial cytoplasm --- Certainty= 0.068(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 55 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>

bacterial inner membrane --- Certainty= 0.000 (Not Clear) < succ>

The protein has no homology to the following sequences in the databases:

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
5 useful antigens for vaccines or diagnostics.

### Example 132

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 263> which encodes amino acid sequence  
<SEQ ID 264; NGS135>. Analysis of this protein sequence reveals the following:

10 GvH Examining signal sequence (von Heijne)  
Signal Score (-7.5): -4.67  
Possible cleavage site: 39  
>>> Seems to have no N-terminal signal seq.  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
15 ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 5.52 threshold: 0.0  
PERIPHERAL Likelihood = 5.52  
modified ALOM score: -1.60  
20 Rule: cytoplasmic protein  
\*\*\* Reasoning Step: 2  
----- Final Results -----  
25 bacterial cytoplasm --- Certainty= 0.457 (Affirmative) < succ>  
bacterial periplasmic space --- Certainty= 0.000 (Not Clear) < succ>  
bacterial outer membrane --- Certainty= 0.000 (Not Clear) < succ>  
bacterial inner membrane --- Certainty= 0.000 (Not Clear) < succ>

30 The protein has no homology to sequences in the databases:

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
useful antigens for vaccines or diagnostics.

### Example 133

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 265> which encodes amino acid sequence  
35 <SEQ ID 266; NGS136>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
Signal Score (-7.5): -3.97  
Possible cleavage site: 15  
40 >>> Seems to have no N-terminal signal seq.  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 11.35 threshold: 0.0  
PERIPHERAL Likelihood = 11.35  
45 modified ALOM score: -2.77  
Rule: cytoplasmic protein  
\*\*\* Reasoning Step: 2  
50 ----- Final Results -----  
bacterial cytoplasm --- Certainty= 0.523 (Affirmative) < succ>  
bacterial periplasmic space --- Certainty= 0.000 (Not Clear) < succ>  
bacterial outer membrane --- Certainty= 0.000 (Not Clear) < succ>

bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology to sequences in the databases:

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
5 useful antigens for vaccines or diagnostics.

#### Example 134

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 267> which encodes amino acid sequence  
<SEQ ID 268; NGS137>. Analysis of this protein sequence reveals the following:

10 GvH Examining signal sequence (von Heijne)  
Signal Score (-7.5): -8.52  
Possible cleavage site: 51  
>>> Seems to have no N-terminal signal seq.  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
15 ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 2.81 threshold: 0.0  
PERIPHERAL Likelihood = 2.81  
modified ALOM score: -1.06  
20 Rule: cytoplasmic protein  
\*\*\* Reasoning Step: 2  
----- Final Results -----  
25 bacterial cytoplasm --- Certainty= 0.374(Affirmative) < succ>  
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

30 The protein has no homology to sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
useful antigens for vaccines or diagnostics.

#### Example 135

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 269> which encodes amino acid sequence  
35 <SEQ ID 270; NGS138>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
Signal Score (-7.5): -7  
Possible cleavage site: 36  
40 >>> Seems to have no N-terminal signal seq.  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 10.66 threshold: 0.0  
PERIPHERAL Likelihood = 10.66  
45 modified ALOM score: -2.63  
Rule: cytoplasmic protein  
\*\*\* Reasoning Step: 2  
50 ----- Final Results -----  
bacterial cytoplasm --- Certainty= 0.415(Affirmative) < succ>  
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>



bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

```

5   ^ **gbp_13559865 gi|13559865|ref|NP_112075.1| \ (NC_002730) terminase
      small subunit [Bacteriophage HK620]
      gb|AAK28890.1|AF335538_42 (AF335538) terminase small subunit [Bacteriophage
      HK620]
      Length = 140

10  Score = 125 bits (313), Expect = 5e-28
      Identities = 56/122 (45%), Positives = 85/122 (68%)

Query: 4   TKRKLGRPTDYTKDMADKICEKIANGSLRSICAEDGVPPMKTIYRWLEANEFRHQYAR 63
          T+ K GRP+DY ++AD IC +++G SL +C G+P T++RWL +E+FR +YA+
15  Sbjct: 3   TEPKAGRPSDYMPEVADDICSLSSGESLLKVCKRPGMPDKSTVFRWLAKHEDFRDKYAK 62

Query: 64   AREKQADYFAEEIIEIADSAQAESAASVSKAKLQIDARKWAASKIAPKKYGDKSELDVKSQDGD 125
          A E +AD EEI EIAD+A ++A V+KA+L++D RKWA +++ P+KYGDK ++ DG
20  Sbjct: 63   ATEARADSIFREIFEIADNAIPDAAEVAKARLRVDTRKWALARMNPRKYGDKVTNELVGKDG 124

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 136

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 271> which encodes amino acid sequence <SEQ ID 272; NGS139>. Analysis of this protein sequence reveals the following:

```

25  GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -1.49
      Possible cleavage site: 32
      >>> Seems to have no N-terminal signal seq.
30  Amino Acid Composition of Predicted Mature Form:
      calculated from 1
      ALOM: Finding transmembrane regions (Klein et al.)
          count: 0 value: 8.65 threshold: 0.0
          PERIPHERAL Likelihood = 8.65
35  modified ALOM score: -2.23
      Rule: cytoplasmic protein

      *** Reasoning Step: 2

40  ----- Final Results -----

      bacterial cytoplasm --- Certainty= 0.301(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
45  bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology to the following sequences in the databases:

```

50  ^ **gbp_16127009 gi|16127009|ref|NP_421573.1| \ (NC_002696) hypothetical
      protein [Caulobacter crescentus]
      gb|AAK24741.1| (AE005943) hypothetical protein [Caulobacter crescentus]
      Length = 184

      Score = 59.7 bits (143), Expect = 4e-08
      Identities = 50/164 (30%), Positives = 74/164 (44%), Gaps = 20/164 (12%)

55  Query: 30   ASGREFRTAYTYTPQWRFSLSFEVLRTKASVNELEKLAGFFNARKGSFESFLYEDPAD-- 87
          ASG E RT+ ++ + R+ ++ ++E+ +L FF AR+G F + DPAD
      Sbjct: 5   ASGHERRTSPWSQSRRLYLIA----TAPRPLDEIAELVAFFEARRGLHGFRFRDPADFK 60

60  Query: 88   -----NAVTDQFVGNTVQGVAR-YQLVRSMSGGFIEPVSAVKERP-----AVKVGGTAL 134

```

-149-

A DQ +G T GV + +QL ++ G E V+ +P V V G L  
 Sbjct: 61 SCAPSVQPAAGDQAIG-TGDGVRKAFQLRRITYGAGGEAVARTIAKPVAGTVTVAVAGVVL 119  
 Query: 135 AYGRDYTEVTDKGVLVFNTPQPPGPRITWTGGFYFRVRFSTDTVD 178  
 5 A G G++ NT P G +T F VRF D +D  
 Sbjct: 120 APGAFVDVTGLITLNTAPPAGAAVTAGFAFDTPVRFDLRLD 163

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### 10 Example 137

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 273> which encodes amino acid sequence <SEQ ID 274; NGS140>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -3.86  
 15 Possible cleavage site: 31  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 20 count: 1 value: -4.94 threshold: 0.0  
 INTEGRAL Likelihood = -4.94 Transmembrane 34 - 50 ( 31 - 54)  
 PERIPHERAL Likelihood = 8.01  
 modified ALOM score: 1.49  
 Rule: cytoplasmic membrane protein  
 25 \*\*\* Reasoning Step: 2  
 ----- Final Results -----  
 30 bacterial inner membrane --- Certainty= 0.297(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>  
 35 The protein has homology to the following sequences in the databases:  
 ^ \*\*gbp\_17987625 gi|17987625|ref|NP\_540259.1| \ (NC\_003317) Hypothetical  
 Phage Protein [Brucella melitensis]  
 gb|AAL52523.1| (AE009572) Hypothetical Phage Protein [Brucella melitensis]  
 Length = 144  
 40 Score = 72.4 bits (176), Expect = 5e-12  
 Identities = 43/119 (36%), Positives = 64/119 (53%), Gaps = 7/119 (5%)  
 Query: 10 RIVEEARSWLGTFPYHHHAMVKAGVDCAMLLVAVYGAV-GLLPEGFDPRFPQDWHLHRD 68  
 45 R++ EA W+GTFY H A G DC L+ ++ A+ G+ PE +P Y DW  
 Sbjct: 6 RVLAEHRWIGTFYRHGASTLGVSCDCLGLVRGIWRALYGVPE--NPGVYAPDWA EVSQ 63  
 Query: 69 CERYLGFTVQFC--RETESQAGDIIV--WRFGRSFSGGILAGGGKVIHSYIGRGVVS 123  
 + L ++ RE +PQ GD+ V W+ G + H GI+A G+ IH+Y G GV++  
 50 Sbjct: 64 GDPMLEAAVRYMVRREEHAPQPGDLLVFRWKPFGFAAKHMGIMAREGRFTHAYQGHGVLA 122

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 138

55 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 275> which encodes amino acid sequence <SEQ ID 276; NGS141>. Analysis of this protein sequence reveals the following:

-150-

GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): 5.35  
 Possible cleavage site: 28  
 >>> Seems to have a cleavable N-term signal seq.  
 5 Amino Acid Composition of Predicted Mature Form:  
 calculated from 29  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 8.86 threshold: 0.0  
 PERIPHERAL Likelihood = 8.86  
 10 modified ALOM score: -2.27  
 Score for OM-PP discrimination: 1.53  
 Rule: outer membrane or periplasmic protein  
 Score for OM-PP discrimination: 1.53  
 Rule: outer membrane or periplasmic protein  
 15 \*\*\* Reasoning Step: 2  
 Outer membrane? Score: 0.152929  
 Outer membrane? Score: 0.152929  
 20 ----- Final Results -----  
 bacterial outer membrane --- Certainty= 0.512(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.320(Affirmative) < succ>  
 25 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

30 ^ \*\*gbp\_5915870 gi|5915870|sp|Q50940|CAH\_NEIGO Carbonic anhydrase  
 precursor (Carbonate dehydratase)  
 emb|CAA72038.1| (Y11152) carbonic anhydrase [Neisseria gonorrhoeae]  
 Length = 252  
 Score = 523 bits (1347), Expect = e-147  
 35 Identities = 252/252 (100%), Positives = 252/252 (100%)  
 Query: 1 MPRFPRTLPRLTAVLLLLACTAFSAAAHGNHTHWGYTGHDSPESWGNLSEEFRLCSTGKNQ 60  
 MPRFPRTLPRLTAVLLLLACTAFSAAAHGNHTHWGYTGHDSPESWGNLSEEFRLCSTGKNQ  
 40 Sbjct: 1 MPRFPRTLPRLTAVLLLLACTAFSAAAHGNHTHWGYTGHDSPESWGNLSEEFRLCSTGKNQ 60  
 Query: 61 SPVNIETVSGKLPKLVNYKPSMVDVENNGHTIQVNYPEGGNTLTVNGRTYTLKQFHFH 120  
 SPVNIETVSGKLPKLVNYKPSMVDVENNGHTIQVNYPEGGNTLTVNGRTYTLKQFHFH  
 45 Sbjct: 61 SPVNIETVSGKLPKLVNYKPSMVDVENNGHTIQVNYPEGGNTLTVNGRTYTLKQFHFH 120  
 Query: 121 VPSENQIKGRTFPMEAHFVHLDENKQPLVLAVLYEAGKTNGRLSSIWNVMPMTAGKVKLN 180  
 VPSENQIKGRTFPMEAHFVHLDENKQPLVLAVLYEAGKTNGRLSSIWNVMPMTAGKVKLN  
 50 Sbjct: 121 VPSENQIKGRTFPMEAHFVHLDENKQPLVLAVLYEAGKTNGRLSSIWNVMPMTAGKVKLN 180  
 Query: 181 QPFDASTLLPKRLKYRFAGSLTTPPCTEGVSWVLKTYDHIDQAQAEKFTRAVGSENNR 240  
 QPFDASTLLPKRLKYRFAGSLTTPPCTEGVSWVLKTYDHIDQAQAEKFTRAVGSENNR  
 55 Sbjct: 181 QPFDASTLLPKRLKYRFAGSLTTPPCTEGVSWVLKTYDHIDQAQAEKFTRAVGSENNR 240  
 Query: 241 FVQPLNARVVIE 252  
 FVQPLNARVVIE  
 Sbjct: 241 FVQPLNARVVIE 252

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 139

60 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 277> which encodes amino acid sequence <SEQ ID 278; NGS142>. Analysis of this protein sequence reveals the following:

-151-

GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -0.49  
 Possible cleavage site: 22  
 >>> Seems to have no N-terminal signal seq.  
 5 Amino Acid Composition of Predicted Mature Form:  
     calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
     count: 0 value: 1.22 threshold: 0.0  
     PERIPHERAL Likelihood = 1.22  
 10 modified ALOM score: -0.74  
 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 15 ----- Final Results -----  
     bacterial cytoplasm --- Certainty= 0.145(Affirmative) < succ>  
     bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
     bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 20 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

^ \*\*gbp\_15794480 gi|15794480|ref|NP\_284302.1| \ (NC\_003116) hypothetical  
 protein [Neisseria meningitidis Z2491]  
 25 pir|F81851 hypothetical protein NMA1587 [imported] - Neisseria meningitidis  
     (group A strain Z2491)  
 emb|CAB84814.1| (AL162756) hypothetical protein [Neisseria meningitidis Z2491]  
     Length = 181  
 30 Score = 358 bits (919), Expect = 6e-98  
     Identities = 173/181 (95%), Positives = 178/181 (97%)  
 Query: 1 LKTD TARMNN LIPEHLAAYAHSDNLQIEGGHRCFSLSCQGRDTFHIRYYGEPFDGLITDT 60  
     +KTD TA+MNN LIPEHLAAYAHSD+LQIEG HRCFSLSCQGRDTFHIRYYGEPFDGL+TDT  
 35 Sbjct: 1 MKTDTAKMNN LIPEHLAAYAHSDSLQIEGVHRCFSLSCQGRDTFHIRYYGEPFDGLMTDT 60  
 Query: 61 DKAPVKIVAVEAVSGDEIVLFDGAEHGYNAMFC DKYSQNKQNR TLTDLDEYTYRVPIHL 120  
     DKAPVKIVAVEAVSGDEIVLFDGAEHGYNAMFC DKYS NQKQNR TLTDLDEYTYRV IHL  
 Sbjct: 61 DKAPVKIVAVEAVSGDEIVLFDGAEHGYNAMFC DKYSPNQKQNR TLTDLDEYTYRVLIHL 120  
 40 Query: 121 YYNIDYEDEYEDFVNSEGQVPLIDGRIISFDSLKRNGFDAISIDLIDEKHSVRELLNEELS 181  
     YYNIDYEDEYEDFVNSEGQVPLIDGRIISFDSLKRNGFDAIS+DLIDEKHSVRELLNEELS  
 Sbjct: 121 YYNIDYEDEYEDFVNSEGQVPLIDGRIISFDSLKRNGFDAISVDLIDEKHSVRELLNEELS 181

45 A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS142 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 140

50 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 279> which encodes amino acid sequence <SEQ ID 280; NGS143>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -2.51  
 Possible cleavage site: 57  
 55 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
     calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
     count: 4 value: -15.23 threshold: 0.0

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INTEGRAL Likelihood = -15.23 Transmembrane 84 - 100 ( 79 - 107)  
 INTEGRAL Likelihood = -8.12 Transmembrane 259 - 275 ( 250 - 281)  
 INTEGRAL Likelihood = -4.14 Transmembrane 159 - 175 ( 153 - 176)  
 INTEGRAL Likelihood = -3.88 Transmembrane 216 - 232 ( 216 - 235)  
 5 PERIPHERAL Likelihood = 1.11  
 modified ALOM score: 3.55  
 Rule: cytoplasmic membrane protein

\*\*\* Reasoning Step: 2

10

----- Final Results -----

bacterial inner membrane --- Certainty= 0.709(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 15 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

^ \*\*gbp\_5764059 gi|5764059|emb|CAB53350.1| \ (AJ010260) NosR protein  
 20 [Paracoccus denitrificans]  
 Length = 724  
 Score = 393 bits (1009), Expect = e-108  
 Identities = 191/379 (50%), Positives = 249/379 (65%), Gaps = 22/379 (5%)  
 25  
 Query: 1 LMVQRVLSVNDKAFVTADLDYELPQAYVYVDDPKAPPVEISAPVEAVPAAASDTASDGI AE 60  
 L+VQR + +K F T DL Y+LPQ Y AP A PAA +D  
 Sbjct: 358 LLVQREVGPVIEKVFTFDLGYQLPQKYLRSIAPAPEA-----AAPAAQAD----- 402  
 30  
 Query: 61 DASAENGVSQNLWKQIWKAKQGQIVVVGIALTILLVFLPQDWIVRYEKWYDRFRAFLT 120  
 E+ QLWK+IW + +I + L +L VF FQ + RYE+ + FR A+LT  
 Sbjct: 403 -----ESQAQAQLWKRIWLDSPKPIAGLAAMLLVLTGVFFQSFSTTRYERAFYVFRMAYLT 458  
 35  
 Query: 121 FTLFYIGWYAQAQLSVVNTLTLSAILTEFHWEFFLMDPIVFILWLFTAATMLLWNRGTF 180  
 TL ++GWYA AQLSVVN + LF +++ F W+ FL+DP+ FILW AA +L W RG +  
 Sbjct: 459 VTLVFLGWYANAQLSVVNLMLFGLSVNGFSWQAFLLDPLTFILWFAVAAALLFWGRGAY 518  
 Query: 181 CGWLCPFGLQELTNRIAKKLGKQITVPHMLHTRLNVIKYLILFGFLAISLYDLGTAEK 240  
 CGWLCPFGLQELTN++A+KL + Q T+P LH RL +KY+I G +SL + AE  
 40 Sbjct: 519 CGWLCPFGLQELTNQVARKLRIPQWTLPLWGLHERLWPKYMI FLGLFGVSLMSVEQA EH 578  
 Query: 241 FAEVEPFKTAIILKFMCDWWFVAFVAVALLIAGLFIERFFCRYLCPLGAGIALPGRFRVFD 300  
 AEVEPFKTAIILKF+ W FVA+A ALLIAGLF+ERF+CRYLCPLGA +A+P R R+FD  
 Sbjct: 579 LAEVEPFKTAIILKPIRAWPFVAYAAALLIAGLFVERFYCRYLCPLGAALAI PARMRMFD 638  
 45  
 Query: 301 WLRRYKMCNCPQCICTHECPVQAIAPEDGIHPNECIQCLHCQVMYHHDTRCPQVVAENKK 360  
 WL+RY CGNCPQ C +CPVQ+I P G+I+PNECI CLHCQV+Y +T CP V+ KK  
 Sbjct: 639 WLKRYHECGNCPQCTCARQCPVQSIHPTGEINPNECINCLHCQVLYQSETTCPVVI---KK 695  
 50  
 Query: 361 KQKQAAAKSGELENVSKQP 379  
 +++ A +G + + + P  
 Sbjct: 696 LKRREAVAAGSMPKLGQPP 714

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
 55 useful antigens for vaccines or diagnostics.

#### Example 141

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 281> which encodes amino acid sequence  
 <SEQ ID 282; NGS144>. Analysis of this protein sequence reveals the following:

60 GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): 1.23  
 Possible cleavage site: 21

>>> May be a lipoprotein.

Amino Acid Composition of Predicted Mature Form:  
calculated from 20

ALOM: Finding transmembrane regions (Klein et al.)

count: 1 value: -0.37 threshold: 0.0

INTEGRAL Likelihood = -0.37 Transmembrane 90 - 106 ( 89 - 106)

PERIPHERAL Likelihood = 10.82

modified ALOM score: 0.57

Rule: inner or outer membrane protein

Rule: inner or outer membrane protein

Rule: cytoplasmic membrane protein

\*\*\* Reasoning Step: 2

Lipoprotein?

Inner membrane?

----- Final Results -----

bacterial outer membrane --- Certainty= 0.790(Affirmative) < succ>

bacterial inner membrane --- Certainty= 0.734(Affirmative) < succ>

bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>

bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology no to sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 142

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 283> which encodes amino acid sequence <SEQ ID 284; NGS145>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)

Signal Score (-7.5): 1.5

Possible cleavage site: 19

>>> Seems to have a cleavable N-term signal seq.

Amino Acid Composition of Predicted Mature Form:  
calculated from 20

ALOM: Finding transmembrane regions (Klein et al.)

count: 0 value: 8.70 threshold: 0.0

PERIPHERAL Likelihood = 8.70

modified ALOM score: -2.24

Score for OM-PP discrimination: -9.24

Rule: outer membrane or periplasmic protein

Score for OM-PP discrimination: -9.24

Rule: outer membrane or periplasmic protein

\*\*\* Reasoning Step: 2

Periplasmic space? Score: 0.924443

Periplasmic space? Score: 0.924443

----- Final Results -----

bacterial periplasmic space --- Certainty= 0.931(Affirmative) < succ>

bacterial outer membrane --- Certainty= 0.231(Affirmative) < succ>

bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

^ \*\*gbp\_5051426 gi|5051426|emb|CAB45007.1| \ (AJ242839) OpcA protein  
[Neisseria gonorrhoeae]

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Length = 263

Score = 531 bits (1369), Expect = e-150  
 Identities = 262/263 (99%), Positives = 263/263 (99%)

5 Query: 1 MKKALLALTIAAISGTAMAQLPDFLGKGEYTVRTDISKQTLKNADLKEKHVKQKNIGFRA 60  
 MKKALLALTIAAISGTAMAQLPDFLGKGEYTVRTDISKQTLKNADLKEKHVKQKNIGFRA  
 Sbjct: 1 MKKALLALTIAAISGTAMAQLPDFLGKGEYTVRTDISKQTLKNADLKEKHVKQKNIGFRA 60

10 Query: 61 DMPFDDIHHGMRFEVSHSRDKKDMYVVTESTTKPFGKDVEEKRTDVYAGYTYTQPISEAT 120  
 DMPFDDIHHGMRFEVSHSRDKKDMYVVTESTTKPFGKDV+EKRTDVYAGYTYTQPISEAT  
 Sbjct: 61 DMPFDDIHHGMRFEVSHSRDKKDMYVVTESTTKPFGKDVEEKRTDVYAGYTYTQPISEAT 120

15 Query: 121 KLRAGLGLGYEKYKDAVANEKGTVSTEREAFTYKAHADLTSDLGGGWYLNPAEYKVDLD 180  
 KLRAGLGLGYEKYKDAVANEKGTVSTEREAFTYKAHADLTSDLGGGWYLNPAEYKVDLD  
 Sbjct: 121 KLRAGLGLGYEKYKDAVANEKGTVSTEREAFTYKAHADLTSDLGGGWYLNPAEYKVDLD 180

20 Query: 181 AKLKHNATVAGVSADINAKTRGWGVGVGANIGKQITDTVGIEAGPFYKRRHFKASGSFVL 240  
 AKLKHNATVAGVSADINAKTRGWGVGVGANIGKQITDTVGIEAGPFYKRRHFKASGSFVL  
 Sbjct: 181 AKLKHNATVAGVSADINAKTRGWGVGVGANIGKQITDTVGIEAGPFYKRRHFKASGSFVL 240

25 Query: 241 DGGNIRVDPTKINEYGVRVGVKF 263  
 DGGNIRVDPTKINEYGVRVGVKF  
 Sbjct: 241 DGGNIRVDPTKINEYGVRVGVKF 263

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 143

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 285> which encodes amino acid sequence  
 30 <SEQ ID 286; NGS146>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): 0.1  
 Possible cleavage site: 51  
 >>> Seems to have a cleavable N-term signal seq.  
 35 Amino Acid Composition of Predicted Mature Form:  
 calculated from 52  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 3.50 threshold: 0.0  
 PERIPHERAL Likelihood = 3.50  
 40 modified ALOM score: -1.20  
 Score for OM-PP discrimination: -15.70  
 Rule: outer membrane or periplasmic protein  
 Score for OM-PP discrimination: -15.70  
 Rule: outer membrane or periplasmic protein

45 \*\*\* Reasoning Step: 2

Periplasmic space? Score: 1.56979  
 Periplasmic space? Score: 1.56979

50 ----- Final Results -----

bacterial periplasmic space --- Certainty= 0.944(Affirmative) < succ>  
 bacterial outer membrane --- Certainty= 0.375(Affirmative) < succ>  
 55 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

60 ^ \*\*gbp\_5051429 gi|5051429|emb|CAB45013.1| \{AJ242839} hypothetical  
 protein [Neisseria gonorrhoeae]  
 length = 109

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Score = 216 bits (549), Expect = 2e-55  
 Identities = 109/109 (100%), Positives = 109/109 (100%)

5 Query: 1 MFKRPEEIIIVLILAVLWLAGTYFLAALFGADAYTVLKITALTLLWSAASFLLWQKKPQPA 60  
 MFKRPEEIIIVLILAVLWLAGTYFLAALFGADAYTVLKITALTLLWSAASFLLWQKKPQPA  
 Sbjct: 1 MFKRPEEIIIVLILAVLWLAGTYFLAALFGADAYTVLKITALTLLWSAASFLLWQKKPQPA 60

10 Query: 61 YLAAARLPDHLVAVSESIGRTRFFTLACIMDVQNHLSPDSRNRLSV 109  
 YLAAARLPDHLVAVSESIGRTRFFTLACIMDVQNHLSPDSRNRLSV  
 Sbjct: 61 YLAAARLPDHLVAVSESIGRTRFFTLACIMDVQNHLSPDSRNRLSV 109

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### 15 Example 144

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 287> which encodes amino acid sequence <SEQ ID 288; NGS147>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -4.09  
 Possible cleavage site: 40  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 25 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 1 value: -2.28 threshold: 0.0  
 INTEGRAL Likelihood = -2.28 Transmembrane 36 - 52 ( 36 - 52)  
 PERIPHERAL Likelihood = 5.20  
 modified ALOM score: 0.96  
 Rule: cytoplasmic membrane protein  
 30 \*\*\* Reasoning Step: 2  
 ----- Final Results -----  
 35 bacterial inner membrane --- Certainty= 0.191(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

40 The protein has homology to the following sequences in the databases:

^ \*\*gbp\_6606516 gi|6606516|gb|AAF19189.1|AF200716\_2 \ (AF200716)  
 trafficking protein B [Neisseria gonorrhoeae]  
 Length = 139

45 Score = 274 bits (700), Expect = 7e-73  
 Identities = 139/139 (100%), Positives = 139/139 (100%)

50 Query: 2 MILLDTNVISEPLRPQPNERVVAWLDSLILEDVYLSAITVAELRLGVALLLNGKKKNVLH 61  
 MILLDTNVISEPLRPQPNERVVAWLDSLILEDVYLSAITVAELRLGVALLLNGKKKNVLH  
 Sbjct: 1 MILLDTNVISEPLRPQPNERVVAWLDSLILEDVYLSAITVAELRLGVALLLNGKKKNVLH 60

Query: 62 ERLEQSILPLFAGRILPFDEPVAAIYAQIRSYAKTHGKEIAAADGYIAATAKQHS�TVAT 121  
 ERLEQSILPLFAGRILPFDEPVAAIYAQIRSYAKTHGKEIAAADGYIAATAKQHS�TVAT  
 Sbjct: 61 ERLEQSILPLFAGRILPFDEPVAAIYAQIRSYAKTHGKEIAAADGYIAATAKQHS�TVAT 120

55 Query: 122 RDTGSFFAADVAVFNPWHD 140  
 RDTGSFFAADVAVFNPWHD  
 Sbjct: 121 RDTGSFFAADVAVFNPWHD 139



Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 145

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 289> which encodes amino acid sequence  
5 <SEQ ID 290; NGS148>. Analysis of this protein sequence reveals the following:

```

GvH Examining signal sequence (von Heijne)
  Signal Score (-7.5): 0.86
  Possible cleavage site: 47
>>> Seems to have a cleavable N-term signal seq.
10 Amino Acid Composition of Predicted Mature Form:
    calculated from 48
ALOM: Finding transmembrane regions (Klein et al.)
    count: 5 value: -15.44 threshold: 0.0
15   INTEGRAL    Likelihood ==-15.44    Transmembrane 157 - 173 ( 142 - 181)
    INTEGRAL    Likelihood ==-12.15    Transmembrane  62 -  78 (  56 -  83)
    INTEGRAL    Likelihood == -6.32    Transmembrane 194 - 210 ( 191 - 212)
    INTEGRAL    Likelihood == -4.30    Transmembrane  87 - 103 (  85 - 104)
    INTEGRAL    Likelihood == -2.60    Transmembrane 121 - 137 ( 121 - 142)
    PERIPHERAL  Likelihood =  2.92
20   modified ALOM score:  3.59
    Rule: cytoplasmic membrane protein

*** Reasoning Step: 2

25 ----- Final Results -----

    bacterial inner membrane --- Certainty= 0.718(Affirmative) < succ>
    bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
30    bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
    bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology to the following sequences in the databases:

```

^ **gbp_15777859 gi|15777859|gb|AAL05955.1| \ (AY048756) putative cadmium
  binding protein [Staphylococcus aureus]
35   Length = 209

    Score = 354 bits (908), Expect = 1e-96
    Identities = 177/208 (85%), Positives = 194/208 (93%)

40   Query: 14  MRCFMFSTVITA AVL YIATAVDLLVILLIFFARANTRKEYRDIYIGQYLGSVILILVSLF 73
      MRC M TV+ AAVLYIATAVDLLVILLIFFARA TRKEYRDIY+GQYLGS+ILILVSLF
      Sbjct: 1  MRCIMIQT VVA AAVLYIATAVDLLVILLIFFARAKTRKEYRDIYVGQYLGSIIILVSLF 60

45   Query: 74  LAFVLNYVPEKWVLG LGLIPIYLGIKVAIYDDCEGEKRAKKELDEKGLSKLVGIVALVT 133
      LAFVLNYVPEKW+LGLLGLIPIYLGIKVAIYDDCEGEKRAKKEL+EKGLSKLVG VA+VT
      Sbjct: 61  LAFVLNYVPEKWILG LGLIPIYLGIKVAIYDDCEGEKRAKKELNEKGLSKLVGTVAIVT 120

      Query: 134 VASCGADNIGLFVPYFVTVLDDLVLVLLVFLILIFVLVYTAQRLANISGVGEIVEKFSR 193
      +ASCGADNIGLFVPYFVTVL + +LL+TL VFLILIF LV+TAQ+LANI G+GEIVEKFSR
50   Sbjct: 121 IASCGADNIGLFVPYFVTVL SVTNLLLTLEFVFLILIFLVTQAQLANIPGIGEIVEKFSR 180

      Query: 194 WIMAVIYIGLGLFIIENNTIRTIIISII 221
      WIMA+IYI LGLFIIEN+TI+TI+ I
      Sbjct: 181 WIMAIYIALGLFIIENDTIQTILGFI 208
55

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## Example 146

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 291> which encodes amino acid sequence <SEQ ID 292; NGS149>. Analysis of this protein sequence reveals the following:

```

5   GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -0.63
      Possible cleavage site: 43
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 2.12 threshold: 0.0
      PERIPHERAL Likelihood = 2.12
      modified ALOM score: -0.92
      Rule: cytoplasmic protein
15  *** Reasoning Step: 2

      ----- Final Results -----
20      bacterial cytoplasm --- Certainty= 0.122(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

25  The protein has homology to the following sequences in the databases:
      ^ **gbp_15675455 gi|15675455|ref|NP_269629.1| \ (NC_002737) conserved
      hypothetical protein [Streptococcus pyogenes]
      [Streptococcus pyogenes M1 GAS]
      gb|AAK34350.1| (AE006588) conserved hypothetical protein [Streptococcus pyogenes
30  M1 GAS]
      Length = 224

      Score = 106 bits (264), Expect = 3e-22
      Identities = 63/151 (41%), Positives = 85/151 (55%), Gaps = 12/151 (7%)
35  Query: 20  LSALQHYAFCPRQCALIHNEQAWAENYLTAQKALHERVDSDE-PETCKGVRFEWTVHVL 78
      LS +QH+ FC RQ ALIH EQ W +N TA G+ LH + D+ E K + + +
      Sbjct: 11  LSGIQHFQFCKRQWALIHIEQQWLDNEATAHGQVLHTKADNPYIKEKRKELLVSRAMPIS 70

40  Query: 79  ADKLGISGILDVE-----VDTKTGR LKP--VEYKRGKPKPDGDEIQLCAQGLCL 127
      + +LG+SGI+D+VE + K G+ P VEYKRGKPK D D +QL AQ +CL
      Sbjct: 71  SAELGLSGIMDVVEFYKDDQGVSLRGKRGKWLPKVVEYKRGKPKKDTDRDIVQLVAQTMCL 130

      Query: 128 EEMTGQTVSEGalWYMQTRHRVPVVFSDGLR 158
      EE ++EG L+Y RV V + LR
45  Sbjct: 131 EETLDCDINEGCLYYHSVNQRVIVPMTSALR 161

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## 50 Example 147

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 293> which encodes amino acid sequence <SEQ ID 294; NGS150>. Analysis of this protein sequence reveals the following:

```

55  GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -0.71
      Possible cleavage site: 19
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1

```

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ALOM: Finding transmembrane regions (Klein et al.)  
 count: 1 value: -0.85 threshold: 0.0  
 INTEGRAL Likelihood = -0.85 Transmembrane 79 - 95 ( 79 - 96)  
 PERIPHERAL Likelihood = 6.52  
 modified ALOM score: 0.67  
 Rule: cytoplasmic membrane protein

\*\*\* Reasoning Step: 2

----- Final Results -----

bacterial inner membrane --- Certainty= 0.134(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has no homology to sequences in the databases.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## Example 148

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 295> which encodes amino acid sequence <SEQ ID 296; NGS151>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): 3.47  
 Possible cleavage site: 23  
 >>> Seems to have a cleavable N-term signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 24  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 14.32 threshold: 0.0  
 PERIPHERAL Likelihood = 14.32  
 modified ALOM score: -3.36  
 Score for OM-PP discrimination: -32.29  
 Rule: outer membrane or periplasmic protein  
 Score for OM-PP discrimination: -32.29  
 Rule: outer membrane or periplasmic protein

\*\*\* Reasoning Step: 2

Periplasmic space? Score: 3.22889  
 Periplasmic space? Score: 3.22889

----- Final Results -----

bacterial periplasmic space --- Certainty= 0.933(Affirmative) < succ>  
 bacterial outer membrane --- Certainty= 0.253(Affirmative) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

^ \*\*gsa\_AAY75310 Neisseria gonorrhoeae ORF 649 protein sequence SEQ ID  
 NO:2094 |WO9957280-A2|21-MAR-2000  
 Length = 103

Score = 35.4 bits (80), Expect = 0.32  
 Identities = 25/85 (29%), Positives = 38/85 (44%), Gaps = 5/85 (5%)

Query: 7 ILTGILLATALPASAHGMHKSPLAMDELPPICQQYFKRAETCYNKAGNKADFARN-NTK 65  
 + T T+ PA H H SK L P C++Y +R Y GN + N +  
 Sbjct: 13 VSTTAAAGTSEPAHRHTKHISKA-NKQMLHPECRKYLEERRAAWYRSQGNVQELRENKKAR 71

Query: 66 FLFQALPAADLGQRKQMCQIAMDSF 90  
 F+ LP A ++K C+ A ++F  
 Sbjct: 72 KAFRTLPHYA---EQKIQCRAYEAF 93

5

The protein was expressed in *E.coli* as a soluble 9.35kDa His-fusion product and then purified.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 149

- 10 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 297> which encodes amino acid sequence <SEQ ID 298; NGS152>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)

Signal Score (-7.5): -5.46

Possible cleavage site: 18

15

>>> Seems to have an uncleavable N-term signal seq

Amino Acid Composition of Predicted Mature Form:

calculated from 1

ALOM: Finding transmembrane regions (Klein et al.)

count: 1 value: -3.19 threshold: 0.0

20

INTEGRAL Likelihood = -3.19 Transmembrane 368 - 384 ( 367 - 384)

PERIPHERAL Likelihood = 0.53

modified ALOM score: 1.14

Rule: cytoplasmic membrane protein

25

\*\*\* Reasoning Step: 2

----- Final Results -----

30

bacterial inner membrane --- Certainty= 0.227(Affirmative) < succ>

bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>

bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>

bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

- 35 The protein has homology to the following sequences in the databases:

^ \*\*gsa\_AAY81609 Streptococcus pneumoniae type 4 protein sequence #109

|WO200006737-A2|24-MAY-2000

Length = 1237

40

Score = 48.1 bits (113), Expect = 4e-04

Identities = 80/312 (25%), Positives = 142/312 (44%), Gaps = 59/312 (18%)

Query: 57 RRQARIRVGNLITDSLEHIRVKALLPLPL----KLPVKRI---NLPRNLPALFVRLRRTI 109  
 RRQ R + ++ L+H RV L P+ ++FV+++ +PR A RL++ +

45

Sbjct: 941 RRQVR-QPQQVLVHQLQHQRVHRLRRQPVHQSQQQVPRQLPHQQVPRLQQAPVRRLOQVL 999

Query: 110 SPRQIGDALPILKLQRI--RLTLHLKPLPLHPQLGLLHIKRPVRIPLRHLAVQRTLVRNL 167  
 +P+ P+ + Q++ RL H + PL L +P R + L QR VRLN

50

Sbjct: 1000 APQF--QPQVVRQPQQVSQRLNRHQVRPLQQVLA----PQPQRQQVHRL--QRQVRVLN 1051

Query: 168 RRIKPPLLQHRLTVRRILRRSRQPFPAPQFDDRIFIMFRHNPARRIKLCRRQLTVQGP 227  
 R + LQ L A P R+ +H +R++ ++ L Q R

Sbjct: 1052 RHQVRPLQQVL-----APQPQRQQVHRLQH---QRVRLPLQQVLAPQPQR 1093

55

Query: 228 IRRSRPLIKLPLRRQRIRPGRHQRTLVRVKITHRLAAPIHIPVKSQRRRRPSARIRRARI 287  
 + R L+RQR+R +HQR + + H+L +H FV+ Q + R + +++ +

Sbjct: 1094 QQVHR-----LQRQVRVLSQHQRVRQPQQAHL-LNLHQFVR-QPQHRQAPQLQQQPV 1144

60

Query: 288 APREIRPGPRIGGKRLIAARKP-QTGIRTPFESTRPAQPPRPI-LNIVTAQIHIPITRR 345  
 + R R+ + + R+P Q +R P R + P+P+ LN H P+ R+

-160-

Sbjct: 1145 RQPQRRQVRRRL---QQVPVRQPQQVPVRQP--QRRQVRRPQFVHLN-----RHQPV-RQ 1192

Query: 346 PGLIIRNGTPHR 357  
 P ++ + H+

5 Sbjct: 1193 PQQVLVHQLQHQ 1204

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 150

10 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 299> which encodes amino acid sequence <SEQ ID 300; NGS153>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -5.48  
 Possible cleavage site: 13

15 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 6.31 threshold: 0.0

20 PERIPHERAL Likelihood = 6.31  
 modified ALOM score: -1.76  
 Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

25 ----- Final Results -----

bacterial cytoplasm --- Certainty= 0.150(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 30 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

35 ^ \*\*gbp\_15832758 gi|15832758|ref|NP\_311531.1| \ (NC\_002695) hypothetical  
 protein [Escherichia coli O157:H7]  
 dbj|BAB36927.1| (AP002562) hypothetical protein [Escherichia coli O157:H7]  
 Length = 188

Score = 73.9 bits (180), Expect = 3e-12  
 40 Identities = 54/169 (31%), Positives = 79/169 (45%), Gaps = 15/169 (8%)

Query: 12 LTQEV LKELLRYDDNTGKLYWAERPRKYFNSGLHYKSWNTGFSGKEVFLYKGR LGYLK LK 71  
 LT + + ELL +D +TG W + + S F GY +  
 Sbjct: 16 LTVKRIFELLSFDKSTGVFRWKVPTQ----GRIALNSVAGAFDSN-----GYSMIM 62

45 Query: 72 IFKKQYNAHRLIWL FVY GKH-ASSIGHINRDKTDNRISNLRDVTHAENMKNRGKFKNN TS 130  
 I ++Y H L++ + + A I H+N +TDNR NLR+ EN +N KN+ S  
 Sbjct: 63 IDGRRYKTHVLV FYITHNRWPAGQIDHVGIRTDNRPENLRECLPIENSRNIRIRKNSKS 122

50 Query: 131 GHTGVYFHKPSKKWQARIMVNRKNKILGLFEHIEDAA-KAREAASKDFG 178  
 G GV +HK KKW R+ + K+K G F+ +E A A EA K +G  
 Sbjct: 123 GCRGVTWHKRQKKWNVRLGFHGKSKHFGCFDDLELAVLVAEEARDKY YG 171

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

55

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## Example 151

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 301> which encodes amino acid sequence <SEQ ID 302; NGS154>. Analysis of this protein sequence reveals the following:

```

5   GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -6.98
      Possible cleavage site: 28
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
10  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 8.12 threshold: 0.0
      PERIPHERAL Likelihood = 8.12
      modified ALOM score: -2.12
15  Rule: cytoplasmic protein

      *** Reasoning Step: 2

      ----- Final Results -----
20
      bacterial cytoplasm --- Certainty= 0.423(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>
25

```

The protein has homology to the following sequences in the databases:

```

30  ^ **gbp_15830449 gi|15830449|ref|NP_309222.1| \ (NC_002695) hypothetical
      protein [Escherichia coli O157:H7]
      dbj|BAA94132.1| (AP000422) hypothetical protein [Escherichia coli O157:H7]
      dbj|BAB34618.1| (AP002554) hypothetical protein [Escherichia coli O157:H7]
      Length = 148

      Score = 42.7 bits (99), Expect = 0.003
      Identities = 27/99 (27%), Positives = 49/99 (49%), Gaps = 10/99 (10%)
35  Query: 37  IRPRKSKRSVEQNRRLLWFLYREISEKVFIDGRRFSQDVWHE-----FLKRRKFIGCIEMP 91
      + ++ KRS QN R+W + ++S +V G+R + + W + +LK K + +P
      Sbjct: 33  VHVKEPKRSKAQNDRMWPMPLNDVSRQVLWHGQRLAPEDWKDLFTALWLTKKLEQRSVPG 92

40  Query: 92  GQ----LMGISTTKLSVREMSEYQEKIISWASMEHGVLW 126
      ++G+ T+K+ M+E E I+ W E V W
      Sbjct: 93  IDGGVVMLGVRTSKMRKASMTPELIE-IMFWFGSERNVRW 130

```

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## Example 152

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 303> which encodes amino acid sequence <SEQ ID 304; NGS155>. Analysis of this protein sequence reveals the following:

```

50  GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -4
      Possible cleavage site: 27
      >>> Seems to have an uncleavable N-term signal seq.
      Amino Acid Composition of Predicted Mature Form:
      calculated from 1
55  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 4.98 threshold: 0.0
      PERIPHERAL Likelihood = 4.98
      modified ALOM score: -1.50

```

\*\*\* Reasoning Step: 2

5 ----- Final Results -----

10 bacterial inner membrane --- Certainty= 0.046(Affirmative) < succ>  
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

15 ^ \*\*gbp\_15801502 gi|15801502|ref|NP\_287519.1| \ (NC\_002655) putative  
endonuclease of prophage CP-9330 [Escherichia coli  
0157:H7 EDL933]  
ref|NP\_309804.1| (NC\_002695) endonuclease [Escherichia coli O157:H7]  
gb|AAG56131.1|AE005344\_7 (AE005344) putative endonuclease of prophage CP-9330  
[Escherichia coli O157:H7 EDL933]  
dbj|BAB35200.1| (AF002556) endonuclease [Escherichia coli O157:H7]  
20 Length = 119

Score = 47.4 bits (111), Expect = 2e-04  
Identities = 38/122 (31%), Positives = 54/122 (44%), Gaps = 8/122 (6%)

25 Query: 71 LILPYFVSANRYWRIWRNRAVRSAEAAAYKETVRRRIA-QGAGAMPSEGAVAVYVRLIPKA 129  
L+LPYP + N YWR + S Y+ V I Q + G +A+ + P  
Sbjct: 5 LVLFPYPPTVNTYWRRRGSTYFVSKAGERYRRAVVLIVRQQRLKLSL SGR LAIKIIAEP-- 62

30 Query: 130 NKDGGANKTVIDLDNALKVTLDALQGVAYHNDRQVRRIAAEYGGEPVTGGGLAVEVGELE 189  
+K DLDN LR LDAL D + G+PV+GG L V++ ++E  
Sbjct: 63 -----PDKRRRLDNLKAPLDALTHAGVLMDDDEQFDEINIVRGQPVS GGR LGVKIYKIE 117

Query: 190 ME 191  
E

35 Sbjct: 118 SE 119

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 153

40 A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 305> which encodes amino acid sequence <SEQ ID 306; NGS156>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
Signal Score (-7.5): -2.61  
Possible cleavage site: 49  
45 >>> Seems to have no N-terminal signal seq.  
Amino Acid Composition of Predicted Mature Form:  
calculated from 1  
ALOM: Finding transmembrane regions (Klein et al.)  
count: 0 value: 7.96 threshold: 0.0  
50 PERIPHERAL Likelihood = 7.96  
modified ALOM score: -2.09  
Rule: cytoplasmic protein

\*\*\* Reasoning Step: 2

55

----- Final Results -----

60 bacterial cytoplasm --- Certainty= 0.307(Affirmative) < succ>  
bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>

bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

5     ^ \*\*gsa\_AAG90098 C glutamicum protein fragment SEQ ID NO: 3852  
       |EP1108790-A2|26-SEP-2001  
       Length = 148

10     Score = 102 bits (253), Expect = 7e-21  
       Identities = 60/147 (40%), Positives = 88/147 (59%), Gaps = 18/147 (12%)

Query: 3    NAYDVADFFLSPFEEEDGEQISNLKQLKLLYYAQGYALAILNRPLFAENIEHWQHGFPVVP 62  
           +A ++A++F++ +E D E +S LKQLKLLYY+QG +A   R LF++ I WQHGFPV P  
 Sbjct: 5    SARBAEWFVAWGDELDAE-VSPLKQLKLLYSSQGEHIAATGRKLFSDKILAWQHGFPVTP 63

15     Query: 63   CIYRTYKKGGSPLPAAHIEPDKYADEEL-----VVLNRVRKEQGQCYTAWALRNKT 113  
           +Y   K YG +P       I+PD++ +E                   L V ++ G Y+AWALR KT  
 Sbjct: 64   GVYSDTKSYGRNP-----IDPDEFVSDEFNWDDYSDVDELVTVWRKYGIYSAWALREKT 118

20     Query: 114 HQEAPWIQT-RQGEVIGI--ALMGEYF 137  
           H E+PW+    QG+ I I A + ++F  
 Sbjct: 119 HSESPWLDWAQGGONIEITDAALKDFF 145

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### 25   Example 154

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 307> which encodes amino acid sequence <SEQ ID 308; NGS157>. Analysis of this protein sequence reveals the following:

30     GVH Examining signal sequence (von Heijne)  
       Signal Score (-7.5): -5.65  
       Possible cleavage site: 42  
       >>> Seems to have no N-terminal signal seq.  
       Amino Acid Composition of Predicted Mature Form:  
       calculated from 1

35     ALOM: Finding transmembrane regions (Klein et al.)  
       count: 0 value: 3.98 threshold: 0.0  
       PERIPHERAL Likelihood = 3.98  
       modified ALOM score: -1.30  
       Rule: cytoplasmic protein

40     \*\*\* Reasoning Step: 2

      ----- Final Results -----

45     bacterial cytoplasm --- Certainty= 0.291(Affirmative) < succ>  
       bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
       bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
       bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

50   The protein has homology to the following sequences in the databases:

      ^ \*\*gbp\_6274533 gi|6274533|gb|AAF06681.1|AF163663\_6 \ (AF058689) Toul  
       [Neisseria meningitidis]  
       Length = 272

55     Score = 546 bits (1408), Expect = e-154  
       Identities = 267/272 (98%), Positives = 271/272 (99%)

Query: 19   MKGMDKLRVQDRLNIRPIFTAGEQEYLTELSDRPLSVLTDSVRNIEEIGIDFVYSPAK 78  
           MKGMDKLRVQ+DFLNIRPIFTAGEQEYLTELSDRPLSVLTDSVRNIEEIGIDFVYS AK  
 60     Sbjct: 1   MKGMDKLRVQQDFLNIRPIFTAGEQEYLTELSDRPLSVLTDSVRNIEEIGIDFVYSSAK 60



Query: 79 LEGNTYNQYDTQALLKLGQTAGGKLYSDAVMLINLRESYRHLLSGLDSPKPFDWLDFLKT 138  
 LEGNTYNQYDTQALLKLGQTAGGKLYSDAVMLINLRESYRHLLSGLDSP+PFDWLDFLKT  
 Sbjct: 61 LEGNTYNQYDTQALLKLGQTAGGKLYSDAVMLINLRESYRHLLSGLDSPEPFDWLDFLKT 120  
 5  
 Query: 139 THSLISENLLKGGSGGVVRRDSVTISGTDYTPLSNPQSLDTLKWLLQEAPKIENPFDR 198  
 THSLISENLLKGGSGGVVRRDSVTISGTDYTPLSNPQSLDTLKWLLQEAPKIENPFDR  
 Sbjct: 121 THSLISENLLKGGSGGVVRRDSVTISGTDYTPLSNPQSLDTLKWLLQEAPKIENPFDR 180  
 10  
 Query: 199 VYLHNNLAYLRYFKDCNKRTARNCMTSLMRSGFFPCVFPSPDYPAYAEAVVAYYETGDY 258  
 VYLHNNLAYL+YFKDCNKRTARNCMTSLMRSGFFPCVFPSPDYPAYAEAVVAYYETGDY  
 Sbjct: 181 VYLHNNLAYLQYFKDCNKRTARNCMTSLMRSGFFPCVFPSPDYPAYAEAVVAYYETGDY 240  
 15  
 Query: 259 GLFKKYFISAYENTVNKYGPQPDVDIFRNFSI 290  
 GLFKKYFISAYENTVNKYGPQPDVDIFRNFS+  
 Sbjct: 241 GLFKKYFISAYENTVNKYGPQPDVDIFRNFSL 272

A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS157 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

20 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

#### Example 155

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 309> which encodes amino acid sequence <SEQ ID 310; NGS158>. Analysis of this protein sequence reveals the following:

25 GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -6.98  
 Possible cleavage site: 18  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 30 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 0.16 threshold: 0.0  
 PERIPHERAL Likelihood = 0.16  
 modified ALOM score: -0.53  
 35 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 40 ----- Final Results -----  
 bacterial cytoplasm --- Certainty= 0.185(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 45 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

> ^^ \*\*gbp\_15791833 gi|15791833|ref|NP\_281656.1| \ (NC\_002163) amino-acid  
 ABC transporter ATP-binding protein [Campylobacter jejuni]  
 50 pir|H81391 amino-acid ABC transporter ATP-binding protein Cj0469 [imported] -  
 Campylobacter jejuni (strain NCTC 11168)  
 emb|CAB75107.1| (AL139075) amino-acid ABC transporter ATP-binding protein  
 [Campylobacter jejuni]  
 Length = 253  
 55  
 Score = 301 bits (772), Expect = 6e-81  
 Identities = 153/244 (62%), Positives = 195/244 (79%), Gaps = 2/244 (0%)  
 Query: 1 MALLSIRKLHKQYGSVTAIQSLDLLEKGEVIVLLGPSGCGKSTLLRCVNGLEPHQGQSI 60

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M++L I L K YGS A++ ++L+++ EV+V+LGPSGCGKSTLLRC+NGLE G+I  
 Sbjct: 1 MSILKIENLQKYYGSHHALKDINLEVKAKEVVILGPSGCGKSTLLRCINGLEEIASGNI 60  
 Query: 61 VMDGVGEFGKDVS-WQATARQKVGVMVFQSYELFAHMTVIENILLGPKVQNRDRAEAEQA 119  
 +D + KD W RQKVGVMVFQSYELF H++V ENILLGP+KVQ R + E +A  
 Sbjct: 61 YIDNE-KIDKDFKEWPRMRQKVGVMVFQSYELFEHLVSVEENILLGPMKVQKRKKDEVLEA 119  
 Query: 120 GKLLERVGLLDKKNAYPRELGGQKQRIATVRALCLNPEVILLDEITAALDPEMVREVL 179  
 LE+VGLL + +AYPRELGGQKQRIATVR+LC+NPE++L DE+TAALDPE+VREVL  
 Sbjct: 120 KIWLEKVGLLHKIHAYPRELGGQKQRIATVRSLCMNPELMLFDEVTAALDPEIVREVL 179  
 Query: 180 VVLELAREGMSMLIVTHEMGFARKVADRIVFMDKGGIVESSDPETFFSAPKSERARQFLA 239  
 V+L LA+EGM+MLIVTHEMGFA+ VAD+I+FMG+G I+E +DP++FF PKSERA++FL  
 Sbjct: 180 VMLNLAKEGMTMLIVTHEMGFAKAVADKIIIFMDEGKIIIEENDPKSFFKNPKSERAKKFLN 239  
 Query: 240 GMDY 243  
 DY  
 Sbjct: 240 LFDY 243

- 20 Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 156

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 311> which encodes amino acid sequence <SEQ ID 312; NGS159>. Analysis of this protein sequence reveals the following:

25 GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -4.16  
 Possible cleavage site: 13  
 >>> Seems to have no N-terminal signal seq.  
 Amino Acid Composition of Predicted Mature Form:  
 30 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 6.47 threshold: 0.0  
 PERIPHERAL Likelihood = 6.47  
 modified ALOM score: -1.79  
 35 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2  
 40 ----- Final Results -----  
 bacterial cytoplasm --- Certainty= 0.312 (Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000 (Not Clear) < succ>  
 45 bacterial outer membrane --- Certainty= 0.000 (Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000 (Not Clear) < succ>

The protein has homology to the following sequences in the databases:

> ^, \*\*gbp\_15794799 gi|15794799|ref|NP\_284621.1| \ (NC\_003116) hypothetical  
 protein [Neisseria meningitidis Z2491]  
 50 pir||B81819 hypothetical protein NMA1914 [imported] - Neisseria meningitidis  
 (group A strain Z2491)  
 emb|CAB85135.1| (AL162757) hypothetical protein [Neisseria meningitidis Z2491]  
 Length = 206  
 55 Score = 265 bits (678), Expect = 8e-70  
 Identities = 131/146 (89%), Positives = 138/146 (93%)  
 Query: 1 MTKLYAQIAKTEAQDDGTVKVWGYASSEAVDSDEGVVAAEAMKAAIPDYMKFGAVREMHG 60  
 MTKLYA+IAK E QDDGTVKVWGYASSE +DSDGEV+AA AMKAAIPDYMKFGA REMHG  
 60 Sbjct: 1 MTKLYAEIAKMETQDDGTVKVWGYASSEIDSDEGVIAAAAMKAAIPDYMKFGAGREMHG 60

Query: 61 SNAAGTAIEINVEDDGRITFFGAHIVDPVAVTKVKTGVYKGFSSIGGSVTARNDLNKSQITG 120  
 SNAAGTAIEINVEDDG TFFGAHI+DPV V+KVKTG VYKGFSSIGGSVTAR+DLNKSQITG  
 Sbjct: 61 SNAAGTAIEINVEDDGITFFGAHIIDPVVSVKVTGVYKGFSSIGGSVTARDDLNKSQITG 120

5 Query: 121 LKLTEISLVDRPANPDVFTCFKADK 146  
 LKLTEISL+DRPANPDV TCFKADK  
 Sbjct: 121 LKLTEISLIDRPANPDVSTCFKADK 146

A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS159 protein and  
 10 nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be  
 useful antigens for vaccines or diagnostics.

### Example 157

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 313> which encodes amino acid sequence  
 15 <SEQ ID 314; NGS160>. Analysis of this protein sequence reveals the following:

GvH Examining signal sequence (von Heijne)  
 Signal Score (-7.5): -8.3  
 Possible cleavage site: 33  
 >>> Seems to have no N-terminal signal seq.  
 20 Amino Acid Composition of Predicted Mature Form:  
 calculated from 1  
 ALOM: Finding transmembrane regions (Klein et al.)  
 count: 0 value: 7.85 threshold: 0.0  
 PERIPHERAL Likelihood = 7.85  
 25 modified ALOM score: -2.07  
 Rule: cytoplasmic protein  
 \*\*\* Reasoning Step: 2

30 ----- Final Results -----

bacterial cytoplasm --- Certainty= 0.407(Affirmative) < succ>  
 bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>  
 35 bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>  
 bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

The protein has homology to the following sequences in the databases:

40 > ^^ \*\*gbp\_2126352 gi|2126352|pir||JC5218 type I site-specific  
 deoxyribonuclease (EC 3.1.21.3) Hsd chain S [validated]  
 - Pasteurella haemolytica  
 gb|AAC44667.1| (U46781) HSDS [Mannheimia haemolytica]  
 Length = 442

45 Score = 97.1 bits (240), Expect = 3e-19  
 Identities = 55/149 (36%), Positives = 81/149 (53%), Gaps = 3/149 (2%)

Query: 26 EVAEYSKNRICSDKLNENHYVGVDNLLQNRGKKLSGYVPSEGMTEYIVNDILIGNIRP 85  
 ++ E +I L + NY+ DN+L N G L+ +P+ + DIL NIR  
 50 Sbjct: 10 DIVELISEKIKIKDLKENYISTDNMLPNFGGITLAENLPNSASCNRFKKDILFSNIRT 69

Query: 86 YLKKIWQADCTGGTNGDVLVIRV--TDEKVNPKYLYQVLADDKFFAFNMKHKAGAKMPRG 143  
 Y KK+W A+ +GG + DVLV+R TD +N +YL+ ++ D F F + A GAKMPRG  
 Sbjct: 70 YFKKRWLAEFSGGCSFDVLMVRSKNTDILLN-EYLFLLIRSDDFINFTVISANGAKMPRG 128

55 Query: 144 SKAAIMQYKIPIPLPEQEKIVAILGKFD 172  
 K A+ + IP + Q+K +A FD  
 Sbjct: 129 DKNAMKGFIFNIPSIEYQKKCIANYFAFD 157

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 158

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 315> which encodes amino acid sequence  
5 <SEQ ID 316; NGS161>. Analysis of this protein sequence reveals the following:

```

    GvH Examining signal sequence (von Heijne)
      Signal Score (-7.5): -5.08
      Possible cleavage site: 36
    >>> Seems to have no N-terminal signal seq.
10  Amino Acid Composition of Predicted Mature Form:
      calculated from 1
    ALOM: Finding transmembrane regions (Klein et al.)
      count: 1 value: -1.59 threshold: 0.0
      INTEGRAL Likelihood = -1.59 Transmembrane 302 - 318 ( 302 - 318)
15  PERIPHERAL Likelihood = 3.76
      modified ALOM score: 0.82
    Rule: cytoplasmic membrane protein

    *** Reasoning Step: 2

20  ----- Final Results -----

      bacterial inner membrane --- Certainty= 0.164(Affirmative) < succ>
25  bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>

```

The protein has homology to the following sequences in the databases:

```

30  pir|E81921 probable DNA-invertase NMA0772 [imported] - Neisseria meningitidis
      (group A strain Z2491)
      emb|CAB84055.1| (AL162754) putative DNA-invertase [Neisseria meningitidis Z2491]
      Length = 321

35  Score = 295 bits (755), Expect = 9e-79
      Identities = 151/322 (46%), Positives = 216/322 (66%), Gaps = 3/322 (0%)

    Query: 14  LRNAVGLDISKLTFDATAIVGNAEYSAKFDNDSKGLDQFSDRLKSLGQCNLHICMEATGN 73
      +RNAVGLDIS TFD I+ KF ND +G + + + +++++CMEATGN
40  Sbjct: 1  MRNAVGLDISAKTFDVVTIINGETDYRKFSNDEQGCKNLKEWISAKREKDIYVCMETGN 60

    Query: 74  YYEEVADYFAQYYSVYVNVNPLKISKYAESRFKRTKTDKQDAKLIAQYCRSAQSESLVKRQ 133
      YYE+ AD A+ Y V V+NPLKI YA+ RF R K DKQDAKLIA++C++A EL KR+
45  Sbjct: 61  YYEQAADCLAEEYHVSVINPLKIKAYAQRFSRVKNDKQDAKLIAEFCQTALIERLPKRE 120

    Query: 134 KPTDEQYRLSRMTAAYAQIRSECAAMKNRHHAAKDEEAAKAYAEI IKAMNEQLEVLKEKI 193
      KPT++QY L R+ + +Q+ + + KNR AAKD K + + +K + L +K+KI
50  Sbjct: 121 KPTQQYSLKRLLSLQSQLEQQT SQKNRIKAADSFVQKIHEKQLKELENHNLNAVKKKI 180

    Query: 194 KEQTEKPN--CKEGVKRLETIPAIGRMATAAVLFHHLTSSKFETSNKFPAAGLSPQOKES 251
      +QT K + KE KRLETIP++G+ TA L +L +S FE + +F A+AGL+P Q S
55  Sbjct: 181 -DQTIKSDKKMKELTKRLETIPSVGKTTAISLMSYLNSTFENAKQFTAYAGLNPQNIS 239

    Query: 252 GTSVRGKGLTKFGNRKLRAVLFMPAMVAYRIRAPPDFIKRLEEKKKPKKVIIAALMRKL 311
      GTSV K K+TK+GNR++R LFM A+VA++ PP F RL++ KKPK +II ALMRK+
60  Sbjct: 240 GTSVNKKSKMTKYGNRRIRGSLFMAALVAFKNNYFFAFTNRLKRAKKPKMLIIGALMRKI 299

    Query: 312 AVIAYHVHKKGGDYDPSRYKSA 333
      V+A++++K D+D +RY++A
      Sbjct: 300 LVVAFNLYKTETDFDKTRYQTA 321

```

A homolog was found in serogroup A *N.meningitidis* but not in serogroup B, so NGS161 protein and nucleic acid are useful for distinguishing between gonococcus and serogroup B *N.meningitidis*.

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

## 5 Example 159

A DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 983> which encodes amino acid sequence <SEQ ID 984; NGS162>. Analysis of this protein sequence reveals the following:

```

10  GvH: Examining signal sequence (von Heijne)
      Signal Score (-7.5): -0.86
      Possible cleavage site: 33
      >>> Seems to have no N-terminal signal seq.
      Amino Acid Composition of Predicted Mature Form:
          calculated from 1
15  ALOM: Finding transmembrane regions (Klein et al.)
      count: 0 value: 4.08 threshold: 0.0
      PERIPHERAL Likelihood = 4.08
      modified ALOM score: -1.32
      Rule: cytoplasmic protein

20  *** Reasoning Step: 2

      ----- Final Results -----

25      bacterial cytoplasm --- Certainty= 0.032(Affirmative) < succ>
      bacterial periplasmic space --- Certainty= 0.000(Not Clear) < succ>
      bacterial outer membrane --- Certainty= 0.000(Not Clear) < succ>
      bacterial inner membrane --- Certainty= 0.000(Not Clear) < succ>

30  The protein has homology to the following sequences in the databases:

      ref|NP_312507.1| (NC_002695) hypothetical protein [Escherichia coli O157:H7]
      gb|AAG58749.1|AE005587_7 (AE005587) putative adhesin [Escherichia coli O157:H7]
      EBL933]
      dbj|BAB37903.1| (AP002566) hypothetical protein [Escherichia coli O157:H7]
35      Length = 1588

      Score = 120 bits (302), Expect = 4e-26
      Identities = 109/359 (30%), Positives = 170/359 (46%), Gaps = 65/359 (18%)

40  Query: 22  AVALGSSSTASGEYSYASGYNSVASGNKSYAAGYASVASAEGSVVIGDSRQVKPEADQGV 81
      + A+G + A G+YS A G + A G S A G +++++ + S+ +G S + +
      Sbjct: 93  STAVGYDAIAEGQYSSAIGSKTHAIGGASMAFGVSAISEGDRSIALGASSYSLGQYSMAL 152

      Query: 82  AVGSKATVKNKAKQRVVVGSEAKVNAERGIAIGKEAKAGGKT'TNTLLDGPAYYADAI AVG 141
      SKA K + +G +K IA+G KA T + +IA+G
45  Sbjct: 153  GRYSKAL----GKLSIAMGDSSKAEGANAIALGNATKA----TEIM-----SIALG 195

      Query: 142  YQAEAGKGGALALGKQAKATKQNGMALGVESEAAGDFSTAVGNESKAKGQGG----- 193
      A A K ++ALG + A+++N +A+G E+EAA + +TA+GN +KAKG
50  Sbjct: 196  DTANASKAYSMAILGASSVASEENAI AIGAETEA-ENATAIGNNAKAKGTNSMAMGFGSL 254

      Query: 194  -----VGLGNQSKAEADFAVAV--GNKAEATKE-----NSLVIGRYARANGN 233
      + LGN S+A AD A+A+ GNKA+ N++ +G + A G+
      Sbjct: 255  ADKVNITIALGNQSQAADNALAIGQGKADGVDAIALGNQSQSRGLNTIALGTASNATGD 314

55  Query: 234  HSVSLGSRSEIKDGVSNVAPGYGVSASENNVSVAYKETPQSTELSYRKIVGVDDGV-- 291
      S++LGS S +G+ NSVA G S+A +N VSV RKIV V +G
      Sbjct: 315  KSLALGSNSS-ANGI-NSVALGADSIADLDNTVSVGNSSLK-----RKIVNVKNGAIK 365

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-169-

Query: 292 -NDFDAVNVRLKAMQGQNMALFSVRSEVRGVAASSAALSALTPLSYDANNPTQFMVG 349  
 + +DA+N QL A+ SV + G AA +T +Y+ N ++ VG  
 Sbjct: 366 SDSYDAINGSQLYAISD-----SVAKRLGGGAADVDDGTVTAPTYNLKNKSKNNVG 417

5

Score = 86.3 bits (212), Expect = 1e-15  
 Identities = 68/253 (26%), Positives = 118/253 (45%), Gaps = 39/253 (15%)

10

Query: 28 SSTASGEYSYASGYNSVASGNKSYAAGYASVASAEGSVVIGDSRQVKPEADQGVAVGSKA 87  
 S+ +G + G + A + Y S ++ +G V IG G+KA  
 Sbjct: 38 SALVAGGMLSSFGALANAGNDNGQGVYDYGSGSAGDGWVAIGK-----GAKA 83

15

Query: 88 -TVKNKAKQRVVVGSEAKVNAERGIAIGKEAKAGGKTNTLLDGPAYYADAIYVGYQAEA 146  
 T N + VG +A + AIG + A G + +A G A +  
 Sbjct: 84 NTFMNTSGSSSTAVGYDAIABGQYSSAIGSKTHAIGGAS-----MAFGVSAIS 130

20

Query: 147 GKGGAIALGKQAKATKQNGMALGVESEAAAGDFSTAVGNESKARGQGGVGLGNQSKAEADF 206  
 +IALG + + Q MALG S+A G S A+G+ SKA+G + LGN +KA  
 Sbjct: 131 EGDRSIALGASSYSLGQYSMALGRYSKALGKLSIAMGDSSKAEGANAIALGNATKATEIM 190

25

Query: 207 AVAVGNKAEATKENSILVIGRYARANGNHSVSLGSRSEIKDGV-----SNSVAPG 255  
 ++A+G+ A A+K S+ +G + A+ +++++G+ +E + +NS+A G  
 Sbjct: 191 STALGDTANASKAYSMALGASSVASEENAIAGAETEAENATAIGNNAKAKGTNSMAMG 250

Query: 256 YGSVASENNVSV 268  
 +GS+A + N +++  
 Sbjct: 251 FGSLADKVNTIAL 263

30

Based on this analysis, it was predicted that this protein from *N.gonorrhoeae*, and its epitopes, could be useful antigens for vaccines or diagnostics.

### Example 160

Further open reading frames were identified in gonococcus <SEQ IDs 317/318 to 8621/8622>. These polypeptide and nucleotide sequences are useful for studying gonococcus, for diagnostic purposes, as antibiotic targets, and as vaccine antigens.

35

It will be understood that the invention has been described by way of example only and modifications may be made whilst remaining within the scope and spirit of the invention.

## CLAIMS

1. A protein comprising an amino acid sequence selected from the group consisting of SEQ IDs 26, 72, 230, 984, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314 and 316.
2. A protein having 50% or greater sequence identity to a protein according to claim 1.
3. A protein comprising a fragment of an amino acid sequence selected from the group consisting of 26, 72, 230, 984, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314 and 316.
4. An antibody which specifically binds to a protein according to any one of claims 1 to 3.
5. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
6. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of SEQ IDs 25, 71, 229, 983, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313 and 315.
7. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of SEQ IDs 25, 71, 229, 983, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313 and 315.
8. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to any one of claims 5 to 7.

9. A nucleic acid molecule comprising a nucleotide sequences having 50% or greater sequence identity to a nucleic acid molecule according to any one of claims 5 to 8.
10. A nucleic acid molecule which can hybridise to a nucleic acid molecule according to any one of claims 5 to 9 under high stringency conditions.
- 5 11. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
12. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
13. A composition according to claim 11 or claim 12 for use as a pharmaceutical.
14. The use of a composition according to claim 13 in the manufacture of a medicament for the  
10 treatment or prevention of infection due to streptococcus bacteria, particularly *N.gonorrhoeae*.
15. A process for distinguishing *N.gonorrhoeae* from *N.meningitidis*, comprising the steps of: (a) contacting a protein, a nucleic acid molecule, or an antibody according to any one of claims 1 to 10 with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.



## SEQUENCE LISTING

## SEQ ID 1

ATGATTAATCATATTGAAAAATATATAGGCACATTTCTCATGGCTCGAAAAAGCGATTTCGGGAAGTCAGTACAAATTAAATATCG  
CAGCTATTTCCCTCTTCCCTAACAGGGATTAAAAACTTATATTACTTTAGGGTTAAGCAAACATGATCTGAATTATAAAGCAG  
ATTTGAAATACCTTTTGTATGTTCTTTAAATATGATGAAATCAGATTTTCCCATTTTAAAGATGGTTAGCAGAAACCATCATTT  
GAGAATAAAAAATCCCTTCTTCGGGGGAGGTTGTTTATTTGCCTAGAAGCATTGTAAATCAACAAAAATGGATGCACTGTATG  
TTTCCGCCCATTTTATTTGACGATGATTTCCAAGTCTGTTATGGCGAACCTACAATATGTTTTCCCTTTGCTTGTCCCTT  
GTATAAACAGGAAGCCGAATTGGTGGAAAAAAGGGTTGGAATGCTTTTGAGCAGTTCTTGCTGGATAATGAAGTTGGCAACCTT  
TCGGATATGAATCGGAAACCGTTTACTTGG

## SEQ ID 2

MINHIEKYIGTISHGSKSDSGSQYKLNIAAIPSSPNRDLKTYITLGLSKHDLNYSRFEILFVCSLKYDENQIFPFLRWLAETII  
ENKILLRGQVYVLPISIVNSTKMDALYVSAPFYDDDFQVCYGEHYNIVFPLLVPLYKQEAELVERKGWNAFEQFLLDNEVGNL  
SDMNRKPFTH

## SEQ ID 3

ATGGACTATAACCAAACTGTTTTATCTCACTTGCAAAAAATTTTGAAACATCATGATATTAAAGATTACTTGGACTTTAGGAA  
GAATTGTTGAAGAACTTCCGATTTCCTCAAGTTTCCAAGTGATTCTTAATCATGAAGATGAGCCTTGGGTTTATGTCAGCTCTGG  
GATAGGTCAATTTTTAGGGCAGGAGTTTATCATCAGCCGTTTGAAACACCTGAACATATTGAGACCTTGGCAATGCTGGCA  
TCTGCAAGTATGCATTATCTGATCAATTTCAATTAGGGAAAACCGTCAATATCGGTAGACCGTGGGTCGAGCAATCATCTTCC  
GGCATTTTCTGATTTCTCTGCTTATCTTATGGGCAAGAGTTGGAATATATGGATAATGTCCGATTTTCTGGTTATTGCCAAT  
TACCAGACAGAAAGACTTTTCTTGAATACTCATTGCGTAGAAGAATTGGAAACGAAATTTGATGAAGCGGTATTGATTATTTA  
GATATAAATCGTGCGAGTACTGTCTGCGAGGCAGGA

## SEQ ID 4

MDYNQTVLSHLQKFWKHDIKFTWTILGRIVEELPDFQVQVIPNHEDEPWVYVSSGIGQFLGQEFFIISPETPEHIETLAML  
SASMHPDQFQLGKTVNIGRPWVEQSSFRHFLISLPYPYQLEBYMDNVRFFWLLPITQTERLFLNTHSVEELETKFDEAGIDYL  
DINRASTVWQAG

## SEQ ID 5

ATGAACCCCGTTTGGATTATTACCGGCAAGAAGCCCGGACAGCCTGCGTAACCGCTGGGTGCTTGCCGCCGCTCTCTGCTTG  
CCGCACTCGCCCTTCTTTGGGTTTCTTCGGCAGCTCGCCACCQGTTCGGTCAAGGTCGATCCGCTGACCGTTACCGTCGTCAG  
CCTGTCGACCGCTGTCTATTTTCTGATTCCGCTGATTGCGATGCTGCTTTCTTATGACGCACTGATCGGCGAAATCGAACCGGT  
ACGATGGCGTTGCTGTTGAGTTATCCCATTTGGCGCAACCAATCTTGCCGCGCAAGTTTGTTCGGACACCTCATCATCTCGCCC  
TTGCCACCACGGCAGGTTACGGATTGGCAGGCATTACGCTGCAACTTGCCAACGGCGGTTTCGACATCGCCGCTTGGAACCCCTT  
TGCGCTGTTGATTGCGCCAGCGTGATTTAGGTGCGGCATTTCGTCTATGCGCTACTTGATTAGTCAAAAGGTCAAAGAGCGG  
GGGACGGCGCGCGGTATTTCCATCGGCGTATGGTTGTTTTCTGCTGCTCATCTTCGATATGGCGCTTTTGGGTATTCTGGTTGCCG  
ACTCGAAACAGGTCATCACCGCGCCCGTCTGTAACCGGTGCTGCTGTTCAATCCACCGACATTTACCGCCTGCTCAACCTGAC  
CGGTTACGAAATACGGCTATGATGCGGGTATGGCGGGTTTGAAGCGGACAAATCGGCCGTGACCGTCCCCGTTTGTGACCGCG  
CAGGTTTATGGGTTATCATTCGCTTGTTTTGGCAGCGGAATTTTAGAAAGCGACGAATA

## SEQ ID 6

MNPVWIITGKEARDSLRNRWVLAVALLLAALSLGFLGSSPTGSKVDPLTVTVVSLSSLSIFLIPLIAMLLSYDALIGEIERG  
TMALLSYPIWRNQILAGKFVGHLLIILALATTAGYGLAGITLQLANGGFDIAAWKPFALLIAASVILGAFLSMGYLISAKVKER  
GTAAGISIGVWLFVVFIDMALLGILVADSKQVITAPVVEVTLVLFNPTDIYRLNLTGYENTAMYAGMAGLSGQIGLTVFVLLTA  
QVLWVIIPVLVLAAGIFRKRRI

## SEQ ID 7

ATGTCAGACGAAAAATTAGAACAAAACGGCTTGAGCCGTCGTTCTTCTAGGTACGGCCCGCGCTTCCGGTCAGGTATTGCCG  
GTGCGGGCTGTTGGGTTTGGCGGGTTGCTCTAAAGACGGCGAACAGGCTGCCGCTAACGCTTCCGGCGCGGCTCCCGTCGCCAA  
GGCGCAAGGGGAATCCAAACCCGGCCAACGTCTTCCGAAGTCGGTCCGGCGAACTCGATCAATATTACGGTTTCTTTTCCGGC  
GGCCAGTCCGGCGAGATGCGCCTGATCGGTCTGCCTTCTATGCGCGAACTGATGCGTATCCCGGTCTCAATATGGACAGCGCGA  
CCGGTTGGGGACGCACCAATGAGAGCTTGAAAGTCTCAACGGCAATATTACCGAAGAAACCCGTAAATTTTAAAGACAGCGG  
CCTGCGCTGCTACCCCAACGGCGACTTGCACCAACCGCACCTGTGCTTTACCGACCAAACTTATGACGGCGGCTATGCCATGCG  
AACGACAAGGCAAAACACCGCGTCTGCCGCGTGCCTTTGGATTGATGAAGGCGGCAAAATCATCGACATCCCTAATGATTCAG  
GTATTACGGTCTGCGTCCGCAACGTTATCCGAAAACCGGTTATGTTTTTGGCAACGGCGAACACATTACCCCTGTGACGGGTGT  
AGGCAAACTGGATGATGCGAAAACCTGGAATGCAGTGTACACCGCCATCGACGGCGAAACCATGGAGATCGCATGGCAAGTATTG  
GTTGACGGTAACCTGGACAACGGCGATGCCGACTATCAAGGCAAAATATCTTTTGCCACCTGCTACAACCTCCGAGCGCGCGCTGA  
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CTTCAAAGAGTTAACGGTGTGAAATGCTGGACGGCCCGCTGAGGCCAAATCCAAATACACGCGTTATATCCCTGTGCCGAAC  
TCTCTCAACGGCTGTAACGCAAGCCCTGACGGTAAATACATCATGCCCAACGGTAAACTGCCTCCAACCGTTACCGTATTGGATG  
TCAGCAAACTGGACGATTTGTTTCCGGCGCAAAATCAAAGAGCGCGATGTGGTCTGATGCCGAACCGCAACTGGGTCTCGGCCCGTT  
ACACACTGCATTTCGACGGTCCGCGCAATGCTTATACGACATTGTTTATCGACAGCCAAATGGTGAAATGGAATATTGACGATGCG  
ATCAAAGCCTACAAGGCGAGAAAATCGATCCGATCAAAACAAAACCTCGACGTTCACTATCAACCGGGTCACAAACATACGACCA  
TGGGCGAAACCAAAGAAGCGACGGTCAATGGCTGGTGTCTTGAACAAATTTCTCAAAGACCGCTTCTTGAATGCCGGTCTCTTT  
GAAACCCGAGTGCGACCAATTGATCGGCATCTCCGGCGACGAAATGCGTCTGGTACACGACAACCGGACTTTTCCGAACCGCAC  
GACTTGTGTTTGGTTGCCGCGTCCAACCTGAACCGGGCAAACTTGGGACCGCAAGACCCGTGGTTC

## SEQ ID 8

MSDEKLEQNGLSRRSFLGTAAASGAGIAGAGLLGLAGCSKDGQAANASGAAPVAKAQGESKPGQLSSEVGPGLDQVYGFSLG  
GQSGEMRLIGLPSMRELMRIPVFNMDSATGWGRTNESLKVNLNGNITEETRFKFLKDSGLRCYPNGDLHHPHLSFTDQTYDGRYAYA  
NDRKANNRVCRVRLDVMKADKIIDI PNDSGIHGLRPQRYPKTYVFANGEHITFVSGVGKLDAAKTWNNAVYTAIDGETMEIAWQVL  
VDGNLDNGDADYQGYKYSFATCYNSEALTVQGASSNEQDWCVVFLDLKAEIGIKAGDFKEVNGVKMLDGRABAKSKYTRYIPVFN  
SPHGCNASPDGKYIMPNGKLPPTVTVLVDVSKLDDLFAKGIKERDVVVAEPQLGLGPLHTAFDGRGNAYTTLFIDSQMVKNIDDA

ATGAAACTAAATACTCTCACATGGGCTTTTGATGACCGTTTTTTCCGTTGCGCCATCTTGGGCAGAACAAACCGGCAAAATACTGAAG  
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CCGCTCCGACCGCAGCGATTATTACTTTGTTACCGAAACATAGACCAAGCCTTCGGTCGCTGAAGGCAAAACAGCAGTTTTTTAC  
GGCAAAGCTTTTACAACCTCCGTTACCGCGCAAGCATCGGGCGAAGGTATACGGCTGACCACTCAATCAGCGACCAAGGCAA  
ACGGCTACAAGAATGGCGGTGGGCGACACGTGATTGGAATACAGCCGCTTCAATCAGGCTTTGGTACTCGGTTTCGTGCCGTC  
TGAAATCAAGAATACCGCCTCACTTATCTGCACGACGACATCAACAACGACCGCCAGCCGAGGTCGTCAACGACGCATTGGAC  
ACCGAACGCCACATCTCCAAACTCAACGTGCGTTGGGGCAATGCCGATTGTAGCAATACGGTCAGCGCGGAAGCAGGCGTCATCA  
AACTCAAACGCCCATGCCGACAATTACTCTTTGCGACAAACAACACGCGCGCAGCAAGTGTTCGTAGAACTTGACCGCAAAAGTGT  
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CCCTCGGCAATTTGGAACCGTACGGCGACAAACCGAAGCGTTTCAACTCGCTTGTGTCATCGTGCAAAACCGTATGAGCGGCAT  
CGTGATGACCAAAAATCCAGCGCCGCCGATTGCAAGGCAATCCCCCTGCTGAAAAAC

MKLNTLTWALMTVF SVAP SWAEQ PANTEE IQPVKTF SPPKP IAPTAAQGYFPENQFORSDRSDYFVTENIDQAFRLKANSSFY  
 GKSFYNSVTAQALGAKVYGVANLNRKTANGYKDGGRDTDWKYSRFNQALVLGFPVSENQBYRLTYLHDDINNDRQPOVVNDALD  
 TERHI SKLNVRWGNADLSNTVSAEAGVIKLKRHADNYSLRPNTPQQVVELDRKVDYFSLKHDADEFKGFHNTAAVSYRNDSONG  
 ERNTHTAMCDFLNGYDFADVHIDRWCIADTLTKYFPDDRKLGLGLSYELNEADIRKNTAQPENKIPGFPASSQQIWKTHYGYD  
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GAGTTTGATCGCGGCATTT

LQAIPLLKTEKHNRIRLTADSRNDYNGYMNSLAGAGWNVGGTLVADKVKDLIIFDRAHQSGTASDKGGIITRNV DARLF TAQA  
YARYNFNPHWAAGIKAAYNYGHNETDGRPPYQIRPFEAAVQADYKNYFAHGSYNIGAATRFVAKQTRGDFDMASGLGIDKREAAK  
GFTVADVYAGVNIKD KYGLRLGVNNVFNKKYVEYISGDHVLALSPSVVYAPGRTYWLSLHAAF

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TTGGCCAACCGCCAAAACGCGCGGAAAAATCGGCAAAAAATACCTACCCGCCCCGAACCCGCCCTAGTCATGGGCTTGGACGGCG  
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MDMKRRDFLKMTAALAAAGVSPSLAAGKEQFTVYGAPAMPSTVIATAALQGLAKQADVSLKIWRSPDQLRAGVASGQFKVMS  
PSNVGVNLRNQGQKVGVMVNIITNGITQLVCKGSAIASPDVLGKKILVPFKNDMPDIVLQALLKKLKIDAHKVSITYAATPPEAV  
GLFPSKGYHAVILPEPMATASLLKGKTIGINVHGFDLVKAWGQAFDTKPLIPMAGILANEYFHAHKAQFDIFHQDLKNALNWI  
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ATGCGCATGGTGGCGTTGTGGCGTGGGGCAGCGCCGTGTTTCGGCGAGTTTATGCTGCCCTGCGCCGGTAGAGGTGTTTCAAAAAT  
CTTTGGATTATTATTAACATTTTCAGGAAAATGAAATCGGGATTTCGCTGTGGCGGTTCGGTAGTGGGTATTTTCGGTTGCTTTGAT  
AGCAGGATTGGCGCGGGGCTGGTGGCGGGGCTGGTGGCGGCAGTTTTAAGACGGCGATGGCGTTGCTTAAGCCGTGTGATTACG  
ATTTTGTTAGCAATGCCGCCGATTATTTGGGTGGTGATGGCGTTGTTTTGGTTTCGGGTTTCGGCAATCCGAGCGTGTGTGTTACCA  
TCATTGTGTGGTTGCGCCGCTGACGTTTGCGAGTGCGGCGGTTCGGAATGGCGAGCGTGAACAAGCAGCATGAGGAGTTGTTTGA  
CGCTTATAAAATTAGGCCGCTCTGAAAAAATCCGCTATCTGTATATCCCGCATCTGACGGGCTATGTGATTTCCAGCGTCGGCGTG  
CGCGTGGCAATGGGGGTGAAGCGGTGATCATGCCGGAACCTTTAGGCGCCAGCAAGGCGTGGGCGCGCGGATTCCGGACGCGCA  
GGCGCAATGCTG

## SEQ ID 16

MAMVALWAWGSAVFGEFMLPAPVEVFQKSLDLLKHFOENEIGISLWRSVVGISVALIAGLAAGLVAGLVAGSFKTAMALLKFVIT  
ILLAMPPIIWVVMALFWFGFNPVSLFTIIVLVAPLTFASAAVGMASVVKQHEELFDAYKLGRLLKIRYLYIPHLTGYVISSVGV  
AVAMGVKAVIMAEELGASKGVGARIADARAML

## SEQ ID 17

GTGAAAGCCTTGTTCCGGCCGAGCGGCTGTGGCAAGACGACGGTTTTACGGCTGATTGCGGGCTTGAAACGCCGAAATCGGGCA  
CGATACGTAATACTTTCCACAAAACGGGTTTTCTGTTTCAGGAAAACCGCCTGCCGGAACCTGACCGCGATGCAGAAATATCGC  
GATTTTTATGGACAACCCAGACGAAGCGGAAATCGTCGCGCTGGCGGCGAAAGTCGGGCTGACTGCGGGCGATTTGAACAAATAT  
CCGACCGAATTGTCCGGCGGCATGGCGAAACGGGTGGCGTTTTTGGCGCTGCTGCTGCGGCTGCGACCTAGCCTTGCTGGACG  
AACCGTTTTGTGCGTTTGGACCGCGATTTGCGCGATATTTGGTTGCTATGCTGGTGGAAAAATCGAGCGGCAGGGCATGGCGTG  
TATACTGGTAACGACGACCGCTTCGAAGCCGCGCGCTGAGCCATGAAATTATGCTGCTTTCCGCTAAGGGCATGAACGTGCAA  
AACGTGATAACCTGCCACGCCGCTGTCCGAACCGGATTCGGCTTTTGAAGAAGTCGTGGTGGCAAGGGAGTTTCAGGGGATTC  
ATTATTATGAG

## SEQ ID 18

VKALFGPSGCGKTTVLRLIAGLETPKSGTIRNTPHKTGFLFQENRLEPNLTAMQNIATFMDNPDEGETVALAAKVGLTAGDLNKY  
PTELSGGMKRVAFRLRLCGDLALLDEPFVGLDRDLRDILVAMLVKIERQGMACILVTHDRFZAARLSHEIMLLSAGMNVQ  
NVITLPTPLSERDSAFEEVVVAREFQGIHYE

## SEQ ID 19

TTGGGGTTGAGGCAAAAGCTCAGGGGGATAATACCAAACCTTAGCAACCTCAATCGGCACATCTGCCGAAGCAAATGCACCCGGG  
CATTGGCTTTAGGGGGAAGTTCTGAAGCATCGAAAAAATTTAGTATAGCAGAAGGCTATCTGGCATCTAGTGATGGCTATGGTGC  
AATAGCGATTGGTTCTGCCGCCAAGATAAAGCAATTTGGAAAAAGGCACAAATTAATCATATTGTGGGAAACGATAATAAAGGTCTT  
TATGTCGATGCAGACGGCAATGTAAACAAAGATAACCGTAAGGACTGAGTCGGAAGAAATATTTCTCTCAAGATACGGTCAAACCTT  
ACGGTGCCTGGTGGCTAGGGTTTAGATCTTCTTACATAATCTTTTGGCAGTTCAATTGGAGCGTTTTCTACAGCCACAGCTAT  
TGAAAGCTTGGCAGTCGGCGACAGCAGCAATCAACGGGCTACCGCAGTGCTACTTTTGGCAGTCACAGCAGGGCTTTGGCAGAA  
GAAAGTTTGGCATTAGGTTATGAAACTCGGGCAAATGCTTATGGTTCTGTTGCTTTAGGTGCAGAACTCTGTGGCGAATGAAGAAA  
ATACCGTATCAGTGAGTTCCGATACATTGAAACGGAATCGTTAATGTGCGCGATGGCAGCGAAGATTAA

## SEQ ID 20

LGLRQKLRTGIIPNLATSIGTSAEANAAPGALALGGSSEASKKFSIABGYLASSDGYGAIAIGSAAKIKQLEKGTINHIVGNDNKG  
YVDADGNVTKITVRTESEKDILSRYGQTYGAVALGFRSSSHNLFASSFGAFSTATAIESLAVGDSSQSTGYRSATFGSHSRALAE  
ESLALGYETRANAYGSVALGAESVANEENTVSVSSDTLKRKIVNVDGTEDL

## SEQ ID 21

ATGTCGCGGATGGCACGGAAGATTTATGATGCAGTAAATGTCCGCCAGTTGAACCGCTTAAGCAAACGTACAAACCGCGTCGGCG  
CAAGTGCTGCGCGCTTTGGCTTCGTTAAACCTGCACAATTAGGCAAAAACGACAAATTCGCCCTTTCTTTGGGCTTTTGAAGCTA  
TAAAAATGCCAAGCGGTGGCAATGGGGCGGTGTTTAAAGCCGCTGAAATGTGTTGCTTAATGTGGCGGGCAGTTTGGCCGGA  
CCGGACCGGGCTTTCCGGCGCGGGGTTTTTGGAAATTCGGCGGCAAACCGACACCTGCGGTTGCCGCACAAAACCGCGCGCATC  
CTGCAAAAGTTTGGCAATTGCGGCGAGGAAGTGGCGCGTTGCGCGCCCGGCAGGCAGAAACCGACCGCAAACCTGCACAAACAGGC  
CGAAATGGAACGAGCTGCAACAGTTGCGCGCGCGCTTGTCCGAATTGAAAAAACAT

## SEQ ID 22

MSPMARKIYDAVNVRQLNRLSKRTNRVGASAAALASLKPAQLGKNDKFAFSLGFGSYKNAQAVAMGAVFKPAENVLLNVAGSFAG  
PDRAGAGVFWKFGGKPTPAVAAQNAHPAKVLQLRQEVAAALRARQAETDRKLHKQAEEMENELQQLRRALSELKHH

## SEQ ID 23

ATGACGGAGGGGAACGGCGCACGGACATTTGCCGGAATCTTTTATGTTTCCATTATCATACTCTTTTCAATGCGCTATTCCAGGA  
AAAAGAAAATAGCTTGTGACGGCTGCTTTTGTGTTTCAGACGACCTGTAATTAACGGCTGCTTATCCAATCTGCTTTTCAAACCT  
ACCTGCAACCGCAAAATCTGCTGCAACCGCTCCCTCCCTGTGGGGGAGGGTTTGGGAGAGGGCATTTTTCAAGTTGCGGCAAT  
TCCCCCCCCCGCTCAAAAAATTCCTTAACCGCCCCAATACAAGCCTTGCAGCTTACTGCCCTCTCTCTAACTCTCTCCACGGG  
GAGAGAGGACTATGATGCCCGCCGGCGGCTTGTATTAGGAATATCTGAATCGTCATCCACGAAAGTGGGAATCTAGAAACCC  
CAACGCAGCGAGAACTATCGGAGAAACCGAAACCGACAGACCCGGATTCCCGCTGAGCGGGAATGACGAGGGGAACCGGCGC  
ACGGACATTTGCCGGAATCTTTTATGTTTCCATTATCATACTCTTTTCAATGCGCTATTCCAGGAAAAAGAAAATAGCTTGTGCA  
GGCTGCTTTTGTGTTTTTACAGACGACCTGTAAT

## SEQ ID 24

MTEGNARTFAGIFYVSIILFSMRYSRKKKIACAGCFLFFRRPVINGCLSNLLFKLPATAKSAATRSPLCGGGFGRGHFSSCGN  
SPPPLKKFPNRPNTSLAAYCPLNSLPRGERTMMPAGLILLGISESSFPKRWESRNPNAARIYRRNRNPTDPSRLSGNDGGERR  
TDICRNLLCFHYHTLFNALFQEKENSLCRLLFVFQPTCN

## SEQ ID 25

TTGCTTATAGTTGTACGGTTTGACATATGCACGGAAGGAAACGCCATGACTTTCTTCAAACCTCTACCGTCGTGCTGACCGCAT  
CCGCACTCGCGCTTTCCGGCTGCGTTGCCGACCCGTAACCGGACAGCAGTCCCAAACAAATCCGCCATGTACGGTTTGGGTGG  
CGCGGCAGTGTGCGGCATCGTCGCGCACTGACCCACAGCGGCAAGGCGCACGCAATTCGCGCTTGCTGCGGCGCAATCGGC  
GCAGGCGTGGGCGGTATATGACTACCAAGAGCAGCGTTTGGCGCAAACCTTGCCGGCAGCAAAATCGAAATCCAACGCCAAG  
GCAACCAATCAGGCTGGTGATGCCGAAAGCGTTACCTTCCGACCGGCGAGCGCGCGTTGGCGGCGACACCGGCAACACAGGTTCCGATGCA  
GAACACTGCCGCACAGACGCTGGTGAGTATCCGACACGACGCTGACCATCAACGGGCGACACCGGCAACACAGGTTCCGATGCA  
GTCAACAATCCGCTTTCGCAACACCGCGCCCAAGCGTTGCGCTACTATCTGCAGACGCGCGCGTGGCGGCTTCCGCGCTGACCG  
TTTACGGCTACGGTTTCGCATATGCCGCTCGCGTCCAACGCTACGGTTGAAGGCCGCGCGCAAAACCGCGCGTCAAAATCCTCAT  
CAACCCCGACCAACGCGCGCTCAACCGCGCACGGCACATG

## SEQ ID 26

MTFFKPSSTVLTASALALSGCVADPVTGQQSPNKSAMYGGLGAAVCGIVGALTHSGKGARNSALACGAIGAGVGGYMDYQBRRLR  
QNLAGTQIEIQRQGNQIRLVMPESVTFATGSAALGGSQAQYALNTAAQTLVQYPTTLTINGHTDNTGSDAVNNPLSQHRAQAVAY  
YLQTRGVAASRLTVYGYGSHMPVASNATVEGRAQNRREILINPDQRAVNARHM

## SEQ ID 27

ATGAAATCGAAACTTACTGTCGTCTATTACGATTGGAAGCAATATTGCAGAAGAAATACTGTCAGGAACATAATGCCTGATG  
GAAATTTTCTTATTCAAGAGATTCTCTTTTCGACCCGAATTGGCTTTAAACGACATTGTTGCCATAGAACGTGAGGATAAGAT  
GCTGTTTTTCGACCACTTGATAAAGCTTCAGGAAATACCAGATAAACATCGTTGTTTGGATCATTTCCCAAAGGATTTATTG  
GCAGCCATAGAAGAACACAGTGGTAAATCAGAAAAATGGAGAGAAATTATTTATCGGTTAATTTTCCGCCCAAAAAATATAATT  
CTGATTTAAAGGAATTTTAAATAGATATGAGGAAGCAATATCCTCAGCTACAGGAAGCTTGTTTGGGCTTCTCT

## SEQ ID 28

MKSKLTVVYYDLESNIAEELSNGNIMP DGNFLIQEIP LFAPNLALNDIVA IEREDKMLFFDHLIKASGNTTINI VVLDHFPKDLL  
AAIEHSGKIRKNGENYLSVNFPPKKYNSDLKGLNRYERANILSYREACLGFS

## SEQ ID 29

ATGGTGCAATGGCAACAATAACCAAGCGGCGCAATCCTTCCGGCGAAACAGTATATCGGGTTACGGGTACGGGTACGGCAAGAAAG  
GCTATCCTGCTTTCAATGAGAGCAGGACGTTTCAAGTAAAGAGCTTTGGCGGTGCAATGGGGGAAGAACGGGAGGCGGAAATCGA  
AGCCGGCCCGAAGCTGCTTTTCAAGCGCGGCAAGGTCAAGATGATGACGCTGTCCGAAGCTATGCGGAAGTATCTTAAAGAAACG  
CTTGAGCGGGTCCGTCAAAGAAAATGGGCTTGCCTTTCTGATGGAGTTCCCGATTGGCGGCATCGGCATCGATAAGCTGAAAC  
GGTCTGATTTCCGGAACACGTTATGCAGAGCGCGCGGAAATCCCCGAACCTGGACATTGCGCCAATCCGGGCTTCTACGGCAT  
GCAGGAGCTGCAATATATCCGTTCCGTGCTAAACACGCGCTTTTATGTGTGGGGCTTGAATAGGCTGGCAGGAATGGATTTC  
GCGGCAACCGGCTGAAACGCTCGAATATGGTTGCGAAATCTGCAATCAGGGACAGATTGCGGACCACGGAAGAACTGCAAAACCC  
TGACAACTTATTTCTGCGGCAATGGCAAGCAGGAAATCTTCCATACCGATGCACCTGATATGTGGCTGGCGATTATATACCTC  
AAGGCGGCGAGGATGAGATTTGCGGCTGCTGTTGACGACTGGCACAATAATGATTGTACCCGGCCGGTTCGTGATTTAAAAAT  
CCGAACGGCAGCACAGGGAATAATAAGGAGTTTGATATTCTGCCATTGCGCTTTGCGGCTCATTTGACGAGCTGCGCGGGAATCGG  
TCAGGAAGCGTATGCTTGCACAAAGGCATCGCCGACAGCCTTGATACCGTGCACCGGAAATCGGTTTCCGCGGCTTGGACGAG  
GGCGTGCAAGGTTCTTGGAAATTAAGACTTGGCTTCCACGATTTACGGCACGAGGCTGCTACCCGTATGGCTGAAGACGGCTTC  
ACGATTCCGCAATGCAACGGGTAAACGCTGCATGACGTTTGAACAGCCTGCAGAGGTATGTGAGCGTACGCAACGCTCGACGC  
GGCTGGATTTAAAGAGGCAATGATGCAGGCGCAAGCGATATAAATCCGGGAAG

## SEQ ID 30

MVQMATITKRNPSGETVYRVQVRVGGKGYPAFNESTF SKKALAVEWKKREAEIEAGPELLEFKRGKVMMLSEAMRKYLNET  
LGAGRSKRMGLRFLMEFP IGGIGIDKLKRSDFAEHVMQRRRGIP ELDIAPIAASTALQELQYIRSVLKHAFYVWGLEIGWQELDF  
AANGLKRNMVAKSARLDRLP TTEELQTLTYFLRQWQSRKSSIPMLIMWLAIYTSRRQDEICRLLFDDWHKNDCTRPVRDLKN  
PNGSTGNKFEFDILPMALPVIDELPEESVRKRMLANKGLADSLVPCNGKSVSAAWTRACKVLGIDKLRFDHDLRHEAATRMAEDGF  
TIPQMQRVTLHDGWNLSLQRYVSVRKRSTRLD FKEAMMQAQSDIKSGK

## SEQ ID 31

TTGCGACAACGGCGCGGCTTTCAGCTGCTTCAACTGGACCGAACATTTCAAACGGACGGCAAACCTGATCAGCCTCATGCACAGG  
GAAGCGGCGGCATGAGGACGACATCCGAACCTGCGTGTATCAGGATTCCGGCACAAAAGGCTCAAACACGGCATCAGGCATAAG  
CGGCACGGCTGCGGCGCGGCGGGAACAAGCGTTTTCAGCGCGGCGAAGACGGCAAACCGCAGCGCTCAGCGCATCCGCAAC  
GCTCCGCCACACCCGACAAGCCAAAGAACGACGAAAACCCATGACGTTTCAAGGACACAACAACCGTAAAAAAGCCGGCGGCT  
ACGCCGAATACATACCGGCGGCGAGCTTGAGCGGCTGTTGCGGCCAAAGTCCGCGGATCTGCGGCGAACACCCGGCGGTATT  
TGACGGCGCGGCGAGGAGCGGGCAGCTGGAGCAGTACATCGAACCGTCCGATTTCGCGCGCTAGAGATACAGGCGGAAGCGTGT  
AAAGCCTTGTGCAAACTACCTGCGGCAAAGTATACACAAACAGCTTTTCTTTATACCGACGGCGAACCGCAAGACTGCA  
CCGTATGAATCCGCGCTTTTCCATCAAGCTAAAGGATTTGAGCGAAGACGAAAAGCCGTATCGCACAGGAATACCCGTGGAA  
GAAATCGGGCGTAGCCGATGAAATCTTCTGTTTAAAGGATTTGAAAACGCGCCGCGCTTCGGATTCTTCATCTGTTCCCGGCG  
ATCGCCTACCGCAAAGCGAGCAGCGATTCCGCGAAATCATCGGCAACCGGCTGGCAGAACTCAACCGCATACAAAACGCGTTTG  
AAGACACGCGCATCGAAGTGCTTTTACTGGTTATCGACAAAGACAAAACCGAGCGGCTGCATCCGCGAAGCTGACGATGCAA  
AACAGACACCTGCTTGGCGCGACACTTGGCAAATCGAACCGGACTTGTGGCAAACCGTGCAAGAACCTGACCGCGGAAGGAA  
AAGGAAGACCCGCTCTTTGGAACACGAATGCCGTGACGCGCGGCAAGCGGATTTGCCCGGAATTTAGGTTTCAGCAAAATGG  
TCAACGAGATAGAAGGCTGGCCGATGCCGAATTTGACGGCTTTTGGCAGCGCTGTGCAACCTGATACAGGACAGAAATACGG  
AAAAAACACTACTTCCCGTGACGCTGCCACTTTTTCGAGGGGCGGCGCGC

## SEQ ID 32

LRQRRRLQLQLDRTFQTDGKPDQPHAQSGGMRTHIRTCVYHDSGTGKSNTASGISGTAAGAAEQAFFSAAKTANRSASAASAN  
APPHDPKPKNGRKPMTFQGHNNRKKAGGYAEYITGSLRLRLVAAKVRRYCGEHPGVFDGAAGSGQLEQYIEPSDFRAVEIQAEAC  
KALLQNYPAKVYNTSLFLYTDGEPQDCTVMNPPFSIKLKDLSDEKSRIAQEPYWKKSQVADIEFVLKLENARRFGFFILFP  
IAYRKSEQRFREIIGNRLAELNRIQNAFEDTPIEVLLLVIDKDKTDGGCIRELYDCKTDTLLAADTWQIEPDLWQTVQEPAPPKE  
KEDPVLLEHECRDAAAKRIARELRF SKMVNEIEGWPHAEFDGFCDLRLNLQAEKYGKKHYFPCSLPLFGGAAG

## SEQ ID 33

ATGCAACAGTAGCAACAAAACCGACGGCAAAACAGATGCTTCCGCCAAACCGCGCGGCGAAGGAATCAACCGCGCAGGAACCGG  
CCGTCAACGCGCGCGGACGGTCAAGAACGTTGACCGGAACCGGCTGTCCGCCCGGTCAAAGCGCAAAAAGAAAACATCGCCCCG  
GATGTTTGTCTGCGCGCAAGGTATCGGAAGACGAAGCCCTGACGTGCGGCATCATGATGCGGCTGTCCCTGCAGGATATGCGCTAT  
GCCTGCAATCAGGAATTAATCAACTTCGCCGAACATATCGTCAAACAGGTGCAACGCTTGGGCTGTACTGCAACACTGACGACC  
CCGCGAACGGGGAAGCGTACTGTTGCTTGCCTGCCGCGAAGCATCGCAGGCGCTCGCTCAATGGACTAAAGATTTTGACAATTTAAG  
CCGAATCAGCGCCAACCTGCTGCTGCGTCCGCTGTCAAATCTCTTCGCCGCGTACGAAGAATTTCTGAAAGACGCGCTGCACGG  
CTGATAGCCGAAGTATCGGCATACCTATGGCCGTGCGGGTTGCCAAGAAAGCCATGCGGTTTGTAGAGCTTGACGCGGCTTTGA  
TTTCGGCGGTTGGCAAAGTCTGCAACGGCGCGGATTCGCGCGCGGAAGCCCGCCCTTAAATGCGCGGCAATTTACAGG  
CCGGATCTACAGCCGCGAACCCTGCTTACGATGTGGGACTTTCAGGCGGACAAGGAGCTTTCGGCGATGTACGGCAAGCCGCTG  
AATCCCGTGCGCCCGGACGCGATAAGCGACGTGCGCGCGCGGATGATGAAAATGCTTGTGCGGACAAAGCGCGCGCTTGGTCC  
GGGCGTAAAGACTCGGAAGACGTATCCGGCATTGGGACAACGGCGCGCGCTTCAGCTGCTTCAACTGGACCGAACATTTCAA  
ACGGACGGCAACCTGATCAGCCTCATGCACAGGAAGCGGCGGCA

## SEQ ID 34

MQTVATKPTAKQMLAAKRAAKESTRQERAVKRAGTVRNVDRNLSARSKAQKENIARMLSGAKVSEDEALTCGIMMRLSLQDMRY  
ACNQELINFAEHVQVQRLGLYCNTDDPANGESVLFACREASQAVAQWTKDFDNLSPNQRLVLRPLSNLFAAYEEFLKDPAR

LIAEVSAYSILAVRVAKKAMAFLELDGGLISAVGKVVNGADSRABARRLKMPYAEFTGRILHAANLLYDVGIQADKELSAMYGKPL  
NPVRRPRRISDVRRPMMKMLVADKGGALVRAVKDSESVIRHCDNGAGFSFCFNWTEHFKRRTANLISLMHREAA

## SEQ ID 35

ATGTACGGAAATGTGCCGGATTAGATTGCTGCTTTACAGGAAACCGCATATAATCAAAAGTATGAAACCGCACACGATACCA  
TTTTCCAAGAGCCAAAGGCTGCCAAGCGCGCCGCTTCTCTGCTGTACAAGGCAAACGGCAGGCTTGAAGTACTGAAGCTGATGAA  
GCTGATGTACTTGAAGCTGAACGTGAGTCTTTTTTACGCTTCGGAGAAGGCTTACAGGTGACGCGTTGGTTTCAATGCCGATGGT  
CCGGTACTCTCCATGACCTTGGATTTCATTAACGGCGGACATGAGTCCGTTCCGAACGGATGGGCAACGTTGGTTAGCGACCCGG  
AAAACAGGATGCTTGCCTTACGCGATCCAAGTATGATTCCGACGCCCCGGGCAAGACTTATCGGCATTATCCGAAGCTGATTGGA  
AGTACTGGAATCGGTTTGGGAGAATTACGCCATTATTCGCGATGGGATCTGCGCAACATGACCCACAACGGGTTATGCCCGGAA  
TGGGAAGACCTCAGCGCTCAAGCCGCCGATTCCCATCAAAAACTGTTGTCTGTGCTTGGTTATGATGACGAACAAGCCGTAG  
CGATTGTAGAAAGGCTGGAAGAACAGGCTTACATCAATCGCGCTTTCGGG

## SEQ ID 36

MYGNVPDLDCILLYRPHIISKMPKPHNDTIFQEPKAAQAAFLLYKANRLEVLKLMKMLYLAERESFLRPFGEGLTGDALVSMFPG  
PVLSTMLDFINGGHESVPNGWATWVSDRENRLALRDPMSMIRTPQDLSALSEADLEVLESVWENYGHYSANDLRNMTNHLCP  
WEDPHGSSRPPIKLLSVLGYDDEQAVAIERLEEQAYINRAFG

## SEQ ID 37

ATGTTTATCCCTGCCGCCCTGCACAAAGACGAACATTCCGCATATGGCGTAACCATCCCCGACCTTCCCGGCTGTTTCTCTTGCG  
GCGACACCGTTGAAGAAGCCGTCGCCAACGCCGTTCTGCCGCTATATGCATATTGACGGTATGATTGAGGACGGAGGTTTCAA  
AAACCTTGCCGTAAGCAGCATTGCCGATTGAGCCAAGAAGCTGATTATCATGGGGCAACATGGGTAATGATTGAAATCGACCT  
GCAAAATCAGTCGGCAGCAAATCCGATTCAACGTCAGCTGGCCGCAATACCTTCTTGATAGAGTGGATGAATATACATCCGCAA  
ATCATGAAACCCGTAGCGGTTTTTAGCCAAAGCCGCCCTGCTTACCATGAATCAGGCA

## SEQ ID 38

MFIPAAHLKDEHSAYGVTIPDLPGCFSCGDTVEEAVANARSAAYMHIDGMIEDGGFKNLAVSSADLSQEPDYHGATWVMIEIDP  
AKISRQQIRFNVSWPYQLLDRVDEYTSANHETRSGLAKAALLTMNQ

## SEQ ID 39

ATGAACCGATATGCCATGCGTTTGGCGTCATACGGTTTATGCCCTATGTCCAAACGCGCGAATTGGCCAAACATCGGCATCATCA  
TAACCCACCCGCAAAGCGGCTGCTTCGACTTTAAATCGAACATCGCTACAGCAGATTGAGCCGTTTTCGCGCGCTTCGATCC  
GCCCCCTATAAAGCGCGGACCCGTGCCCTTTGAAAAGAAATTACAGCGGATTAGAAACCTGGCGGCACACTCCGCGCCCGATCAG  
ATACGCGCCATGCCCCGACCATCTGACCCGCCCGCGCGAAGCCCTGATTATGGCCGCCCAACCGGGCGTAACCTCGCCCCGACA  
GGGGCAGGAATGAACCGCTGTTGATTATTTGTGCGCCGCGAGCTTCGCCAAAAACCAACCGAAGCAGAACTTACCCGACA  
AATACAGGCAATGTTAAAGCCGCTTCAGACGCGCATACCCCTTCAAAGAAAGCACAATCGCGCAGCCGTGAGCTTTACGCGCTCC  
ATCCCTTGGTGCAAAAGCGGAAACCGCGAAATACGGAAATCATCAAGCCTATCTATTTCGGACGGAAGACCCCTGCCGACA  
TCTATTACAAGTCTGATAAGCGGATTGCCGCGCATAAACCGTTGCGGCGCGCGGATACATCGACCGCTCTGAAATATTGTTGCG  
CTACGAACCCGCGGAGCGTCCCGACAAGGCACAAGAAAGGCATTGCTTGACGTATCGGGCGACCTGGAGGAACAGGGCATACAG  
CTTGCCGATAACCGAAGCGAAGGCAAAATCATCAGAACTTTGCCCTGCGGC

## SEQ ID 40

MNRYAMRFVIRFMPYVQTRFANIGIIITHPQSGCFDFKIEHRYSLRFRFRFPAYKAATRAFEKELQIRINLAHSAFPDQ  
IRAMPDHLTRPREALIMAAQPGVTLAPDRGQELNRLFDYFVARSAFNQPEALTRQIQAMLKPLQTAYPFKESTIGDPSGFHAS  
IPLVQKAENGEIRKLIKPIYFGRKDPADIYYKSDKRIAGIKRLRRGGYIDRSEILFAYEPPERPDKAQEKALLDVSGDLBEGQIQ  
LADNRSEKIIIRNFACG

## SEQ ID 41

ATGAAAAAAGAGAATTAAATGAAATTGAGACGGCTGAATGTGCCGAATAAAAGAAATTTTAACTCAAAAAAGAAGAACTTA  
AGCTAACCAATACAGCTGGCAGAAGCTGTAGGAGTTACTCAAAGCGCGGTGAACCATTTTAAATGGCACCAACGCCTTAAA  
CGCTCCATTGCAAGCCAGTTTGCCAAATCTTGCAAATCTGTTTTCGGATTTCAGCTCCGACTTGCCGAAGAAATAAGCAGT  
ATGTCTCATCGGCATTGATGGAGATAAATGTCTGGCACTGCAAGCAGACATCTCGACACCAACACCATCACCTTCAACCTATACG  
ACGTATCAGCCAGTTGCGGTGATGGGGTAGTCAACCCGACTATCCGCAACTGCTACGCTCGATTGAGATTCCCAATGACGCGCT  
ATTTCGAGCTTTTGGGGACAAACAATCTGACAAACGTGCGAGCTTATGCCCGCGGACGGCAGCAGCATGGAGCCGACCATCCACAG  
AAATCGATAACTTTAATCAAAACAGAGCTTAGCAAGTTTCAGACCGCGCGCATCTACCTGTTTACCTTTGACGGTTATACCTACA  
TCAAACGCCGTGTCAGAGGCAAAGCGCGCGGATACACGCTACCAGCGACAACAGGCATTACGCCAAGTCGGATTTTCTGATAAA  
CCCTGAAGAAGCCGACAAATCCACATTACCGGCAAAATTTGGAAGTTTTCGCCGCTTGATTTTTAGACCTT

## SEQ ID 42

MKKRELNEIETAECAELKRIFNSKKEELKLTQYKLAEAVGVTQSAVNHYLNGTNALNASIASQFAKILQIPVSDFSRLAEIIS  
MSIGIDGDKLLALQADNLDNTITLNLVDVSACGHGVNPNPDYPQLLRISIEIPNDALFELLGTNNLTVNQLMPPDGDMSMEPTIPQ  
KSITLIKTDVSKFQTGGIYLFITFDGYTYIKRLSRGKGGAHATSDNRHYAKSDFLINPREADKFHIGKFWKVLPLDFLDL

## SEQ ID 43

ATGAGTGCAGGCTGATGGGGATGGCTTTCAAACCGGTATCCCGAGGGGGCAGCGTTTTGTTTGGTAAAGTTGTGCGACTGCGG  
CCAACGACGATGGCTTGTGTTATCCGTCGCAAGAACGCTGGCGGAAGATACGGGCTTCGCCGAACCGCTACGGCAGCATAT  
CAAGTGGCTGAAGGATAACAATTTCAATCAAGTCCGCCCGCGCGCAGAGGGGGCGGAGAGGAAGTCGACATCTACCGCATCAAC  
GTCGCCCTGCTTGAAAAATGCTATGCGGAGGCGGCAAAACGGAAGCGCGCGGCAAGGCAAAATGTGGGAAGAACCATTGGATT  
ACGAACCTTCGGATTTGAACCGTTCGATTACGAACCTTCGGATTTTGAACCGTTCGGATTACGAACCTTCGGATTTTGAACGCTAA  
GAACCATCAGATTTTGAAGCATGAACCATCAGATTTTGGCGTAAGAACCATCAGATTTTGGCGTAAGAACCATCAGATTTTGAAGC  
GGCGAACCATCAGATTTTGGCGTAAGAACCATCAGATTT

## SEQ ID 44

MSARLMGMAFKTGIPRGQRFVLVKLDCDANDGLCYPSQETLAEDTGFAETAVRQHIKWLKDNFIFKSARRQRGRERKSDIYRIN  
VALLEKCYAEAAKRAARQAAMWEEPLDYEPSDFEPSEYPSDFEPSEYPSDFEPSEYPSDFEPSEYPSDFEPSEYPSDFEPSEYPSDFEP  
GEPSDFALRTIRF



## SEQ ID 45

ATGGCTTTGAGGAACGCGTCTGATTTCTTGGGGGCTTACGGCGCGCGGCTCGGGTTCGAGCGGAGGCAATGCGCGGAACACGGCG  
GATACGCGCGGCGAAAGCGTTTTCGCGCGCGTGTGGACGGGCTGCCCGGCTGCCGGAAGCTGGAGGCGCGGACGAAATGGCGGC  
ATACGCGGAACGCTGCGCGCGGGCGATGCGCGACGCGTGGAAAAACGCATCGGGCGTTGGGCGATCGCCCCCGGGTTTCA  
AACTGCCGGATTGAAAACTACGCGCTCAGCGATTTCGATCCCGGGGATGGCGAGGGCGAAGCGCGCCCGCCGAGTATGCGGCAA  
ACTTCGCGCGATGTGTTCAGACGGGGCGGAGCATGATTTTTCGGGCGAGGAGGGCACGGGCAAAACCACTTGCCTGCGGCAT  
CGCCCCGGAAGTCAATCGCGCGCGGCAAAAGCGCGCTGGTCATCAGGTGGGCGATATGCTGCGGACGGTCAAGGACAGTTTCGGC  
GGCGCGCGGAGGCGGGGGCGGTCGGGATTTCGTGAAGCCCCGATTGCTGGTGTCTGGACGAGTTTCGGCGCGGGCAGTCTGTCTGG  
AAACGGACGGCGGATTTCGTTTTCGCTCGTCAACGCCCGGTACGAGCGCGCTGATGCCGATGCTGGTGTCTGACCAACCTGACGGC  
GGAAGCCTTCGCGGAAAAACCCGACGCGCGGATCAGGGACAGGCTGCGGGACGCGCGGCAAGCTGATTCGCTTCCGACTGGGAG  
AGCTACCGTGGC

## SEQ ID 46

MALRNASDFLGAYGGVVRERRQCAEHGGYAAKSVLRGVWTGCPACRKLAADEMAAYAEFLRRGAMRDALEKRIGRSGIAPRFR  
NCRIENYAVSDSIPGMARAKAAAAYANFADVLQTRSMIFSGRRGTGKNHLACGIAREVIAAGKSALVITVGDMLRITVKDSFG  
GGGEAGAVGIFVKPDLVLDEFAGSLSETDGRILFSVNARYERLMPMLVLNLTAFAFRENTDARIRDRIRDGGGKLIPFDWE  
SYRA

## SEQ ID 47

ATGAATATAAAGAATTATGTCTAACTATACCAACCATCCCGTTCTCTTTATTGGAACAGGTATGAGTTTGAGATACTTAGATA  
ATTCATATACTTGGGATGGTTTATATCTAAATTCGAATAGATTATTTGGAGATGATAGGGAATATTTGAACATCAATCAGC  
GTACTGTGAAGATGGTAGATTCCAATATGAAGAGATTGACAGGAATTACAAAGTAAATTTGATAAAGTTTGAAGAAATGACCCCT  
GATGGTAGATTTAAAGAAATAATGATAAGTTCTTTGAAATATGAGGCGGGAAACACCTTGAGCAGGTTTGAAGATTTATATAT  
CCACCCCTGCTCTCACAATTGAATTATAAAGATAATTCTAATACAGAATTATCTGAATTAAGGAGGAGAAAAATGTAGGGTC  
AATCATTACCAACAAATTATGATAAATTAGCCCAAGATATTTTGAATTTAACCCTAATTGGTAATGATATCTTTTAAGCAAC  
CCTTATGGCTCAGTATACAAATACATGGTTGTGTGGACGATCCATCAAAATTTATTATACCAAAAGGATTATGAGAAATTTA  
AAGAAAAATGAACTTATTAGAGCCCAACTATTATCGTTATTTATTCACAATCCAATCATATTTCTTGGATATAATGTTGGTGA  
CGAAAAATATCAAGAAATTTTAAAAACAATCTTACTTATGTAGAACAACACTCTCTTCAGCTAATAAAATTCGTAGGAATTTT  
TTACTCGTAGAATATGAACCTGAGTCTAACAATGAAGATATTTGTTGAACATGATATAGATATAGATATAGATATAGATATAGATAT  
TTAATAAAATCAAAACAGATAAATCTCTCAAAATTTATAAGCTCTTGCAGAACTAACACTACCAATCTCAGCTATGGATGTACG  
TAAATTTCAATCTATAGCAAAGGAGATTATACTGGCGGTAACTATAAGTTAGCTTTACGGAAGATATGGACAATTTAAATAAT  
AGCGATAAAGTGGTTGCTATTGGTTCAACTAAAATATCAGCTACAATTTCAAAACAACATCAGAGATGATGTCAAATTTATTTCA  
AAATAATTGAAGAGGAAAAATTCACAATCTTCAAAATTAATAGATAAACATAGTATAGCATCTACGCAATATTTTCTATTATG  
ATTTAGTAGGATATGTTCTGATATACATAAAGAAGCTGTACTAAAACGCCAAACAAAGAAAAATTAGATCATTTTATTGAAGAA  
ATAAATAGGCGTTGTAAAAATAATCATTCATCCATCCAATCAATTTTAGATGATGAAATATTTTCAAGACATATAAAACGATG  
CGATTGCTTGGGGAATATGGAATAACCAACTTTTCAAGATGAGGTTGAAATTTTAAAAATTTTGTGAATAAAAAAATAC  
GCACTATAAAGACTACTATGTATGTTCGATTATAAAAAATATCGGATACCTGTC

## SEQ ID 48

MNIKEFMSNYTNHPVLFITGMSLRYLDSYTWGDLISKIAIDLFGDDREYLNISRYCEDGRFQYEBIAEELQSKFDKVLENDP  
DGRFKEINDKFFENMRAGNTLSRFKIYISTLLSQLNYKDNSNTBELSELKKARKNVGSIITNYDKLAQDIFEFNPLIGNDILLSN  
PYGSVYKGVDDPSKIIITKKDYEFKEKYELIRAQLLSLFIHNPFIIFLGVNVDENIKEILKTIITYVEQNSPSANKIRNF  
LLVEYEPESNNEDIVEHDIDITGFSTIRINKIKTDFNSQIYKALAEITLPISAMDVRRKPSIAKEIYTGNNIKVSFTEDMDNLNN  
SDKVVAIGSTKTIISYNFQTTSEMSNYFKIIEEENSQLLKIDKHSIASTQYFFIYGFSTRICSDIHKAVLKRQOKEKLDHFIEE  
INRRCKNNHSSIQSILDDENISDTYKNDALAWGIWNNQLSEDEVENYLKNFVNKKNTHYKRLLCMFYDKKYADTV

## SEQ ID 49

ATGCTCTTCAAACTCCGTTACCTCGCATCAGTATTGGCATTGTCTTCACTGTTGGCGGCATGCGGCGGTTCAGGAAAAGTCTGCGG  
CAGGCGATGCTTCTCCTGCTTCCGAGACGGAAGCGGCTTCCCAAGTACAGGCTCGGAAGCGGTTCCTTCCGCTTCATCGGCCTC  
GCCCGAAGACCAAGACCTTTTGAACGCGCGCAAGGTGTATTCCAACCTTTGCGGACTGTGGAAGAAATGAGAAAATCCGTCCG  
TTTACCGAAGAACAGGTCAAACCTCGGACACCAACTCTGGTATGAACCAAGCGCTTCCAAAGCAATACCGTAAGCTGCAACTCTT  
GCCACAACCTTGTCTCCGCGCGGTGTGGACAATATGCCGACAGTCAGGGGACAAAGGGCAGTTCCGGCGGACGCAACTCGCCTAC  
CGCATGGAATGCTGCGCTGCTGGGCAGCCAGTTTGGGACGCGAGCTGCCCGGATGTTGAAGAACAGGCTGGCGGGCTTTGGTG  
AATCCGGTGAAGATGGCGAATGATTTCGCAAGAGCGCGGTTCGAGCCGCAAAATCGCCAAAGTTCCCGAATATCAAGAAATGTTTAAAA  
AAGCTTTTCTGTAAGACGCGCGGTTTCGTTTAAAAACATCACTACCGCATTTGGTGTGCTTTGAGCGTACCCTGCTGACGCCGAC  
CAAATGGGACGAATACCTCAAAGGCAACGTCACGCCCTGAGCGAACAGGAACGAAAAGGCGTGCAGCGCGTTCATGGACAACGGC  
TGTATTGCTTGCACAAACGCTGTCAACCTTGGAGGCAGGACCTTCCAGAAATTCGGTCTGCTTCAAGGGCCGTATTGGAATTTCA  
TTGAAGATCCGAAACGCGACAAAGGCCGTGCTGACGTAAACAAAAAACCGAAGACGAATTTTCTTCCGTGTTCCGGGGTTGCG  
TAACGTGGCTAAACTTATCCGTATTTCCACAACGGCAGCGTGTGGGAGCTGGATAAGGCAATACCATATGGGTAAGGCGCAA  
TTGGGTAAAGACATTCCGAAAGAAGATGTGGATAACATCGTCTGATTTCTGAAATGCACTTTCCGCAATGTTTCCGAATCAGCGC  
GCACGATGCCGGAACCTGCCCTGACCGCACCGATGGAATCTAAGCCGGAACAAA

## SEQ ID 50

MSFKRLRYLASVLALSSLLAACGGQEKSAAGDASPASETEAASQVQASEAVPSASSASPEDQDLLKRAQGVFQPLPTVEEMQKIRP  
FTBQVQLGHQLWYEPRLSKGNTVSCNSCHNLASAGVDNMPTSQGHKGQFGGRNSPTALNAALLGSQFWDGRAADVEEQAGGPLV  
NPVEMANDSQEAAAIAKVPEYQEMFKAFPEDGAVSFKNITLALGAFERTLLTPTKWDEYLGKGNVNLSEQERKGVRAFMNG  
CIACHNGVNLGGTTFQKFLVQGPYKFIEDPKRDKGRADVTKTTEDEFFRVPGLRNVAKTYPYFHNGSVWELDKAVTIMGRAQ  
LGKDIKREDVDNIVVFLNALSGNVSESARTMPPELPLTAPMESKPDNK

## SEQ ID 51

ATGACCGCCCTCACACTCTACCGGTGCGCGGCAGACGTACAGGCGGCGCTGGATTACTACTTTGACAGCGAAACCGAGCGCGGAAG  
ACACGCTGGAAGCCGTATCGGGCAGTTTCGAGGTCAAAGCCCAATCCGTTATCGCTTATATTAATAACCAAGAAATCACGGA  
AATGCTTGAAGGGCAGATCAGGCAGATGACCGGGAAGCTCAAGCGGCAAAAGCGCGGAATCAAAGCCTGAAAGACTACTTGGCG  
CGCAATATGACAGGCGCGGGCATTACCGAAATCAAAGCGGATGACGGCACTTTTAAAGCCTCGTTCCGCAATCCGAAGCCGTCG

TGATCTTAGACGAAGCACAAATCCCCGCCGAATTTATGCGTGAGGCCGTCAAAACCGAACCGGACAAAACCGCCATCAGAAAAGC  
GATTGAAAGCGGTTCGGCAAGTAGCAGGCGCGAAGATTGAAGGGCGGAAGAATTTGCAGATTAGA

## SEQ ID 52

MTALTLYRCAADVQALDYFDSETEREDTLEAVIGQFEVKAQSVIAYIKNQEITEKMLEGHIHQMTGKLKAAKARNQSLKDYLA  
RNMQAAGITEIKADDGTFKASFRKSEAVVILDEAQIPAEFMREAVKTEPDRTAIRKAIESGRQVAGAKIEGRKNLQIR

## SEQ ID 53

GTGCAGGCGGATTTAGCCTACGCCGCCGAACGCATTACCCACGATTATCCGGAACCAACCGCTCCAGGCAAAAACAAAATAAGCA  
CGGTAAGCGATTATTTAGAAACATCCGTACGCATTCCATCCACCCAGGCTGTCCGTCCGCTACGACTTCGGCGGCTGGAGGAT  
AGCGGCAGATTATGCCCGTTACAGAAAGTGAACGACAATAAATATTTCCGTCGACATAAAAGAGTTGGAAAACAAAGAATCAGAAT  
AAGAGAGACCTGAAGACGGAATAATCAGGAAAACGGCAGCTTCCACGCCGTTTCTTCTCTCGGCTTATCAGCCGTTTACGATTTC  
AACTCAACGACAAATTCAAACCTATATCGGTGCGCGCGTCGCCACGTCAGACACAGCATCGATTGCTACTAAAAAAT  
AACAGGTACTCTTACCGCTACCTTAGTGATGCTGACGACGAGTTACGGTTTATCCTGACGACATCCGCAAAAAACACCTAT  
CAAAAAAGCAACAGCAGCCGCCGCTTGGGCTTTCGGCGCGATGGCGGGCGTGGGCATAGACGTCGCGCCCGGCTGACCTTGGAGC  
CCGCTACCGCTACCAACTGGGGACGCTTGGAAAACACCCGCTTCAAACCCACGAAGCCTCATTTGGGCATGCGCTACCGCTT  
C

## SEQ ID 54

VQADLAYAAERITHDYPEPTAPGKNKISTVSDYFRNIRTHSIHPRVSVGYDFGGWRIAADYARYRKWNDNKYSVDIKELKNQN  
KRDLTENQENGSHFVAVSSGLSAVYDFKLNDFKFPYIGARVAVGHVRHSIDSTKKITGLTAYPSDADAAVTVYPDGHPQKNY  
QKSNSSRRLGFGAMAGVIDVAPGLTLDAGYRYHNWGRLENTFRFKTHEASLGMRYR

## SEQ ID 55

ATGGACGGCGTTGCGGCGGTAGGCGGCATTGTTGACCGCGCCGCCACCGTTTCGCGTTTCGGCACAACCGCGCAAACTGCCAG  
CCGCCGAACACGGTTGCCGAGCCGCCAACCGCTTGCAGCGACACATAAAGCCCGTCTGCCAACCGTCGTTGCGTTCCGCC  
GGCTTGTTCGCGGTAGCGTTGGCGGTACGTTCCAGCGACACCGAAAGCTGCGACCGGCGGCTCAGCGGTAAGATGCGCCAA  
CTGCACACCCGCCCGTGCAGCATATACGGCGCAAGCGCGGTCGGCAGGCGGTTTCGTTTTCGCATCAAAGCCGTCGCTA  
CCCGACAATTGCGCCTGATAAAACGGCAAAACCCACCGTCTGCCGCGCATTTTATACTGCCAGCCCAATAAGCCCTGCCGA  
AAGCATCGTCATAAGCCGATTGCGGCTGAAATAATAGCTTGTGCCCGGACATTGGCGCGGAACAGCAGATAATGGTTGTCCGC  
CAGCGCAGTCAGCTTTCCGCCCGGCTCATAATCCAACCTGCGCGACGACAGGTCCGGTAACGCTGCATATCCGGCTGCCG  
CCGCCCTGCAGGAGTATTGCGCGCGGCATTGTTGGCGTTTGTTCACAGAAGGGCTGATGCCGCCGAAAAATGCCAGCCG  
TCAGCCCTCCGCTTTTTCGGAAACGCCCCACATTTTCCAAAACCGCGCGCGCAATCCAATTTTGGCGCTCCGCAAAATG  
CAGCCCTGCCGACTTCAGCCGGAATCGTCAAACCTCCGCCCGCGCAATCCAGCAAAACCGCTCGTCTGCCGCTATTCCTG  
TGCAACGCCCGATAGCGCGCCACCGCTCCGCCCGCTTCCGCCAATTTGCCAGCAAGCCCGCGCTGCCGTACAAACCG  
CATCATAATCCGGCAGCTTGGCATACAAATCCGCCAAGCAAGCGATCAAATCCGCCCTGATTGCCGTTGAGCGCGTCCGCCAAAC  
GTGTTCCAAACTGCGGCGCGACAGCAGGAAATCCCGCTCGATTACGCGCAACCGCGTTTGGCGGAGAAATCCCTTCCGGC  
GGCATTTCCCGCCCAACCTCCGAGCGCGACGCTGGGCGCGCAACGCCCGCATCGTCCGAACGTCCGGCAAGCCGGCGGCAT  
ACGCGCGACCGCACCCCAACACACAGCGCGGCACAGCCGCGATACCGGATACACACTATCCTTCAATTTGCGCTTCTTAA  
AAACACCGCGCGGCGCGCGCAGAAACGCCCGCAAGCCCGCGCGCGGCGGACGCGGCGCATCATATAGTGGAT

## SEQ ID 56

MDGVAAVGGIIVDRAAHRFAFRHKPRKLPAAEHGCRAAQPPCQRHIKPVLPVFAFRPALFAVALAVTFQRHRKLRLPAAQAVRMRQ  
LHTRPVRQHIRRKPAVGRFRFRIKAVATRQLRLIKRQNPRLPRIFILPAQISPAESIVISRFAAEIACAPDIGAEQQIMVVR  
QRSQLRPRLIIQPCRTDRSGNAAYPAAALQAVLRRGIVGVFVHRRADAARKMPARQPLRFFPETPHIFQNRRLQIQFCRLRKM  
QPCRLQPEIVKLRRRQIQONPLVCRIPVQRPIARHLRLRPSRQFRQSPRPAVQHRIRIIRQLGIQIRQRSDQIRLIVERVAQN  
VFQQLRARQQEIPVDYARTAVCGRIFFRRHSRPTLRSLTGAQRRRIVPNVQAGGIRADRTPTNQTQPAYPIHTILQFAFLK  
KHRTAAAEPTQAPRAADAHHIVD

## SEQ ID 57

ATGAACATTACCATAGCCGCCCTACTGCTCGCTGCCGTCCGAACCGCATTTCAACCGCTTTTGGTATCTGGCAGAACTATTGT  
CGCAATCGCACGACGTGTGCTGATTACCAGCAACTCAAGCACTACGACAAATCTTTCAGACGGCCGAAGATGCTAAGGCCG  
CTCACAAGGCCGTCTGAAAGTATGCTGTTGGAAGAAAGCGGATACAGCAAAACGTTCTTTAGGACGCGTGACCAGCCATCAC  
CGCTTCGTCAAACATTTTGAATAATGGTTGGAACCTGCCGTCCGGCGCAACAGACGTCGTCTATTCCGCTATCCGCTGATG  
CCACCAACCTGCTGTTGGGCAACACAAAGCGGTTTGGGTTACAACTGATGTCGATGTCAGGACGTATGGCCGGAGTCTTT  
CTCCTCTGTCTGCGCTTTTGAATAAATCCCGCAACCTACTGCCCTTTGCTTACGCGCCCAACCGGCGCTACCGCTACGCC  
GACCGTTGGTTCGCGTATCGCAGACCTATCTCGACCGCGCAAGAAGCCATCCGAACGTACCGCGCAAGTCTCTATATCG  
GTGCGGATTTTGGCGCCATCGCCCCCCCCCGGATTCGCTCCAAACCGTCCGCTTTTCTACTTGGGCACGCTCAGTTACAA  
CTATGACGTGGAACCGTGTGCAAGGCGTTCGCAAGCTGTTGGACGACGGGGAAACGTCGAATTGCACATTATGGGCGGCGG  
CCCGATTGGACAGGCTCAAACATATGCTGCGACGGCATCAAGTTTACGGCTACATCCCTTACGCGGAAATGATGTCGGTCC  
CCAAAGGCTGCGACATTGCCGTCAACGCCATCCACTTACGCCCATCGAGTCGATTACCAACAACTCTCCGACTATATGGCTTT  
GCAAAAACCGATTCTGAACAGCGAGGTCACGACGAAGTTGCGGAAGTCTTACCCTGCTGCCGACGAAAACCTACCGTTCCGGC  
GATGTGGACGGTTTCTGTCGAAGCGGCAAGATATTTGAAGCGCAAAAACGACCTGTTAGTCCGACGAAATCGTCCGCCGCT  
TCAGGCACGACATTTCTATCGGAAATCGTCAACCTGATTGAAGATTGGCAATGAG

## SEQ ID 58

MNITIAAPYCSLPSEPHFNRFWYLAELLSQSHDVLITSNFKHYDKSFRRPEDAKAASQGRKLVMLLEESGYSKNVSLGRVTS  
RFVKHFEKWLNCRPGEQDVVYSAYPLIATNLLGKHKARLGYKLIVDVQDVWPEFSVVPFLKKIPHNLLFPASRANRAYRYA  
DALVAVSQTYLDRAKEANPNVPGVYVIGADFAAIAPPPFRSKTVRFYLGTLNNDYVETVCKGVRKLLDDGENVELHIMGGG  
PDLDRKQYACDGIKFYGYIPYAEMMSVAKGCDIAVNAIHSYAMQSITNKLSDYMALQKPIILNSQVHDEVAEVLTLPHENYRSG  
DVDGFVQAADILKRKNDFVQSDIVRRFRHDI SYRKIVNLIERLANE

## SEQ ID 59

ATGGGCGGCATATCTGGCAGGCTGCATCCTGCCACCGGAAAAATTTGCACAACTGTTTTCATTATTTGAAAAACAAAGGTTTC  
CCATTATGAAATCATCTGACTACTTCTATGTCGGGCTGGGCGGCACAGAAACCGCCACCGTCCGCTCCGGCGGCTGCTCAA  
ACGCGACGGGCACGACATCATCTCGCCTCTCGGACGGCCCTTTGTCGGAGAGGCGCAAGCATCGGGCATCCGTTGGCAGCCG

GTTGATTTTACCGGGGCGGGCTTGCCGGCTACCTTAAAGCACCTTTGCCTACGCCCGGATGCTGCGCCGGAACAACCGACA  
TCATCGACTGCCAAATGGCGCGCGTCGTCGCCGCTTGCCTGCGCCAAATTCGTTTACCGAAAACCAAATCATCTGCCA  
CTCGCACGGTTTGGACGCGGCAACCTACCCAAAACCGCAAACCTCTTCGACAAGCTGGGCGGTACATCATCGGCAACTGCAAA  
CAGAAACCGGAAAAGCTCATCCGCCACGGCTTCCCGCGCGCGGATTGCCTACGCTACAACACCCCCCGGAATTTTCATTTC  
GGAAAACCGAAAAGAAATGCGCGGTACTCGGCACACTTTCCCGTTTGGACACCGTCCGTGCGGTGCATCTGATGTTGGATATTTT  
GAAGAAAATGGTTGGCCGCAATATACCCGTACGCTGAACATGGCGGGCATAGGAGAAGAAATGGACAACCTCAAAGCCCAAGCC  
AAACGTTTGGGTATTGAAGACAAAGTGACCTTCCTCGCGCGCGTCCGCGATTGACCGGCTACTTCAAAGAAGTCGATATTTAG  
TGAACACGCGCATTCGCTAGGTGACCACGGCGCAGGTGTCGGAACAATATTTTGAAGCCGCGCTTACGACACGCGCTGCTGT  
GACCTACAACATGGCGGGCATTTCCGAAATGGTCATTACCGGCCAAACCGGCTACTGCATTCTCTTCGGCGATGACGAAGCGTTT  
ATCGAAGCCGTCGATACACTCATCAAGCATCCAGAGTTGCGCAGCCAAATGGGCAAGCCCTGCACAAACATGTCGAAACCTTAT  
GCTCCGACGACGAAATCTACCGACCAACCATGGCTGCGTACGAAATG

## SEQ ID 60

MKIIILTTSMGLGGTETATVRLGRLLKRHGHDIILASSDGPVFGAQAQSGIRWQPVDFYRGGLAGYKSTFAYARMLRREQPDII  
DCQMARVVPACALAAKIVSPKTKIICHSHGLDAATYFKTAKLFDKLGAYIIGNCKHEREKLIIRHGFAGRIAYAYNTPPEFHF  
TEKECAVLGTLRLDTRAVHMLDLILKMMVGRNI PVRLNMAGIGEEMDNLKAQAKRLGIEDKVTPLGGVRDLTGYPKEVDILVN  
TPHCVDHAGVGNINILEAGLYDTPVVTYNMAGISEMVTGQGYCIPFGDDEAFIEAVDTLIKHPRLRSQMGKALHKHVTCLCS  
DDEIYRTTMAAYEM

## SEQ ID 61

TTGAAAACCGTGCGGCGTTTTCGTGGGGCAGCCGCTATACCGAGTTTGATTTCACCGATAAAATTTTCAGACGGCCCCGGCACGG  
TTTACCAAGTCCGCGCGCGCGTGTTCGACAAAATCCTGATTGAAGAAGCCGCAACAAGCGGTTGAAGTACGTTTCGGGCACGG  
CGTAACCGCGTTCGACAACAGCGCGGATTTCGCCGCTTGAACATCGAAACCGACACCGCGAGAGCTATGAAGTACCGCGAAA  
TTCGTCTTGGACGCAAGCGGTACGGACGCGTGTCTCGCGCGCTGCTAAACTTGGAACGCCCTCGCACCTGCGCGCGCGCAAA  
CGCATTTACGCAACATCGACGACAACTTACCCACCGAAATTCGACCGCAACAAATCCTGATTACCAACCATCCGCAACACCG  
CGACGTGTGGATTGGCTGATTCCCTTCGGCGCAACCGTTGTTCCGTGCGCGTGGTTCGGCACACCCGCAAACTTGCCGGCGAA  
TCGGAACCGGTGTGAAAAAATTTGTTTACGAATGCCCGATGTTGAGCGAAATTTTGGAACAAGCCGTTTGGGAAAACGATTTC  
CGTTCGCTCCATCAAGGCTATTCCGCCAACGTCAATCACTGCACGGCAGGCTTTCGCGCTGTTGGGCAATGCGCGCGAGTT  
CCTCGACCCCGTGTCTCGTGGCGGTAAACATCGCGCTGCACCTCCGCGAACTTGCTGCGCATCTGCTGACAAAACAACCTCAA  
GGCGAAGCCGCGGATTGGCAAACCGAAATTTGCGCAACCCCTGATGATCGCGGTAGACGCGTTCGCGACCTATGTGGACGCGTGT  
ATGATTTCCGCTTCCAAAACGTCGTGTACCGCGCGGACCGCAGCCGGAATACCGCGTATGCTTTCTTCGATTTTGGCAGGCTA  
CGCGTGGGATACCGAAAACCGGTTTCGTGGCGAAATCCGAACAACGCTGACTGCCCTTGTGAGAATGGGTGCGTCAGTTGGAAAGC  
GAA

## SEQ ID 62

LKNGAASFWSGSRYTEFDFDKFSDGPGTVYQVRRVDFDKILIEBAKQGVFVRFHGVTAFDNSGDFARLNIEITDGTESYELTAK  
FVLDAAGYGRVLPRLNLETPSHLPPROTHTHIDNITHPKFDRNKILITTHPQHRDVWIWLIIPFGDNRCVGVVGTGPKLAGE  
SETVLKKFVYECPLSEILDKAVWENDFPFRSIQGYSANVKSILHGRHFALLGNAEFLDPVFPSSGVTIALHSAELAADLLTKQLK  
GEAADWQTEFAEPLMIGVDAFRTYVDGWYDFRFQNVVYAPDRSPEISRLSSILAGYAWDTENPFVAKSEQRILTALSEWVGQLES  
E

## SEQ ID 63

ATGTTTTCAGCGCAACAGTTAGGACAAGCAATATCAGAAGCGATTAAGAGAAAAATGTCAGTCAAAAGGAGGTGCGGATCATT  
TTGGGGTGAAACAGCCAAGCGTTTCAGGTGGGATAAAAAATGGACGAATAGATAAAAAACATCTAGATAAAATTAATTGATTATTT  
CTCAGACGTAGTAACGCCAAGCCATTTCGGCATGAAACATTAGAGTCTTAAATCGAATGAACAAAGTAGCATACGTTTCCCC  
CGCTTAAATGCCGAAGCGACCTGCGCGCAGGCACGATTAACGACCACTATATCGAGGTTGTGGATTATGTAACCGTCGCTGCCG  
CATGGGCGCGGGAGAACTGGGCGGAAACCTCAACAAATCCAAGTCATTACAGCCCGTGGCGACAGCATGGAGCCCAACATCGA  
AAACGGCGACGTAATGTTGATACCGCGCTCGAAGCCTTCAGTGGCGACGCGCTCTACCTGCTTTGGTATATAGACGGCCTT  
AAGGCCAAGCGGCTGCAATCCACCGTGGCGCGCGCTGATGATCATCAGCGACAACAGCTCATACCGAACCAGAACCGTGGCGG  
GCGAAGATTTAAACGCCGTACGCATCATCGACGCATACGCGCGCATGGCGTTTGGAGCCAGTTC

## SEQ ID 64

MFSGEQLGQAISEAIRKKNVSQKEVADHFGVKQPSVSGWIKNGRIDKKHLDKLIDYFSDVVTPSHFQIETFRVLKSNEQSSIRFP  
RLNAEATCGAGTINDHYIEVDYVTVAAAWAREKLGGNLNKIQVITARGDSMEPTIENGDMFVDTAVEAFDGDGLYLLWYIDGL  
KAKRLQSTVGGGLMIISDNSSYRTETVRGEDLNAVRIIGRIRGAWRLSQF

## SEQ ID 65

TTGATGATGAAGCCGCTCTGAAAGTTTGAGAGCGGCAGGCAGGCCAATCGCGTATTACCGAAAATTTGGCAAAGCCTTTGGGCGGTG  
TAAATGCGGCAATATTATTCGGGCATTCTTCTACTGGAACGATAAGACGCAGTATGAATCAGGCATTACCGAACAGCGGAAGA  
AATTGAAATTGAAACCGGGCTGTCCGTTTCAGGAACAAAGAACGGCACGGGCAAAGCTGAGGGAACGCGCGGTATTGATTGAGACT  
GAAAAACGAATTGAACACCGCATTTACTACAACTGAATTTAGACGCTTTTGATGATTGATGTTGCAACATTTCGGGGGTGGGG  
AATCAACAGCCCCGAAATGCAATATCAACAGCCCCGAACTTCAAAATCAACATTTCGGGGGTGGGGAATCAACAGCCCCGAAATG  
CAATATCAACAGCCCCGAACTTCAAAATCAACATTTCGGGGGTGAGGAATCAACAGCCGTTATAAGAACAGAAGATTTAACAGAA  
GATTTAGCAGTATATACCCCTTACCCCAACAGCGGAAACGGCAAAGCGGTTTGAACGCTGACGCGTTTGTTCGCTGACG  
CGGAAACGTGCGGGCGGGAACCGGCGAACCAGTTTCGCGCAAGCGCGAAAGCGACAGTAACGGCAACGGCGGCTTTTCGGGAAA  
ACCGAAAAATGCGAATGTTCCGCGCGCGCGCAAAACCCACGGCGTACCGCTTCAGGAAATCGCGGATTGTTACAACAGAAATTTG  
GGCGGCGGTTGCCAAGCGTCCAAGTGTGAACGACACGGCGCAACCGGCGATTGCAAAACCGGCTGGTGGCAGATGCTGGGAACGG  
CGGCGCAACAGCGGAAGGTGAGGTTTCGGGGACAAGGAAACCGGTTTGGCCTGGTTTTCGCGGTTTCTTCGGGAAAGTGGCGATGAA  
CCCGTTTGGGATGGGCGAAAACCAACAGGTTTGGCGTTCGATTGGAATTTCAAGCGGGCAATTTTCGTCAAAATCCTT  
GAATGCATCCGCTTAAACGAACAGCGCGCAAGGGGAAGGGCA

## SEQ ID 66

LMMKPSESLRAAGRPIAYYPKLAKPLGGVNAAILFGHFFYWNDKTQYESGIYRTABEIEIETGLSVQEQRTARAKLRERGVLIET  
EKRIEHRITYKLNLDLDAFDDMLQHS GGESTAPKCNINSPQLQNHSGGGESTAPKCNINSPQLQNHSGGSESTAVIRTEDLTE  
DLAVYTPLPNAGNGKGLNADAFVSADAETCGRETGBEPTSPKAESDSNNGGLSGKPKNANVPRRRKTHGVPLQEIADLYNEVL



GGRLPSVQVLNDTRKRAIANRWCEMLGTAAPNGKVRFGDKETGLAWFAGFFRKVAMNPFWMGENQTGFVAVGFDWIFKAGNFVKIL  
 EWHPPKTNQAARGRA

**SEQ ID 67**

ATGGCACTAGGGCAATTTCGACGATGTTGAAACATCAGTAATTCGCAGTTTAAGTTCTGCAAGCCTGTATATGTTACGCGCCGGA  
 TGTTTTATCAAGGCGCGGCTATGTTTGGCAGCGGGCGAATCACCATGCGCCAATCTGCAACGCGCTCGAGCGTGTTCACACGG  
 CGAAACGAAACGCTGATTATCAATATTCGCGCCGATACCTCGAAACGAAATCGCGGTCTGAACTTTATCGCGTGGGCGATG  
 GGGCGGTGCCTGATGCGAGTTTATCCACGCGAGCTATTTCGCGCGCGTGGCGGTCAATAACTCCGTACAGATTCCGAACTTGG  
 TGCAACACGAAGAGTATCGGGCGATTTTCTCTGATTGCGACTGCGAGCGGAAAGCGGCCATCCTGGAACCAACCGCAGGCGG  
 CGTGATGTACGCAACAGGTGCGGGCGGTACGATTACAGGTTTCGGTGCGGGCAGGCATCGGGAGGGATTTCGCGCGTGCATCATC  
 ATTGACGACCCGCACAAAGCAGATGAAGCGCGAAGCGAGGTTCAGGCGGCGAAGCGTCATCGACTGGTTTCAAAACACGGTCAAT  
 CCGGGAAGAACAGCCCTGACACGCGGATTATCTGATTATGCAACGCTGCACGAGAAAGACTTGGCGGGCTGGCTGCTTGACCGG  
 CGGCAACGGCGAAGAGTGGGAACATTTGTGCTGCTGCCATTTCAGGAAGACGGCAGCGCGTTGTGGCTGAAAGCATGATATT  
 GAAACATTGCGCCGAATGGAGCAGGCGCGCGCTATGTTTGGCGGGCAGTATTGCAAAACCTGCGCGCGCTGACGGCGGT  
 CGTTCAACGCTGACAACCTGCAATTTGTCAAGGCGTTGCCCTGCCGGAATATCAGATGGGTACGCGGTGGGACTTGGCTTCAAC  
 CGCAACGGCGCGGACTACACGGCAGGCGGAGGATTACGCAACACGGCGCAAAAGACGGCGTGAACGAAATATCCATCCCGCAAG  
 CGGTACGGCGCGGACGAGCGGGACGATATTACGCAACACGGCGCAAAAGACGGCGTGAACGAAATATCCATCCCGCAAG  
 ACCCGGGCGGACGAGCAATCGCAACACTATACCTGACCGCCAGTTGGCGGGTTTTCCTGATCCGCGCGCGCGCAATCGGG  
 CGACAAGGTTACACGCGCGGACCGTTTCGCGGCACAGGTCAACATCGGCAATGTGATGGTGTGGATGACGGCACATGGGACAG  
 GACGCGCTGATTGCGGAATGCGCATGTTCCCGAACGGCGCGCATGACGACCAATAGACTGTTTGGCGCGTGGCTTGGCGAGC  
 TGCTGGATACCCGACGGCGCATGATTGATTCTCTGCGATCGCAGGTTCGAGGCTGTGAAA

**SEQ ID 68**

MALGQFDDVETSVIRSLSSALYMFTRRMFYQRRGYVWQRANHHAPICNALERVFNGETKRLIINIIPRYSKTEIAVVNFIAWAM  
 GRVPDCEFIHASYSALAVNNSVQIRNLVQHEEYRAIFPDALALAGESGHHWKTTAGGVMYATGAGGTTTGFAGRHREGFGGCI  
 IDDPHKADEARSEVRRQNVLDWFQNTVESRKNSPDTPIILIMQRLHEKDLGWLDDGNGEEWEHLCLPAIQEDGTALWFERKHI  
 ETLRRMEQAAPYVFAQYQLQKPAPPDGGTFKPDNLQFVKALPAGNIRVWRWDLASTANGGDYTAGRGLVTEDEGRYLIANVRG  
 RYGADERDRILRNTAQKDGVTKISIPQDPGQAGKSQTLVLRQLAGFSVSAGPESGDKVTRAGPFQAQVNIQNVMLDDGTWDT  
 DALIAEMRMFPNGRHDDQIDCLGRAFGELLDTRTGMDIFLRSQVEAVK

**SEQ ID 69**

ATGAGTAAAAAGACACCTTTATCGCAAGGCTTTATGCCCCGCTTGGCCCGCGGCTCCGTTACGCCTTTACCGGCAACGCGGACG  
 GGTGTTTCGACGCGGGCGAGCCTCCGCGCCCTGCGCGCAGCAGGAGGGGCGGCGGTTGATTACGAGCCGTTCTACAACGT  
 CGGGCATTCAGCCGCGCGAAGCTGAAGCGGTAGGCTTTGCGCAATTACGCGCCCTGCGCGCAACTACCATGATTTCGCTTTG  
 GTGATCGAGGCGCGTAAAGACCAATGGAGTGCCTTAAGTGCAAAATCCAAAGCGCGACGTCGAATCAACCGAAGACGACGAAT  
 CGCAACGGAAGACCGAAGGTGCGATGAAGCGGTTCGCTTCTCCGTCGCGCGGATAAAGAACATACGTGGCGGAGTGGCTGCG  
 CATCTTGCTGGAAGACCTGTTGTTATGACGCGCGTGCATCTACCGCGCAAAACACTGGGCGGCGGCTGTACGCCCTCGAA  
 GTGATGGACGGGGCGACGATTAAAGCGGCTTTTGGACAATACGGGGCGTATGCCGTTACCGCCCGATACGGCGTATCAGCAATCC  
 TGCACGCGCATGGCGGCGGTGCGATTACACGGCTGACGAGTTGATTACCGTTTCGCGGAATAACCGAAGTTACAAGGTTTACGGCTA  
 TTCGCCCGTCGAGCAAATCATCATGACCGTGAATATTGCTTTAAACCGGAGGTTTCACGCGTGGAACTACTACACGGCGGCGAGC  
 GTGCCCGATGCTTTAGTCGCGCGTGCCTGAAACGTGGTTCGCGGAGCAGACATCAGGCGGTTTCAAGAATACTGGGATTGTGCTGT  
 CGGGCGAAACGGCGCAGCGCGCAAAATGCGTTTCGTGCGCGGCGAGTTGTCCCGAACTTCCGCGAGACGAAGCAGCCCGGCT  
 GAAGGACGTTTACGACGAATGCTGGCGCGTGTCTGCTTTCGCTTTAGTGTGAGCCTACGCCGTTTCGTGGCGCAGGTAAC  
 CGCAGCGTGGCAGACGAGCCGCGAGCAGTGCCTTTCAGACGGCATGGGCAGCCTGAAAAACTGGGTAAAAAGCCCTGATTGACG  
 ACGTGTCTGCGCGTTACATGGATATGGCGCGTATGAGTTTACCGCCGACGAAATCCGCGCCGAAGTGGGCAAGGAGCCGTTACCGGGCGAG  
 AATCTACGCCATCTACAAAAACCGCAGGCTTTGACCGCCGACGAAATCCGCGCCGAAGTGGGCAAGGAGCCGTTACCGGGCGAG  
 GGGCAGCCTGAACCGGATAAGCAAGACGGCGGAAAGCCCGAAGACCGCGCAACCAAGGGGCTGAAAGGTTGGGAAAGTCCGAAA  
 GCGCGATGAGCGAAGACGAATCTGCCGCGCTTATTGAGGCTTATTGCTGACACGCATTGACGGCTTGGCGCAACAAATCGCGGC  
 GCTGATTGAGGGTTCGCGCGCTGATTGGCAGGCGGGGATTGGCGGCGGAATTGAGCGCGCGGCGAGGGGTTGTGCAACGCGC  
 TTGGATTTTGGCGATTGGTTCGGGATTGTCCGATGTGCTGAGCGGATATCAGGCGTGTGCGGAAGACGGGGCGGTGCGCGCT  
 TGTTCGCGTAATGCTGAACCTGCGCGCGTATGTTTACGAACTTCGACGCGCGCGCTCAAGTGGGCGCATGAACGCGCGC  
 CGAAATGCTGCGCATGAAGCGGGCGGGCGGGCGGCTTGTCCGAAATCTGCGCGCGAGTGCGCAATCACCAGGGGACGCGCGAA  
 ATGATACGCGCCCAAGTAGCCGAAGCCATGCGAAACGGCGACAGTGTGCGAGGAATTGGCAGGCGCGCTGAAAGAAATCCCATGCTT  
 TCGGCAACGCGACGCGCCGAACCATGCGCGAAGCGAAGCGCGATGGCGGACGGTATGGGCAACCTGATAGGCTGGGAAGGAAC  
 GGGGCTGTTGCGCGCAAGCAGTGGATAACCGCAAAAGACGACAAGGTGTCCGATGTCTGCAATGCCAAGCGCGGATGGGCGTA  
 ATCGGTTTGCACGAGCCTTCTCCACGGTTCGCTGACGATACCGGTCATCCGAACTGCCGCTGCGCGGTGTGCTGCTTTTGG  
 CAGGGGATATGCCTGAATCT

**SEQ ID 70**

MSKKTPLSQGFARVAAGVRYAFTGNADGWFDAGEPPAPAAQQAEGRRFDYEPFYNVGHSKPREREAVGFAQLRALADNYDVLRL  
 VIEARKDQMECLKWTIQKRUVESTEDDESQRDKRVDEAVAFRRSPDKEHTWADWLRLLEDLFVIDAPCIYPRKTLGGGLYALE  
 VMDGATIKRVLNDTGRMPLPPDTAYQQLHGMMAVDYTADELIRSRNRSYKVYGYSPVEQIIMTVNIALKRQVHALEYTAGS  
 VPDALVGPETWSADDIRRFQEYDILLSSGETAQRRKMRFPVPELGSNRFETKQPLKDVYDEWLARVVCFAFSVEPTFFVAQVN  
 RSVETSRQSLSDGMSLKNVWALIDDVLARYMDMAAYEFVWKGESLNPKEQAEIYAIYKNAGILTAEIRAELEKEPLPGQ  
 GQPEPDKQDGRKPEEPNQAELKESPMSEDESALIEAYLLTRIDGLAEQIAALIEGAADVQWQAGDLAAELSRAGVAVANG  
 LDFGDWSGLSDVVEPIIRVVAEDGAVALLRVMPPEAGMVTNIRSAVKWAHERAAEMVMKRAGGGLVRNPAAEQWITEGTRE  
 MIRAQVAEAMRNQDSVQELAGRLKESHAFGNARARTIARTETAMADGMGNLIGWEGTGLVAGKQWITAKDDKVSVCNANGMGV  
 IGLHEFFSHGALTIPGHPNCRCAVVPVLADMPES

**SEQ ID 71**

ATGATGTCGGGATTCTCCCCAAACCTAAGACCATTATCTTAAGCCTTGCAGGTGCATTTGGCGCATTTGGCTTTTGCAGACACCC  
 CGAACCAATACCGAACAGCAGAAAGAACTGAATACCATAGTCCGTCATGGCAACGCGAGTGGCGACCAAAAAGGCGCGGACGACGT  
 GTATTACAAAACGTCTCCAACGCTACGTCGGCAAGAATACCTCGAACCGTACCGCGTCCAATCCGCGCGGACGTAATCAAA

GGCCTAAACGGCGTGTACAAATGAACACCCGACCGCGCGGCCATCACGCCCAACATACGGGTATCACCGGCAAGGGCC  
GCATCCCGGTACCATAGACGGCACCGAACAAACCATCGACGTATGGATGAACAACACTACGGCGTGGCGGACCGCAACTACCTCGA  
CCCCGCCCTGTTCCGAGCATCGCGGTGAAAAAAGCCCCGCCCTCACGCGCGCGGTGAATCGGGCGTGGCGGTGCGATGTCC  
ATCCGCACCATCGAACCTTCCGACATCATCCCCGAAGGAAGAACTGGGGAATTGAAGTCAAAACCGAGTTTCCGGCAACACCG  
TGGCGCAGAAAAACGACCTACGCCAATTCCTTAGGCCGCGACTACCGCACCTCTCGCCCATAGGCGCGACGGCGGACGGGGTATC  
GGGTATGCCCCGATGATTGACCGGTATACCTGGCAAACTTCCCCACCGCCCTGTTGTTGGACGAAGGCATAGCCGACAGAA  
TTCCTGGGCGGTAAAGCCACACCAACTTCAAAGCAGCAGCGCAGCTGATGTTGTCGCGCGCTTCAAACCGACATTACAGACG  
GCCCTGGCCGATACAGCCACCGCCAAAAGGCAACTACTACGCGGGCAACCGCGCTATCAAAGCTACCTCAACAACCCCATTTA  
CGGTGCGGATGCTGTTACGACAGTATCTGACAAATCATGGCGGGAAGATATACTCTGCAAACTTCCGCCAGCCTGGTG  
CCAAATATGGCGTCTGTTCCGGCCGGCGAAGAAATCATGAACAGCCACACCGACACCAAAATCTGCTGCTGAAAAACAAT  
GGTATCTTCCGATAACCAAAAAATCAGCTGCAATATATGGACAAACAAATCGGCTTCGGCGAAATCAACCCCTGATAACGGC  
ATGGATACTCGGTTTCGCCGAACAATCCCTAAACGAACCTGTGACGAGGACCGGGCATAGGGACGAAATCGACAGCAAAAC  
TACAAATCGGCTACGAATGGAAGCCGCAAAACAACAAATGATGATGACCTTCAAGCCGATGTTGGCGGTGAAGACCGACAGTA  
ACCGCATCAGCAGCGCGCCAGTCGTCGCGCTCATTAAGTCCGACTTGTGATTACGACCTTTGGTATTGGTGAACATACGCAA  
AAAACCGCTCGCCCAACCTGCGGGGGAAAGCTGCGAAAGCGCGATGACGTGGAACGCTACGGCTCGGCGGAACCCATGAAGAA  
GTGCTGCGCATGATAGAAGACAGCCCGACAAATCGCCCGAAGCTGGCAGAAATACGATGAAAACAACCGTGGCATTACCGACC  
GCTGGATGGGGCATACGGGCGGCTACTACACCATCACGCCCGCCGATAAAATGTGCTGACCGACAGACCAACCAATCGGCAA  
AATGATGAATCTGCCGAACCTGAAGCAAAAGCTGAATCAGGAACGCTACTACATCGAACATCCCGACCGCATCGTTCCCGGC  
GCGCGGACGCTACCGAGCTCGTCCGCAACGGTTTCAACCTCAGCAACCGCTCCGCTTTCCGACAAACTCAGCTCACCCTTG  
CCGCGCAGCTACCGAGCGGCAACGTTGGAAGAACGCAACCGCATACCGCGACAGCAATGATTGATGAATACTTTCCGCGTACTGAC  
CCGCATGGCGGCTTTGGCGGGCCGAGTCCGCGAAGAAAGCGCGAATGGGGCGGCAACCTGGTATTGATTTGGAACCGACTTCC  
CGCTGAACATACAGCGGGCGTGGCTATCAGAATTATAAGGGGAACAATATCGAACTGGCGCGGACGCTGCGCGACGCAACC  
CTTGGTATCAGTACGGCTGGGTTCGGACAGCTATGTTACCGGCTTAATGATGCCGTATTACGAATTGGCGGATGAAGAAGATAT  
TGCAACCAAAAGCGGATGTTGACGCTTTATGATCCCGATAGAGCTGATGGGCGAGTTGACAGATATCAAGACCTTAACCGCGT  
TTTAAGGAAAAACCGTTACGATTGTTGATCCGATGATCTCGTTGATCAGGATACCGGCTTTACCGCAAACTGATGGAA  
ATTTGTTGATGATGCGGACCGCAATAAAATACCGATGATCTATATGATGCTGCGCGCAACAGATCATTTCAATGAATGCAGG  
CAAAATTTGACCCCGGCAAGTACAAATTACGCGGAAATGTACCGGAAAGAGTAAACAATCCGAGGGGAAAGCGGACGCTAT  
CGCGGTATATCCAGGATCGCATATCTACATAACCCCGCTCGGTACGCGAAGAAATGGAACGATGCGCAATGAAACCAAA  
TTCCGTCAAAAGAAGCAACAATCAGGCACTGGAATTCAATAGCGACCTAAACCGTACCGCTTGGATCCGGCATCAATTCGGCGA  
AGCCGACCGCTGGCGCATGCGCGAGGACGCGCGCATCTCTGGTCCCGCATGCTGGCGGTGACGATGATCTTCCGCAAC  
CACCCTCTTCCGCGCTATGCGCGCATGAGCGCTTCCCGCTTTACGAACTGACCGCGCCACCGGTAGCGGAGGCTGT  
ACGGCAGCGAGCCGTCGCGCAATACAGCTGAAGCCGGAAGAACCAACTGGGAAGTCCGCTACAATTTCAATTTCCGCCCC  
GCATTTCCGCAAACTGCGCAAGGCGACCTCCGCTCACCTACTACAGTAATAAAATCAAAACCAATCGATACATCCAAATGAA  
GACGGCGGTATGATCCAAATACGACAAGGCGTACGCAAGGGGGTAGAATGACAGAGCCGCTCGACAGCGCGCTTCTTCGCT  
CCTTCGGCGGACGATACCGCTTGAACATATGGTGTGCGACAAGGGTATCGCCTTCAAATTCGACTATTACCTGCAACGCTACC  
CGAATGCTTGAAGGTGGCTTCGGCTCAGCGCTTCTTCAGTCTTGGCAGCGAAATATTGCTTACCGCTTATGCTCGGACG  
CGCTTCTTCAACGAAACTGGAATTTGGGATGCGCGCATCCATCACAGCAAGGCGGAGCGGAGAAATTACGACAAGCTGATCG  
CCGACGGCGCGGGGAGGTGATGCGCGCAACGGTAAACCTACCGCTGGCATGACAGCACCTTTTGGATGCTATGCGCGCTA  
CCGCATAGGGAAGCATATAGACTTGAACCTCAGCGTAACCAACCTTGCCAACCGCTATTATCTAGACCGATGTCAGCACCCCG  
GTCCCCGGCGCGGAGGACGATTACCTTCGGCATCAAGGGCAGGTTT

## SEQ ID 72

MMSGFSPKPKTIILSLAGAFGALAFADTPNNTEQQKELNTIVVHGKRSADQKGADVVYKVNVSNAVVGKEYLERYRVQSGDVLK  
GLMGVYNNMTRTAGGAIPTNIRGITGKGRIPVTIDGTEQITIDVWMNNYGVGDRNYLDPALFRSIAVEKSPALTRGVKSGVGGAMS  
IRTIETPSDIIPEGRNWGIEVKTEFSGNTVAQKNDLRQLRGLRDYRLTSPIGATADGVSGMPDVLGTGVTGKPSPTALLLDEGLADTK  
FSGGKSHNTNFKDDRQLMLSAFKTDITDGLAAYSHRQKGNYYAGRGYQSYLNNPIYAGADACYDQYPKSWREKDLCKSSASLV  
PMAVLFRPGEIIMNSHTDTKILLKNNWYLPDNQKISLQYMDNKIGFGEINPLITAWILGFAEQSLNEPVOQAPGIGTKIDSKT  
YKIGYEWKPNKWKIDLQADMWRVKTDSNRHQSGGFGVGVITSDFDYDLWYWCNIRKPSNLRGSCESAMTWNAYGSAARTHEE  
VLRMIETDPKIKKLAEDYDENNRATIDRWMGHGTGGYITIPADKNVLTDTQINQIGKMMNLAEKQKLNQERYIIEHPDRIIVPG  
ARQRTDVRVNGFNLNRLRLSDKLSLTLAADYQRETLERTDTADSNDLMNTFGVLTRMAALGGPQSARKREWGANLVFDWKPTS  
RLNIQAGVRYQNYKGNNIELARQRAARNPWYQYGLGSDSYVTGLMFPYELADEEDIANQKRLQLYDFDRADGQVABYQDLNRR  
FKEKNGYDFDPHDTLVGQDTRFYAKSDGNFVQYADGNKNTDVLVYLRKQIIPMAGKFPDGPVKQITPEMYRERVNPNQKSGSY  
RRYIPGSHIYITPGSVREEMERMANENQIPSKEDNNQALEFNSDLNRTAWIRHQFGEADRWRMPQBQRAHSWSPLAVSYDLADN  
HRLFARYARMSRFPSTLYELTAATGSGGLYGGSETVAEYSLKPEKSTNWEVGVNFNFAHPFAKLQGLRLTYYSNKLKNIQIDTSNE  
DGGMIQYDKAVSKGVELQSLDSGRFFASFGGTYYRLKHMVCDKGIKFDYQLQVRPECLBGGFGLSRFFQSLQPKYSLTLDVGT  
RFFNEKLELGMRAIHHSKAERRNYDKLIADGAGQVYARNGKPYGWAATLLDAYARYRIGKHIDLNFVTNLANRYLLDPMSSTP  
VPGPGRITITFGIKGRF

## SEQ ID 73

ATGAAGCATCACAATTAACCTCGCGTCTCTTCTGGCCGCTGCTTTCCGGCTCTGCTTATGACAGTAGAAGTTAAAGCGGGGATT  
CAAGTAAAGGGCAATTAATCAAGCTCCGAATCCGATTTCCTACCCTTTGGTTCCGGGTGCTGCGGACATCAAGGTACGACAGG  
CAACGGCTTGTCAAATCCATCAACCTCGAAGCCGCGCCCGCGCAGCGCATCCGCAACAAATACGGCAATGCGCCTATCAACGGC  
GGCAATCAGAACCAATGTAAACGGTGGCGCAATTCGAGATATCTGCAACCCGGCGACATCAACCCGATTGCGGGCTGGTTCT  
CGAAACTAGACTCGCCCAAGTGTGGTATGAAAAACGTGCCAACACACCGAAGTGTTCAGCGTACGCCAAATGGCCGACCCGCT  
GCTGCGGATTGCGCGGAAATTCGGCGGCATGACTTTTGCCAAAGTGGCGACGGCGGCAACCAATGTCTTCTTCGGCGAATGGGGC  
CCGCGCAAGGCAACAGCAATCAGATTACCAACAGCACTGATTTAAATATGAACGACGGCAACCGCAGCGTTGGTTTGTGGGTG  
AGAATCCGACTAAAAACACAGAACTTGACTGCGGTACCTATAAGCTTGTGCGGATCAACAGCAACGACCGCGGCAAGAAACGA  
TTTCTATACCGTGAATACAGCCACATTCGGCAGCGGTGACAAAGGTTTTATGAGTGGAGAAGTGAACACACGGATGATGGG  
GAATTGAGCTTTAACGGTGTGAAATTACCAATGCTGACGGCTCGTTCAACAGCATCCAGGCCGAATAACGAAGGCATCAAG

GCCAATTCTACGGCAATGGCGGGCAGCCATGGCGGGCTATGCCACTCGCGGAACCGACAACAAAGGCGATGATGTGGCCTTCGG  
CGGCGCGAAAAA

## SEQ ID 74

MKASQLTLAVLLAAAFGSAYAVEVKGDDSSKGQLIQAAESDFLPFGSGAADIKVSTGNGLSKSINLEAGPAQRIRNKYGNAPING  
GNQNTNVNGAANSRYLQPGDINPIAGWFSKTRLAQVWYKERNANTEVFVSRQMDPLLPAPKFGGMTFAKVPTAATNVFFGEWA  
PRKGNNSQITNSTDLNMNDGNRTVWVFGENPTKNTNRLTAVTYNVVGINKHTPGKNDFTYGEITATFTGTDGRKFGMSGELEHTDDG  
ELSFNGVEITNADGSFNSIPGRNNEBKGQFYNGNAAAMAGYATRGTDNKGDDVAFGGA

## SEQ ID 75

ATGACCCACCGCCTCTGCCTGCTTTTCTGCGGCTCTGTACGGTCTGCCTTGCCTCCGTCCAACGATGCCGCGGACGAAACGCC  
GCCGCTGCTGGACGAGGGCAGCCGCCAAACGACGCAATACCGCGAAAGCGGTTCGGCTGGACACGGAACAGGCACGCGGGGAAGT  
AGAGGAAAAACGACGGCTATATTTTCGATAGGCGGCGAAATCTACCAAGTTCGGCGATACGCGGGAAGAACTGGAAAGCGCAATTTAC  
CACGCCCTCAATGCGCGGCGAGTGGCACAAGGTGCGGCGAGTTTCGCGCCCGCTACGCCAACTGCCCGGCACAGCCGCGCTGA  
TTCATTTGGCGGATGCGCTGCAAAAACGGGACGAAGGGGATTTCGCGCGCGGGGGAACAGTTTTCAGACGGCCTTGGAAAGCCGA  
ACCCGACAACCCGCGCCTGCTGCTCGAAGCGGGGCGGTTTATGCGGAAGACACCAAAACAAAGAGTCTGCCGCGCGGTTTGTAG  
AAAGTTCTGAAACCGGACATTCGCCGAGAAACCCGCCCATTCGTGGAAACTACCTGTCCGAACTGGGCAACGCCGCGCTGGC  
ACGGCCAAATCAGCCTCGCTACGCTATAACAGCAATGTAAACCAAGGCAACGGCATCAACCAATCGGTGTGGGAAATTCGGGG  
CATGTGCTGTATGGAGCGCACCTGCGCGCGCAACGGATTTCGACCTTCTCATCTATAGCGGACCGCGGAAAAAACCGTCCCG  
CTCAAAGGGAATCAGCGGTACAGGTGCGCGGTGTACTGTACGGCAACCGCTACACGGAAGAACAAAGATTCGGCGGCTATTC  
CGGATTACGGCTATCGCAACGGTTTCGTGTACGCGGATACGCTATGCGGACGCGATGCGGACTGGTTCGCGCACACTCTCCCCGACTGG  
CGAATACGATTTCGCAACCGCCACACCCACTACCGAGCATGGGGTTCGGGATGCGGACTGGTTCGCGCACACTCTCCCCGACTGG  
CGCATTAACACACATCGCGGAGCAAAAAGACCGGATACGCGGACAAAGCAAACTTATTTTGGCGATTTCAAACAAATACGAAC  
TCGGCGCGGGGGCGGAATTTCCATCAGCTGAAAGCGGCGCTGCTTGTAAATTTTCGATGCGCGACGCAAGCCATTCGCCAAAA  
ATCCTCTTCCAGCAAGAATATACGGCTCGGCTGGCGCGTATAGGCTTTTTCGGGCGGTACTTATTTAAACGCGCGTCTGCTC  
TACCGCGCGAGCTGTATGACGCGGCAAGTTTCGTCAGCGATAACAAACGGCGCGCGACAAGCAATACATCATGATGGCTGCGG  
CGGTTTTCGCGCAATGGAATATCAAAGGCGTATATCCGAACTGCGTTTCAGGCGAACAATCGCACACAGCAACGCGGTGTATTA  
CCGCTACCGCCAAACGAATGGCTGTTGGGTTTTAAATATCGGTTT

## SEQ ID 76

MTHRLCLLFLPLCTVCLAPSNDADERRRLLEDGSRQTQYRESGWLDTEQARGEVEENDGYISIGGEIYQVGDTEEELESATY  
HALNARQWHKVRQFAARYAKLPRHKPALIHLADALQKRDEGDFRAAGNSFQTALEAPDNPRLLLEAGRFYEDNQNKESAAAFE  
KVLKTDIPIAETRPIVENYLSLGKRRRWGQISLGYGYSNVNQNGINQCVWEIAGMCLMERTLPAPTDSTFSSYSATAEKTVP  
LKGNHGVQVRGVLGNRYTEKDKDSAAMPDYGYRNGSLYAGYAYADARSSFSLLPYFEYDFRNRHTRHWAGADADWSRTLSPHW  
RINSHAGAKTGYGGQSKTYFADFQYELGAGAEFSITLKSGLLVNFDARKAYPEKSSSSKEYTARLGAYRLFSGGTYLNAVILL  
YRRSLYDAASFVSDNKRDRDKQYIMMAAGFPQWNKGVPELFRRTIAHSNAVYYRYRQNEWLLGFKYRF

## SEQ ID 77

ATGAACCAAGAGGGATTACCGCTCACGGAATGCCACGATTACCCCTCAAGGCGAAAGAAAAACAATAAAATTACCGTGGAAAAACG  
CCGCATACAGCAGCGACGGCATTTTCGACTCTGATTACAGAACGCGGGGCAAGACCCGGAACAGGGATGATGAAATAAAATCAT  
ACTGGAAGCCGCGCGGCGATAATATGTTTACCATGAAATCCGCGGATGCGGATGCGGATTATGTAAACAATTCCAAAGTATTAACG  
GAGACACCATATTATAAAGCAACAGAGGTTTCAACGGCATTTTTGCGCTATGCGGACAAATCGCTGGTCAAACCTGATTGGCGAGA  
ATAATATCGTTAAGAGTGAAATCAGTGAAAAATCTAAGGCATTAATGGGGGATTTCGCCATATCGGCATTTATTCTAGGCAAAA  
CGCGAAAGTCGAATTGCTGCGAAGAGCGACATATCGTACAAGCGGGAATTGGGGCTTATACCTCAACCAACTCCTCAATTTCC  
CTCAAGGGGAAAAATAATGTGATTTCAAACCCGAAATATAATGTTTTGCGCTACAAAAAGGCAAGGTTGATTGACTGTGCAAA  
ATAAAAAACACATTATCTGATGCGGAATTTGGCGTATATGCCCTTAACACCAAGTATGGTTAATTTGTCTTCAAAGATAATAACGA  
GGTAAAAAGCACCAAGTGGGTCTGTATTCGCAAGACGCGGTTCAATCAATGTAGATAGGAAGGATAATATATTGAAGCGGAC  
GCGGTTGCGCTTGGTGGGAAAGGTGGAAGTCAAAACATTCGGGCAAGCGGTACAAACCTGATTAGTTTCAAAAAGCTTAGGAATTC  
ATGCTGAACAAGCTGCAAAAATAGCCATAACCGGCGCAAGCAATACAATTCATGCAAGCAATGCCGTATTCGTTTATTAGACAA  
AAGCGAAGTTAAGATTGACGGTCAAAATACCATTTGACTCCAACGTTGCCAATCTTGCAAGGCAAGATGGTTCAATTGGAAT  
TATAAAGACGATACCCGATACAGGGGCAACCGTATCTGATAAGGGTTTGGTAGCCATCAAACTTGAATAACACGAATATTG  
TTGCCGACACTATTCACTATAAAGCGATGTCTTGGCGGTAATAAGGGTAAAGTGAATTAGATTTCACGCCGAACATCCTTTT  
AGCGGGACGTTTGGATAAATTTAGCGGCTTAAACCGATTCCAACATAAAAAATTTATTCGAAAACATGTTTGCATAAATTTAGACAGC  
AAAAGTCGCGGCGAAATTAACTTAATTTAGCCAAAGACGCATTATGGACGATGACAGGTCAAAGCTGGCTGGATAAATTTGAAG  
GACAAGGCACTATCGATTTAATAATGATGCTAAAAACAAGTGGACGCGCTTACATATCGCGGAATTGGCGGGTGCCAAATAAAT  
CTTGATGCTATGTAATAAGACGGCATTACAGCGATATGCTCTATGTGAAAAAAGGCATTCGACACCGCAAGAGTCGTCGTC  
AAAAATCTGTCGAAGTGCTCGACAGTATGAATTACGGCGCAACGTTTTCGCTTTCGCTACAGTAACAAACTCAAAAAATGAATTTG  
TGAACCGTAAAAAATATATTGACGATACGCACCTTATGGAGGATGCCCTGACTGTGCAATACTCCGCACATAACGGCGATAAAAA  
CAACAAGGATGACTATAATAAATCCTTTAACGGCTCTGAAATGACGGCGGAAAAAGCTGGAGACGATTATGTCAATAAAACCTAT  
ACCGACAACAGGCAAAATGTCTATTGTTGCAACAGGCTACCGGCAATCCGAGCCGAAATGTCAAAAATATCAATGATATGTTTCG  
ATTCAACCGCACATTATGCGTTCACTTTGGATACTTATGCCAAACGCGAAGGGGAGCGGGCTTTTCAACGTTGGATAAAAAAGA  
AGGCGATTGGATAAGGCTGACGCATACCCGTTGTGATCAATCCAATCGGTTTATAGGTTTCAATAACAAGATTGGAATTCGGATAT  
GACCGATTACGCTCAACGAGCAGGAGAAAAACGCAAAATGGGCTCTGTACAACTACTACCAATACATAGATAAAGAAGGAGACGAAC  
ATACGTTTGGCAAGGACAAAATCAGGAAATATGAATTGGCTCTGTACAACTACTACCAATACATAGATAAAGAAGGAGACGAAC  
AGGGTATATCGACAATGTATTAAAAATAGGAAAACTGCGTAACCGTGTGATTGACGCAATCATATGGGCAATTTATGGGCAAG  
GGAAAAATATAGCAACACCTATTCTCTATCAGCACCGAATACGGCCGCGTAAATTTTGGATGACGATAAATTTGTCGGGATT  
CACCAGCAAGTACAGTTGCAATATTCCTATTGAGAGGTACCGGCTATCGGATCGATAACGGCATAAACGTCATTTTAAAGCCAGC  
AAACAGCCTGATAGGCGGCTTGGGTTTGGATGTCGTGAGAAAATTTGACGGAGGCAAAAAACTTTCTATATCAAAGGCAATATC  
TTTCATGAATTTTGGGCGAGTCGTTCTTTAAGGCATTTGAGGCGAAAAAGTCATTATGCTCAAAAA

## SEQ ID 78

MNQEGITAHGNATITLKAKENNKITVENAAYSDDGISTLINRTGARPGTRDDGNKIILEAGGDNIIVTMKSGDADADYVNNSKVL  
ETPHYKSKRGSNGIFAYGDKSLVKLIGENNIVKSEISEKSKALNGGFRHIGIYSWQNAKVELSAKSDNIVQGGIWLGLYSNNSSIS

LKGNVINSNPKYNVFAKKAKVDLTVENKNTLSDAEFGVYALNTSMVNLSSKDNNEVKSTQVGLYSQDGGSSINVDRKDNIIEGD  
 AVALVGKGGSQNIRASRTNLISSEKSLGIHAEQAIAITGASNTIHASNAAIRSLDKSEVKIDGQITIDSNVANLARQDGSIHNLN  
 YKDDTRITGATVSDKGLVAIKPLNNTNIVADTIHYKGDVLAVNKGKVELDFTPNILLAGRLDNFSGLTDSKHKNLFENYVANLDS  
 KSAGEINFNLAKDALWTMTGQSWLDKLEGGQGTIDFNNDAKTSGRALHIGELAGANKFLMHLNKGDIHSDMLYVVKGTSTPQEVVV  
 KNLSEVLDSMNYGERLRFATVTNSKNEFVNGKKYIDDTHLMEDALTVEYSAHNGDKNNKDDYNKSFNGSEMTAEKAGDDYVNKTY  
 TDNRQNVYLKQATGNPSRVKNINDMFDSTAHYAFTLDITYAKREGERAFSTLDKKEGDWIRLTHTRVLIQSNARFHNNDPFIY  
 DRPSLNEQEKRRKWSISLDYGHGRTSLWNTFGKDKIRKYELALYNTQYIDKEGDETGYYIDNVLIKIGLRNRVRIARNHMGQLWGK  
 GKYSNTLFSISTEYGRKFLDDDKLWRITPQVQLQYSYLRGTGYRIDNGINVLNLSHANSLIGRLGLDVVRKFDGGKCLFYIKGNI  
 FHEFLGSRSFKAPEGKSHYAQK

## SEQ ID 79

ATGCGCTTCCCCCTCCCTATTACCAATGCTGTGCTAAAAATTACAAATGGCGCAATGGAATTCAAATCAGAAGATATTGGAACCA  
 TAAACTAACAAGCTACTTTTACCTAAAAAAGACACATCATTAAACACCCGAAGGGACTACATTATTATCAGGCGGCAC  
 GCTAACCTTATCTAATACAGGTATTCTTTATCGGTCACAACTCTGTATTTGAAAAGGAACATTACCAACGGCGGCATCATT  
 ACCTTGGCAATCAATCTATGCAGACAACTCACCATTGAAGGAAATTATGTCGGTAAAGACGGTGTGTTAAAGTCAATACAG  
 AATGGAATCGCCGGGTGATGATCAAGGAGGAAATTCTCAATCTGATTACTGGAATCAGGCGATGCTTCAGGAAAAACAAC  
 GGTCAATTCAGTGGGTAAAGATGGCAAAGAAAAATATTATCGACGGTTCGATCGGCGAATTTCCGACCGCTACAAACCGCATGCC  
 GCCGTGTTAAGGTTTTGGGACAAGACAAGGGGGCGGAAACCGGTAAATTAATATCGAAGACGCTAAACATACCTACACAATGC  
 GCGATACTTTTAGCGGAATGCCAAAACACAGGGGGCGGGGAATTGCAATTGGTTTCACACAAGATGAGGCGGGCGGACAGA  
 ATACTTCTGGACTTTAACACCGCCGAATCAAGATAAAACCATCATACGCGCAAGCGCACCGGCTACGCATCGTTCCACGCTCAA  
 AACTTGGAAATCAGGCTATGCGATGCTGGATACGCTCCACCAACCGCGTGGCGAAAATCAAACCTTTCTCGGGACAGGCAAGGCA  
 ATTATCGGCGAGATGCGGAAGCAACAGACATAAAGGCTACCAAGGCACCGTGGGTG

## SEQ ID 80

MRFLPITNAVLIKITNGAMEFKSSEDIGTIKLTAKTFHLKDDTSLTPEGTTLLSGGTLTSLNTGISLSGTTSVFEKGTFTNGGII  
 TLANQSYADKLTIEGNYVGKDGVLKVNTEWNSPGDDQGGNSQSDLEITGDASGKTTVIVSGKDGKENDIDSGISIGELSDRYKRS  
 AVVKVLGQDKGAETGKLNIEDAKHTYTMRTDFSGTAKTTGAGELQLVSHKDEAGATEYFWTLTTPNQDKTIITPSAPAYALVPRQ  
 NLESGYAMLDLTHQRRGENQTLSDRQGNRYQDAEATDIKATKAPWV

## SEQ ID 81

ATGATTCTTGGCTCCCTTGTCCGCTATTACCGCCGTTTGGCAACGGAACCGATGAAACGGGCAACCCGAAAGTGCCGTCTTATG  
 GTTTTAGCGAGGAGAAATCGGCTGGATTGTGGTGTGGATAAAGAAGTTCGTCTGAAACCGGTTGTGCCGAATCTGACTGCCGA  
 TAAAGACCGCGAGCCGAAGCTGATGAGTGTGCCGCGCCCTGAAAACGCAACGTCGGGTATCAAAACCGAATTTTTTGTGGGATAAA  
 ACCGCTACGCGCTTGGCGTGGGAAGCCAATAAAAAACAAAGCCAGCCAAAGAAAAACCGTTTACGCGCTCTGAAAAAACCTTTG  
 AAGCCTTCAAGCAATACCATCTCGATTACTGCAAAACAGCGAAGACGAAGGTTTACAAGCCTTATGCGGTTTTCTGCAAAACTG  
 GCAGCCTGCACATTTTCGCTGCCGAAACCTGCCGTGCCGAATGCTTGATTCCAACACCGCATTTTCTCTGAAAAACCGACCGCT  
 CTATATCCATAAAGCGCAAGCCGCGCAAACTTTGTGGCGAGGCTGCTGAAAGTGATGAAGCACTCGAAAGCTTATGCTTGATTA  
 GCGGCGACACCGCGCGGATTGACGCGCTGCATCCGGCGATTAAAGGCGTGTGGCGGGCAAAGCTCCGCGGCTTCGATTATTTT  
 GTTTAATAAAGAAGCCTTTTCTCTTTCGGAAGAGCAAGGCGCAAAATGCCCTGTTCGGAACAATCCGCTTTTGCTTACAC  
 ACCGCGCTGAATCTCTTGCCTCGCGAAATAATCACTGCTGACCATAGGCGATGCCAGCACGGTCTTTTGGCGGGAAGCGG  
 ATGATATAGTGGAT

## SEQ ID 82

MILASLVRYRRLATETDETNPKVPSYGFSEEKIGWILVLDKEGRKLTVPVNLADKKPQPKLMSVPRPEKRTSGIKPNFLWDK  
 TAYALGVEANKNAEAKERPFTPSEKTFEAFKQYHLDDLQNSEDEGLQALCRFLQNWQPAHFAAENLPAEMLDSNTAFSLEKPTA  
 LIHKREAQTLWAGELKSDALESLCLISGDTAPIARLHPAIGKVFVGGQSSGSIISFNKEAFSSFGKEQGANAPVSEQSAFAYT  
 TALNYLLRRENNHCLTIGDASTVFWAEADDIVD

## SEQ ID 83

TTGGCGCGCGGACGGAACAGCCGATGTTTTCGGGTATCCCGTCGGAGGACGGGGCGGAATTTTGGATACGGGCGTGATGC  
 CGGACCGTTTGGCGCGTCAGTATGCGGACATGGCGGCTAAATACCGGGCAAGCCGTCGGAGGCGGTGGGGATTGATCCGGATGA  
 CGGTGCGGTTTTCTGCGCGCGCTGCTTTGGCGGCGGATTTCGGGCGCGGTGTGCGGTCTGCGGTCTGACATATTGAAAGCCCGG  
 TCGGTTCGCGGATGATGCGCGCTCGGACGCTCGGCGGATGCGGACAGGGGCGGTGTTCCGTCCGCTTACGGAATGTGCGCCCGG  
 GCGGTGCGCGCGCGGTGCGGCTTTCGTTGCGCGCGGCGGTTCTGCGCGCGCTGCTTCCGGCGGGATTGCGCGTGTGCGCGCGCT  
 GCCTGCGGGCAATACTTCGACGCTTTGGATACGCGCGGGCGCAAGGCTTTGGCGAAGGAGGCGGGCCTTGATATTAAAGGCGGT  
 GCGGATTTCCGGCAAATCGCCGCGCTGTGCGCGGAAAAATCGAGCAGGCGTATCACGCGCGGATTGAGGCGGATTATCAGGCGG  
 CTTCGGAAGCCAAACAGGGTTACCTGCCGCGCGCGCTGCGTATGGCGGATGCCGTGCTTCTTAAAAAGGGTTTTCCGTCCG  
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 TATACGCGGACGCGGATTATGCGCGGGAGGCGGGTATGGCGGATATGCGCGGACATTATCTGAGGGTTTGGCGGAATCGGCGG  
 GGGCTGTACGCGCTTACCGTGCACAACATCCGGAATCGGCGGATGTGTTGGACAGGCTTAACCGTGCCTTTACGGTTACCGCGG  
 CAACAACGGTTGGAGCGTGCGCTGTTGAGCCGCGAGGGGAGCGTTTGCAGGGGTTCCGACGCGGTTGCCGGATGACGCGCGG  
 TCTGAGGCGCTGTGTCGGCGCGGCGAGGGTTTACCCCGGCTTTACCCACGGAAGATAAGGGTTTGGCGCAGGATGTGCGGCGAG  
 ATGTGCGGCGAGGTTTACCCAAAGGCGGCGGGTTTGAACCTTGATGCGGGGCGGATGCAAAATCGCGGCTGCTTTCAGGTTT  
 GCCAGGTTCCGCGTTGCGTCCGCAATGCGCGCGCGCTGCGGCAAACTTACAGGTTTCGGGCGCGCGGAGGTTGCGCGCGG  
 GGCCTGTCCGCGTGTGAAACCTTTCGGGACGAGCGCGGGAACGTTGCGCTGTTGCGGGCAAACGCCCCGATACGGTGTGTC  
 CGGTATTGAATCCGAGGTTGCGGAATCGGCGGCGAGGTTATCGCCTAAGAAACGGATGGCGGATGCGGCGGCGGATTTCACGCG  
 CGGTTTGGCGGCGGACAGGCGCAGGCGGAAAAGGCGGTTGTCCTTTGGGGGCGCGCAATACCGTTTTCGAGCATAACGACCGG  
 AGGCATATTGATGCGCTTTCGGGCGTGCGGGCGAGGCGGCGGCAAGGCGGATGCCGAGGAGTTTTCGCGATATGGCCGCTCCTT  
 CCAACTCTGACGCGCTTGTCTCCGACGCTGCGGTTATTGAAAGGGGCGGAGGCGGAAACCTTTCGGGCGGGCGGTTTGTCCGA  
 AGCGGTGCGCTCCGAGCGGGTCCGGATTATCGTCCGACGCAAGCAAGGCGCGGCGGCAAGGCGGCGGCGGCGGCGGCGGCGG  
 GCGCGCGCGGCGGCAAAACCGCGG  
 AAAATCGGCAACCGAAAGCGCTTTCGGATAAGGTGCGGAATATCGAAGCGGGAATCCCGCTTCGATGGCGGAAAGGCGAA  
 GTCGGCGCGGCGCAAGGCGCGGCAACCGAAAGCGCTCTGAAAGACGGGCAAGCCAAGCCTGAAACGTTTCCGAAAACGGCT



TCGGACAATCCGGAAGAGGCACGGCGCAAGGCGCGTGTGTTGCAGGGAGGGCGCTGTTTATACGGTGAAAGAGCGTCAGGCGCCGC  
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TGTGCGCCCGCTGTCCGAAACGGCGCCGACAGGCGCAGATGCTGTGTGTCGAGCGTGTGGAGGGCTGGTTTACGGCGAGGACG  
GGCAAAATCACGCTGGTGGCGGAAAACCTTACGCCGGAACGTGCGGTATGGGCGGCGTGGCACGAGCTGGGGCACAGGGGGCTTTG  
CGCGGATGGTTTCGCCAAGTACCCTGAAGAATTGGAACGTGCGGACGGCAACGGCCGTATTTCGGCGCATTCGGGACGCGGTGCA  
GGAAGGGCGCGAAGGCACGGGCGATGCGGCGGCTCGGTGCGCCCGCGCGGTGGAAGAGGCGGTGCGGAGCTTTATGCGGCG  
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TGGCGCGTATCGGCGCCCTGTTGCGCGCTGTGCTGCAACGCGCTGGCGGGAAGGCCGCGGTGCGATGTCGCGGACGCGGATGTGTT  
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CGGCGCAAGACGGTTCGCGCGGAACGTTCCAAGTCGGAAGGCTTGAAGCTGCGCGTTCGCGGAACCATCCGTATCTCGGGCA  
GGGAGGTTCCGGAAGGCGCAATTTGCGCGAATATAAGCGCAATGCGCTGGAATACGGCAATCTTTGCGCGGGCTTATGTGAA  
TAAGGACACGGGCGTGAATCAGTTTGGGACGTTTCGGGCATCAGTGAATATTTCGCTCACGACTATAAGGACGCGGAACATTTG  
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GGAGCCTCTGAAAGCAATCGCCTTTATCGGGCATTTGATGATAAACCGCTGTTGCGAGATTTTGAAGACAAAGATGCGGGCAAGG  
CGCGCATTCGCGATTGTTGACACGAGGCGGTGCGTTTTCCTGCGCGGAACATCAGGCGCGCAATCGGCGCTATAACGGGTAA  
AAAAATCCGATTGAGAAACGCGCTGAAAGACCGCTGGGATGCTTCAAGGGGATTACGCTCCAGTTTTCGGGCGGCGCGAGATC  
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TTACGGAGGCGGCAAGGTTGTGAGGAAATGGGGCAGGTTGAAGGAGGAGGATGCGAAGCGCTTTCGCGCATCCGACGCGCTTTGGATATT  
GACGCTGCGGAAGGTGGATGCGGACCCGCTGATGCGAAAGGATGCTCAGAAAGCGTTTGGACGCGATCCGACGCGCTTTGGATATT  
CGGACCGGTAAATCGAGAAGGCGGAGGCGCGCTTTCCTTCCGCGGTGCGCGTATTGCGCGTTCGCGATGCGCGTTACAATAAGG  
CGCAACGGCGCGCGGATAAGGCGGCTTATGCGCTGGAGAAGGCGCAGGAAAACACGCTCGGGAATTTTGGCGGATGAGGCGGA  
CATGCGCTGCGCGCTGTTTATGCGGATTTCGAGGCGAAGCGGCGCTTTCGAGGCGCGCGGGCGGATGTCGCGCGGCAAGG  
CGGGCTAAACCGGATGCGGTACGATGTTGGAGCAGGCGCGCGGATGTAAGCGTTTGGAAAAGGATGAGGTTTCGGGCGCAAA  
AGGCTTTGGAGGGGCTTTCCTTTCGTAACCGCGCTTTTCGCGCGTTCCTGATGTCGCGCGCAGAGGTTTACGCGAAGGCGCGGGA  
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CGCTGAAGGAGCGTTTTCGACAACGAGCTGGGCGGTGTGATTTCCTTTCGCGCGTTCGCGGATTCGCGGATTCGCGGATTCGCGGATTCGCGG  
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TTTCGCGGTTGTGAACCTGTGCGCAGACGCAATGGTGGCTTATCCGTTGATGCGCGGAGAAGTTCAATACGATTGAGGACAGTTTGAACGGGATGAGA  
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ACGTTTTCGCGGCTACCGTTTCGCGAAGGCGGCGGCGGCGGACAGCGAGGCGGCTTTCGAAACAGGCGAAAAGGCGGATGAG  
ACGGGCAATTTTACTATGCGCGCAAAACCGTCCGCGCTTATGATGGGCAATGCGGCGAAGGTTGCGGAGGCGGTAAGACGCTGCGCGGG  
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GTGACGACGATTACCCGTTGGGATGCGGAAGCGGCTTTCGCGAATATGTTGGCGGATGCTTTCGCGGATAAGGCGGCGAGGTT  
GGCCAAGGCTTCAGCCGCTGACGCGCGTGGACGCTGTCGCGGCGTTTGGGCTTGAACAGTTGGTTTTCCTCCGATATCCAAGAC  
GGTTTGGAGGTAAGAAGTGGGCGAATCGCTGGTGGTTCGCGAGTACGGGCGCGGTGGTTCGCGCGGATTCGCTGCGCGGACG  
CGCTGCGGACAAGTCATCCGTGCCAAGGACGGCAACACACTATCCCTTATGAAAAGCTGG

## SEQ ID 84

LARGTEKQPDVSGIPSEDGAFLDTGVMPDGLARQYADMAAKYRAKPSAVGIDPDDGAVSAAALAADSGAAVPSAVSDDMEAR  
SVADDAPSGRSADADRGVPSAYGNVRPGGAPRGAASVAPGGSAAASGGIARVAPLPAGQYFDGLDTRGRKALAKEAGLDIKGV  
ADFGQIAAFVRRKIEQAYHARIEADYQAASEAKQGYLPPFVRMADAVFVPPKGFVSPADALDKESRRRFDALPEWVRRAQTVAD  
YTADGIMRREAGMADMRGHYPEGLAESAGAVRAYRAQHPESADVLDRLNRAVYGYRRNNGWSVPLLREGERLQGVRTALPDDGA  
SEAVVGGGRGLTRALPTEDKGLAQDVRQDVRQGLTQGGRLTPDAGADANAAALQGLPGSAVASGNAPARRQNLQVRARAEGAAP  
GLSASENLAGTDGKRAPVAGKRPDTVLPVLPQVAESAGRVSPKKRMADAAADFTRRLAADRRRPEKAGVPLGGGEYRFETDR  
RHIDALGAPVGRPKGGMPEEFADMGPSNSDGLVSDGRRYLKGREABTLRAGGLSEAVPSEPGRDYRPTQEARAPAKVMARPRD  
AADAGKAPAGRAQPARAKDTPVAGKAAAANKAATEKPSDDKVRNIEAGKSRFDGKGKSAQAATEKPSSEKTKAKPETFAKDI  
SDNPEEARRKARVLQGGPVYTVKERQAPQGFALREHAESIKRRLAESIGGLAERVDAVAVSETAPDKAQLLSQRVEGWFDGRT  
GKITLVAENLTPERAVWAAWHELGHGFAADGFAKYREELERADGNGLIRRIADAVQEGREGTGDAASVRPAVEEVAELYAA  
QRTGGWAGIENRYGVKVGNGLRKGIAGVLARIGALLRVLQRLAGKAGGMSDADVFAMLADLHGNVEGARDAPWGNHRAVMFA  
RAEDGAAERSKSESLEKLRAETIRISGREVPEGNLREYKRNALLEYKSLRGPYVKNKTGREISLGRSGITEILRHDKDAEHL  
QSIAAIPOIENAVYIDTLPNEDLAKNGDIQGYEYVSVGLNVGGADYTVRAAVVSRNGNRYDHLTKIEKNLLSLLDVSTT  
GASEKSPLSGIDDKRLQLILQDKDAGKGGIADFDEAVRFSRAANIEAAIGRTTGKSLDLRNALKDRWDASKGIQLQFLGRRI  
EDIYGVGLDGLKEYGRLSELFGADANKAVTEADKVVREWGRLKEEDAKALADLMHDAATLAKVDADPLMRKDAQRLDGIIRLADI  
ADGKIEKAAAVASAGARIARADAAYNKAQRAADKAAAYALEKAQEKHGREILADEADMRLRRLFYADSEAKRLRRAGADVAES  
RAKTDVVRMLEQARADVRLKLEKDEVGAQKALEGLALLNRRFAGLPDAQVRVYRKARDYRAHFQVVRDALAERLARAGQDAETVR  
RLKERFPNELGGVYFPLARFGDYLVVVKDADGNSANVSRAETLSAEKLRDALKADFGAGFKVSPVMKSRDYIRSRDAVSGSFM  
ELGEAVGMLDLDPARARLNDTLTQLYLSLPDTSWAKHGIHRKGVPGFSDDARRAYAQNMGSGANYLAKLRYADRMABQLDVMQ  
DFVDGRKYEFGDQRLQORVADEMRRKHEAVMNPNSKLAQALTGFGLWMMGMSPAVAVNLSQTAMVAYPVMAAKWGYAGAAR

ELLRASQIGLRFGEKFTNTIEDSLNGDEKAAFRKAADYGVIDLQAHDLAVANGDPGLAGSAWQKVMKAAWLFHHAKEFNROV  
TFVAAYRLAKRAGADSEAAFEQAKATYDGHFYDAAQNRPRFMMGNAKVFLFKQYSONILYALGRNAYLAFKGDKEARKTLAG  
LLVSHAMASGILGLPFVSTLLAVASMLGSDDDDPWDAEALRNMLADAFGDKAGEVLAKGFSRLTFLDVSGRLGLNLQVLPDIQD  
GLEGKKWABSLVVGSTGAVVGAGIGAADGVRTRSSVPRNTANTLSLMSKW

## SEQ ID 85

ATGAGTGATTGGTCAGATACGATCCGTTGGAACACGGGCGGCTTGTCGGGGGTTTGAAGGAGTACCGCGGCTTTACGCAAAAGG  
ATGCGCGGGCGGCCCGACGATACGGCGTTGACGCGCGGTTTAAAAATTCTATGCGTTTCGGCGGATATGGGTTGGAATGCCCT  
TACGGGCGCAAAAGAGGAAGTGGGCGGCTCAAGGCGGAGGATATGGATTATCGGAAGATTACAGAGGGGCGCAAAATCCCAAGCG  
CGCAGGGAGTTGGGCGAGGCTTGGGAAAAGGGCGGGGTTGTCGGCGCGGCTGTGCAATGTGTGGGGGAGCTTAAGAAGGACT  
GGCGCGAGAAGGGTTTGGACGGCGCTTGAAGATGTGGGCGAGATGGCGGTTGCGGTGCTGGAGCAGGCGCCAATGCGCTTGT  
CCCTATTGCTACGGCAACCGCGCGGCATATTGGGCGCTTTGGCGGGCGGTAAACGCGGCTGTGCGGCTTATGCGGGCGCGACC  
TTGGGCAATACGCTGATGAATACGCGGGCAGCTGGACAGGGCGGAGAGGCGGGCGGCTCGACCCTGCGGACAAGGATGCGG  
TGATGGCGTTTATCGGCCGAGGTGCGCGGGTGCCTTGAATAATGCGCGGTAAGGGCGGTTGTCGGCGCGCGGATATGGC  
GGCGATGAACTTTGGCGCGAGTATTTGAATATGGGCAAGAGGCGCGGGAAGCGCATTTGAGAAAATGGGTGTTGCGCGC  
GCGGATAAGGCGCGGTTGCGGCGCTAAGGGAACGCTGAATTTGCGGCGCTGGCGAAGGAGTCTGCCAAGGCGGTTTGGGCG  
GTGCGGCACGGCACGCGCGGCTTATGCGACGGAATCGGCGGTTAGTTTGGCGGAGTATTTGGTACGGGGCTGGCAACGG  
GGAATGGGACGAGAAGGGGCGGCTTTGGAGGCTTTCTCTTCTTTGGGCGATTCTGCGGTGGGGTTTGGCGGACGAAGGCTTAT  
GCGGCGTAACCTGACCGCTCAGGCGCGCGCGGCGGACGGAAGGCGGGTGCAGGGGGTATCGGGGCAACAGGAAGGCGGGC  
AGGCGGGCCCCGAAGGGCGCAGGCGTTGCGTTCGGCGGCACAGGCGGCTGCGGACGGCGGCACAGGCGGCTGCGGACGGAGGC  
GCGGAACAGGGCGGCGGCGGTTTCGATACGGCGCATCAGCATAGTCGATCGGCTTTGCGGCGAGTTTGGCGACCGTACGAAGC  
AGGAGGAGGCGGGCGGTTTTCAGCGCGCTGCGGACGGCAATACGCGCACGCGGAGGAATTGGCGCGGGGACGGAACAA  
CGCGGATGTTTGGGTATCCGTCGAGGACGGGCGGAATTTTGGATACGGGCG

## SEQ ID 86

MSDLVRYDPLEHGRVLVGLKEYRGFTQKDARAAADDTALTRGFKNSMRMARMGNALTGDKELGRLKAEDMDYRKIQEGRKSQA  
RRELGEAWERGGVGGGLSNVWGLKDWREKGLDGALEDVEMAGAVLEQAPNALVPIATATAGGILGALAGGNAAVGAYAGAT  
LGNITLMEYGGQLDRAAEAGVDPADKDAVMAFIRGAPGALKNAAVKGAUVGAADMAAMKLGGSILNMGKKAAGKALEKMGVAA  
ADKAAVAAGKTPEFAALAKESAKGGLGAARHAAAYATESAGEFAGEYLGTGLANGEWDEKGAALBAFSSSLGSAVGFAGTKAY  
AAVTDPLRPPRGTEGGCAGGYRQEGGQAGPGRGAGVACGTTGGCGRRHRLRTEARNRAARVSIRITISIRILCGSLRITVRS  
RRRRGGFSAALPTAIRRTRNRWRAGRKNRSMFRVSRRTGRNFWIRA

## SEQ ID 87

ATGGGGACGGACGTACCGGAAACAGGCGTATTGCCCGATAAAAACGGCGAACCGCTGACTATCGGGGAATACCGGCTGTTTGTCTG  
GTGAAATGATGAACCAACCTGCATGGCGTGCCGTTGCCGACAAGGAAATGGACTACGCCGACGGCAGGCTTGACAACGAGCT  
TTTACAGAAACAGCGCGAGTTGGGCTTGCCCCCGCGCTTGAACCTGATTACCCCGACCTGCTGTGGTACAGGATATGAG  
GCGACGATACGGACGAGTGGCGCGTGACGGCGGACGGCGGAAACCGGCGGGCGGACGTCGCGGACGATTGAATTTCAAATCA  
ACCGCGCGAAACGGCAAAGCGGTGCCGACAAGGCTTGTTCGGACGCGTTACAGGGGCGAGATAGCCTGCGGCATCGGCTGGGTGGA  
GGTTACACGCAACCCCAACCTTTTCAGTTTCTTATGAGTGGCGGCTCATCCACCGCAACGCCATCCATTGGGATATGAAATCT  
TACAAATACGACCTGTCCGATGCCCGCTGGCTGATACGCGCGCGCTGGCTGCTGCCGGAACCGCTGGCGCAATTTCTCCCTGAAT  
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ACTGGCGGACGCTTGGGGTATTTCGGGGCGCAACCGCTCAGCGAAGAGTTTGGTTCAATGAAACACGCGCGAACTGGCGGTG  
GCTGAAGTATGCTACAGGCGGTGGGTAAACGGCAGACTGCTGCGCGACAAAAAAGAGGCGCACGTTGAGTTTACGCGCGCAA  
ACCCAAACCATCGGGAGATGGCGGCAACCGCGCGGTATTGTTTGGCGCTTCCGTCGCCGATGCGCGCGCCTTTGTCTGTTGG  
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ACCGCATCCCCTACGGATATGTCGCAATATGAAATACGCGCAGGACAACCTCAACAGCACCAACAGCAAATTACGATGGGGTT  
TGTCGGCAATACGACCGGTACGCAACAAAGGCATAGTCGATGCTCGGACGAACAGTTCCGCGCAATATCGCACGGGTGGAGCG  
GGCATCGTGTGACAAACAAATAGAGGCGCGCCAGCGCGCGCGCTTTTCGACGTCAGCGCGGATTTCAATTTGTGCGGACAGCAT  
TGGCAGATGCTTCAAGACAGCGCGCGACAATACGGCAGATCAGCGGATTACCCCGTCAATTTATGGGCAACCGGGGCAACGCCA  
CCAGCGGACGGCAGGAAAGCATCAAGTCGAGCAGTCAACAGTCGCTGGGCTGGTTATGGACAATTCGCGCAGAGCGGCTC  
ATTGTTGCGGCGAGTTGCTGCTTGGGATGATTATCGAGGATTTGGGCTCGGACGAGCAACCGTTCGTCATAGAAGGGGACGCGCTC  
ACGCAAGGGCGGACGCTGTCATCAACAGGCTGAAACCGACCCGTAACCGGCAAGGCTTATTTGTCCAACGACCTGCAAAACA  
TACGGCTGAAAGTGGCTTTGGAAGACGTGCCAGCAACTCTACCGCAGCGAGCAGTGGGTGCGATGAGCGAGGCGGTCAA  
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AAAATCAAAGAAGTCCGAGTGCAGGAAACGCCCGAACAATCGAGGCGCGTATCGCGCAGGCGGTGCAGGACGCATTTGGCAAAAT  
CCGGCAACGACATCAAACGGCGGGAATTGGCGCTCAAAGAACAACGTACCGCGAGCGAAATCAAGGAATCGAAGCGCGGCGGT  
ACAAATCGGCGGTGAGGCGGCTTACCGCGGCGATGAGGCGGGCGGCGAGATAGCGCCATGCCGCAATCGCACCCGTTGCCGAC  
GCGGTTCATGAGGCGCGGATATATCCGCGCGGCGGCGGCGGCGGACGATCCCGGCTTCCCGCTCCCGGCGATGCCGCTGAAACGC  
AAATACCGCCCCGAAGGCATCCCTGAAGCCTACGGCGCGGATACCGGCCGATGACGGCGGTGCGGCCAAGAGTGCGAATCACGC  
CCAAACAGGCATGGAAACGCCGAGCGGTGTCGGAACCTC

## SEQ ID 88

MGTDVPETGVLPDKNGEPLTIGYRLFVGEEMNQPAWRAVADKEMDYADGRQLDNELLQKQRELGLPPAVENLITPTLLSVQGYE  
ATIRTDWRVTADGETGGRDVADALNFKLNRAERQSRADKACSDAFRQIACGIGWVEVTRNPNPFEPFYECGVIRHNAIHWDMKS  
YKYDLSARWLIRRRWLLPERLAQFFPEYAGHFAMGRGGSOWRISGEMLDGGGNTGLADAWGISGRNTVSEEFWFNETTRELAV  
AEVWYRVVNTADCLRDKKTGRVVEFDGANPNHREMAANGAVLFAASVPRMRRFVVGDLVVRDEPTPYPHQKFPYVVPFGFREDN  
TGIPYFRRWYADQNLNSTNSKLRWGLSAIRTVRTKGVLDMSDEQFRRNLARVDADIVLNKIEAAGPARGFVSRDFELSAQH  
WQMLQDSRATIRQISGITPSFMGNRGNATSGRQESIQVEQSNQSLGLVMDNFRQSRSLVGELELLAMIIEDLGSDEQTVVIEGDAV  
TQGRTVVINRPETDPVTGKAYLSNDLQNLRLKVALEDVPSNYSRSQLGAMSEAVKSLPPEYQAAVLFPVMSLMDIPFKDKVIE  
KIKEVRVQETPEQIEARIAQAVQDALAKSGNDIKRRELALKEQRTASEIKEIEARAVQIGVQAAAYAAQAGQIAAMPQIAPVAD  
AVMQGAGYIRPARGDDPGFPVPAMPFETQIPPEGIEPAYGADTGPMTAVPPKSANHAQTGMETPTVSDNL

## SEQ ID 89

ATGACGGGAAAGACGGTTGATTGAAATTGCCCGCAAACTGGACGGGCTGTTCAAGCCTTGCCGGGTACAAGGTTATGTACGGCG  
GGCGCGCGCGCGGCAAAATCGCACGGCGCGGCATCCGCACTGCTGGCGCTGGGGGCGCAACGCCCTTTGCGTATTTTATGCGCGCG  
CGAAATTCAAAAATCGATGCGCGATTCCGTACACCGCTGTTGAAAGACAAAGTGGCGCAGTTGGGTTGGGGCATTCTACGAA  
ATAACCGACTTCGAGATACGAGGCGCAACCGCACCGCTGTTGTAATTTTCGGGCTGCGAGTCGCATACCGTGGACAGCATCAAA  
CGTTTGAAGGTATCGACATCGTATGGGTTGAGGAAGGGCACGGCGTCAGTAAAAAAGCTGGGACGTGCTCACGCCGACCATACG  
CAAAGAAGGTTCCGAAATTTGGATTACCTCAATCCCGATATGGAGACGGACGAAACCTACCGGCGTTTATCGCTATGCCGCTCC  
GAAGACACTTGGCTTTGCGAAATCAACTGGCGCGACAATCCGTGGTTTCCCGAAGCATTGAACCGGGAGCGGCTCAAAGCACAGC  
GTTTCGATGAATAAAGAGGACTACGGGAATATTTGGGAAGGCAGGCCGCGCATGGTATCGGAGGGGGCGGTTTACCGGCATGAAAT  
ACAGGACGCTTTTCATTCCGGACGCGTTACGCTCGTCCCTTATGATTCTTCTTGGCCGTCATACGGTTGGGATTGGGGCTGG  
AAGCATGCCATGACCATCGGGCTGGTGCAGCGGATTGACGAGCGTGCGCATCATAGGCTACATCGAAGACACGCACCGGACGT  
TGGACTGGTATGTTGCCGAATTGGAAGAGCTGCCCTACCGGTGGGGGACGGACTTCCTGCCGACGACGGCAGGACGCGCAACTT  
CCAAACAGGCAAAAGTACGATGGAGATTTTGACCGGACTGGGGCGCAAGTCGGTTTTCGTGCAAAACGCGACCGGTATCGAAGAA  
GGCATCAGGGCGCGCGGATGCTGTTTCCAAAGTGTACTTCGATAAAGACAAACAGCGCGGCTTTTGGAAATGCCTGAAACGGT  
ACGGCCGCAAAATACATGCGAAACAGGCGTGGCAATGGGGCCGTCGACGACGAATATTCGACGGCGCGGATATGTTCCGCTA  
CCTGGCGCAGCGGTTGATTAAATGGATACAGGCAGCAATACGGGATACCGGAACGCCCGTATCGGATTGGAGGCTTTAT

## SEQ ID 90

MTGKTVDLKLPALDGLFKPCRYKVMYGGRRGGKSHGAASALLALGAQRPLRLCAREIQKSMRDSVHRLKDKVAQLGLGHFYE  
ITDFEIRGANGTLFVFSGLQSHTVDSIKSFEGIDIVWVEEGHGVSKRSWDVLTPTIRKEGSEIWTILNPDMEIDETYRRFLAMPS  
EDTWLCEINWRDNPWFPEALNRRLKAQRSMNKEDYGNIEWGRPRMVSEGAIVYRHEIQDAFHSGRVTLPVYDSSLPVHTVWDLGW  
NDAMTIGLVQRDLTSVRIIGYIEDTHRTLDWYVAELEKLPYRWGTDPLPHDGRTRNFOTGKSTMBELTGLGRKSVFVQVATGIEE  
GIRAARMLFKVYFDKDKTARLLECLKRYGRQIHAKTGVAMGPLHDEYSHGADMFRYLAQAVDLMDTGSNTGYTETFPVSDWRLY

## SEQ ID 91

ATGATGAAGCCGTCTGAAAGTTTGAGAGCGGCAGGCAGGCCAATCGCGTATTACCCGAAATTGGCAAAGCCTTTGGGCGGTGTAA  
ATGCGGCAATATTATTTCGGGCATTCTTCTACTGGAACGATAAGACGCAGTATGAATCAGGCATTACCGAAGCAGCGGAAGAAAT  
TGAAATTGAAACCGGGCTGTCGTTTCAGGAACAAGAACGGCACGGGCAAGAGCTGAGGGAACCGCGCGTATTGATTGAGACTGAA  
AAACGAATTGAACACCGCATTTACTACAACTGAATTTAGACGCTTTTGATGATTGATGTTGCAACATTCCGGGGGTGGGGAAC  
CAACAGCCCCGAAATGCAATATCAACAGCCCCGAACTTCAAAATCAACATTCGGGGGAGTGGGAATCAACAGCCCCGAAATGCAATATCAACAGCCCCGAACTT  
TATCAACAGCCCCGAACTTCAAAACCAACATTCGGGGGAGTGGGAATCAACAGCCCCGAAATGCAATATCAACAGCCCCGAACTT  
CAAAATCAACATTCGGGGGAGTGGGAATCAACAGCCGTTATAAGAACAGAAGATTTAACAGAAGATTTAGCAGTATATACCCCT  
TACCCCCAAACGCCGAAACGGCAAGGCGGTTTGAACGCTGACGCGTTTGTTCGCTGACCGGAAACGTCGGGCGGGGAAC  
CGGCGAACCGACTTCGCGGAAGGCCGAAAGCGACAGTAACGGCAACGGCGGCTTTTCGGGAAACCGGAAATGCGAATGTTCCG  
CGCCCGCGCAAAACCCACGGCGTACCGCTTCAGGAATCGCCGATTTGTACAACGAAGTTTGGGGCGCCGGTTGCCAAGCGTCC  
AAGTGCTGAACGACACGCGCAACGGGCGATTGCAAAACCGCTGGTGCAGATGCTGGGAACGGCGCGCCAAACGGCAAGGTGAG  
GTTCCGGGACAAGGAAACCGTTTGGCCTGGTTTTCGCGGTTTCTTCGGAAGTGGCGATGAACCGGTTTGGATGGGCGAAAC  
CAAACAGGGTTTGGCGTGGCTTCGATTGGATTTTCAAGGCGGCAATTCGTCAAAACTCTGAATGGCATCCGCTAAACGA  
ACCAGCGCGCAAGGGAAGGCA

## SEQ ID 92

MMKPSLSRAAGRP IAYYPKLAKPLGGVNAAILFGHFFYWNDKTQYESGIYRTABEIEIETGLSVQEQRTARAKLRERGVLIETE  
KRIEHRITYKLNLDAFDDMLQHS GGGEPTAPKCNINSPELQNHSGGGEPTAPKCNINSPELQNHSGSGESTAPKCNINSPEL  
QNHSGSEESTAVIRTEDLTEDLAVYTPLPNAENGKGLNADAFVSADAETCGRETGEPTSPKAESDSNNGGLSGKPKNANVP  
RRRKTGHVPLQEIADLYNEVLGGRLPSVQVLNDTRKRAIANRWCEMLGTAAPNGKVRFGDKETGLAWFAGFFRKVAMNPFWMGEN  
QTGFVAVGFDWIFRAGNFVKILEWHPPKTNQAARGRA

## SEQ ID 93

ATGAGCAACGGCGCGCGTTGGACGGTTACCAATGATTCAATGCTGAAAGAGTTGGATTGTCGGAAGACCGCGAGGTCGAATTTA  
GCGACAACAATAAATTCGTCAAAGTGTCCGTGAGCAAGCTCAAGGGCGATGGCGCGTGTCAAATGTATGGCGACATCGTCAA  
AGGAGAATCGGACAAGCTGATTACCGGAAAGGCAGCGAAGGGACGCACATCATCGAATATATGGACGATGCCAAGGCAAAAACG  
ACGGGAAGGGAATATCTGAACTGGTCGAAAACAAGGGCAATCAAGAAGACAATAAAGCATCAAATAAAGCATCATACAAATTGA  
ATGTCGCTGTACGGAACAGGGAGGGTGGTGTTCCTTGGCTTGGGTGAGTCGGGTGCTTCCAAAAGGTCAATATTTCCACAGACGG  
TAAGCGGGACTTCTACCTCTACCCGGATACCTGACGCCGGCGCATCGAGCAGCGTCCCTTCGGCGAGGCGTTGTATCAGTTG  
AACCGCGTTTCCGATGAAACGCTGGTGCAGCGTATGGGCGAAATCCACGCCGACGGAATGCCGAGGAAGACAACAGTTTGGGA  
TCAAACGCGTCCGGCGAAATTTCCGGCAGCGCAGCGATTACCGCGTGGGCGTTACGGCAACCGCTATTTGGGCTTTGCCGG  
CGGCTTCAACAGGACGGGGTTCCGGCGATAAATGGATTCAATACAAAGGGCTGATGCTCCGCCACCTCCAATCGTCCCTACGCTTC  
GAAGACTACGTCGGCAGCGGCAAAATCTTACGGCAGGGCGGCGAGGTGTTTATTCGCTGGCTCAACCGGGAAGCAGGGCTTAT  
TA

## SEQ ID 94

MSNGARWTVTNDMSMLKELDLSEDAQVEFSDNNKFVKVSVSKLKGDDGVFKMYGDIVKGESDKLITRKSGEGTHIIEYMDAKAKT  
TGREYLKLVENKGNQEDNKASNKASYKLNVRCTEQGGWCFALGESGASKVNIISTDGKRDYLYPDTLTPGASSSVLFGEALYQL  
NAVSDETLVQRMGEIHADGMPQEDNNVWIKRVGGKFSGRSDYRVGGYGNRYWGFAGGFNRTPGDKWIHYKGLMLRLHLQSSYAS  
EDYVGSKILRQGGRCFLRLAQPGKQGLL

## SEQ ID 95

ATGACCGATATTTTCACTCCATCCAAACGTTCTTCTGATGTCAAAAATCCATAGCAAAGAAACCAACCGGAAGTATTGGTAA  
GGAAATTTCTTTTCCCAAGGTTTCCGTTATCGGAAAAACGATAAGCGCTATGACGGCAACCGGATATCGTTTTCCTAAATA  
TAAACAGTCGTGTTTATACACGGCTGTTTTCGACAGGGCATTCTTGTAAATAAAGGACATATCCCGAAAAGCAATATGGATTTT  
TGGTTGGAAAAATCAAAAAATCGCGAACGTGATATTAATAAAGACGAGCTGGAAAAGATTGGTTTCAAAGTGATGTGTCG  
TTTGGGAGTGCGAATTAATAAAGCTATTGTAGGGAGCGATTAAATCGGTTGGTCGAGGAAATAAAGATGCCGTC

## SEQ ID 96

MTDIFTPSKRSFVMSKIHSEKTKPEVLVRKFLPSQGFYRKYRKNDRYAGKPDIVLPKYKTVVF IHGCFWGHGSCNKGHI PKSNMDF  
WLEKITKNRRERDIKNETELEKIGFKVIVVWECELNKAICRERLNRLVVEIKDAV

## SEQ ID 97

GTGAAAGGTGAAAGCGGAGTTGATATCGAAAAATTGAAAAACAAATTGCCAGAAAAGGAAAGAGAACCGGTAGAGTTATTTTGA  
ATCGTTTGGAAAGATTTCGGAGCTTACAAATAAAGAACAAAGCGGAAGTAATCTCTGCCTTACATAGTATTATTCCAGAATATCCTTA  
CTATCATTGGCGGCATTTCATCAGGATTTCATACCTGCTGTAACGATTTTACAAATGAAAAGAAGGATTATTTAAGTGCTGCA  
ATCGAGGCAGTTAAAGTTTTCGAAGATAAGGTTTCAAGCAGACAGGCTTTCATAGCATAGACGGAAGAGAAATTGATTGAAAAAG  
CCTTCGGGAGTAAAAAATCTATGCTTCTATTAACGAATAACAAAACGAGGCGGAACAAAATTTAGAAGATGGTCTTTGAACAGCT  
TGCATGCGGAACATGGACTGGATTAGAAATCCTGTGCAACATGAGTTAAGAGCAAATTTATCTCCTAGTATTTTAATGACAAG  
GATGCTTTGGATTAAATCAGCTTAGTTTCATATTTATTGAGAAAAGTGAACAAACAAAAAACGAGCTAAACCTACATCGCCT

## SEQ ID 98

VKGESGVDIENWKNKLPKEREPEVEILNRLSELTNKEQAEVISALHSIIPEYPPYHWRHLHQDLHTACNDFYNEKKDYLSAA  
IEAVKVFEDKVQRKTGLHSIDGRELIEKAFGSKKSMLLLNNKTQAEQNLEDGLEQLACGTWTGFRNFPVQHELRLANLSPSIFNDK  
DALDLISLVSYLLRKVEQTKKRAKPTSP

## SEQ ID 99

ATGTCCTGAAGAAAAATTGAAATGAGTTTCGAGCCAACCGTAATCGAACATTTGGGTGTAAAGATGTATTTCGCACACTGTTTCCTG  
CGATTGCCGAGTTGATAGCGAATGCCTACGATGCATGTGCTACGGAAGTGGAAGTTAGGTTATTTCGATAAACCGGAGCATAAAAT  
CGTTATTAAAGATAATGGCATAGGAATGAGCTTCGATGAAATCAATGATTTTATTGAGAAATCGGTCGGAACAGAAGGGAAGAA  
AAACAAGCCTCCCGTGGCGAAGAATTCCAACGGGTAAAAAAGGTCTTGGTAAATTGGCATTATTACAGCTTGGCAACAAAATCG  
AAATCTCTACTATCCAAGGAACGAACGGGTACTTTACTTTGGATTATGCAGAGATTAAAAAAGTGAGCGTATTTCATCAACC  
GGAGTTTCAGAAAGAGTCTGTAAACCCAATACCGAAACGGAACAACTATACTTTAACCGAGCTGACGAAAAAACAAGGATAC  
CCGTTAGATAAATTATGTGGGGCATCTTTCCCGTTTATTGATTTTCGGCTCAGGATTTTAAATCAAAGTAAGCTTGAACGGCT  
CGGAACCAAGAATCATTGACGGAACCTAAAATATAATCTTGTTTACCCACAATTGGAATGGGAATACAGGATCTAGCAACCAA  
TATTTTCATCGTTATCTTCAAATTCGAACAGTATGAATACAGCGGATTAATACAAGGTAAGTTTATTACAACGGAACAACTTTA  
AAGAATAATATGAAAGGTATTACGTTGTTTGCCACGGCAGAAATGGTAAATATGCCCGAGTTTTCAGTGATAGCGAATCCAGCC  
ATTTT

## SEQ ID 100

MSEELKMSFEPTVIEHLGVKMSYHTVPAIAELIANAYDACATEVEVRLFDKPEHKIVIKDNGIGMSFDEINDFYLRIGNRREE  
KQASPCGRIPTGKGLGKLALFRLGNKIEISTIQGNERVFTFLDYAEIKKSERIYQPEFQKESVKPNTENGTTITLTTELTKKQGY  
PLDNYVGHLSRLFDPAQDFKIKVSLNGSEPRIIDGNLKNLVTPQFEWEYQDLATNISSLSKFEQVEYSGLIQGKFITTEKPL  
KNNMKGITLFPANGRMVNMPEFTDSESHF

## SEQ ID 101

TTGGGAATGGAACCGCTTTCCCAAAATTATGGCAGGACATCAAGACGAGACGGATTTTATGCATAGTTGTGCGGGATTATCCG  
ATATCAATTTGAAACGATTGGCTTTGATACCTAAAAACGGAGGAAACCGTTTGGCTTTTGGCGATATTTCCGAATTACAGCTGGA  
ATGTTTATCGGAAAAGACAATAGTTTAAAGACAGCTTCGGTAGGCTATGGTGGGATAAGCCCGACCTACCATAACGACCAAA  
TTCTTTAGCATTTCCAACGGGCGGTTTGCCCATCTGAAGAAGATAGGGCGTTATCCCTGCGAGAAGGTGCAACATTGCAATCGT  
TCCCTCGTAACATAGTCTTTAAAGCGGCAGTAGGGACAAGATAGCCCGTTTGATTGGTAATGCCGTTCTCTCCGATGTATACGGA  
AAAAATAGGCAGGCAATTGTTGATAATATCGAATGT

## SEQ ID 102

LGMENGFPKIMAGHQDETFMHSAGLSIDINLKRLALIPKNGGNRLAFAHIPQLQLECFIGKDNFSDTFGRLLWWDKPAPTITTK  
FFSISNGRFAHPEEDRALSLREGATLQSFPRNYVFKAGSRDKIARLIGNAVPPMYTEKIGRAIVDNIEC

## SEQ ID 103

TTGCAGCCTGAAACCTTTGAAAAAGAACTCGGCTTAAAAAAGAAATGATGATGATTGATTCTTATAGGTTGTAGTCTTGTCAAT  
ATTGGAGTGTTATTCAAACAGACAAAAGAAAATCGGAAAAATCCAAGAGTTTGCTTTTGGAGTTTCAGCGGTTTGTAGAATATTT  
CAATCCCGGATATGTTGTTGTAGAGAACGTACCGGAATTCTGAGCAGAATGAAAGAAAGCGGGCTTGATAATTTCAATAAGTTA  
TTGGAAGAAAAAGGATTACCGTCCATTTCGGTATTCACAATACGGCTGATTACGGAATTCCTCAAGCGGTAAAGATTACGT  
TAATTGCAACAGAATAACCAAAAAAGCTGGAACCAAGTCAAGTATTCGGGCAACCGCTTACGGTACCGGATGTTTGGGAATG  
GAAACCGCTTTCCCAAAATTATGGCAGGACATCAAGACGAGACGGATTTTATGCATAGTTGTGCGGGATTATCCGATATCAATT

## SEQ ID 104

LQPETLEKELGLKNDLILIGCSPCQYVSVIQTDRKSEKSKSLLEFQRFVEYFNPQYVVENVPGILSRMKESGLDNFIKL  
LEEKGFTVHFGIHNTADYGIPQSRKFTLIANRITKSWNQSSIRANGLRYAMFWEWKTAFFKLWQDIKTRILCIVVRDYPISI

## SEQ ID 105

ATGAATTTACCTTTTCGGGCAATGGTGTCTGATTAGGTGGCACACTTTTAAACACCTGAACATTTAGTGGGTGATCTTACCATTG  
ATACTCTGAGAGTATTAGAGCAAAAGGCGTAGATATTATTTTGGCAACAGGACGCAATCATACCGATATGTCATCCATTCTTGG  
AAAAATCGGTCGCGAAGCGTTCGGTTATGATTACATCAACCGGTGCTCGTGTACGGGATTACAGGGTAATTTGCTTTATAGCAAT  
AGTTTGCCTGAAGAATTAGTTCTCGAGCTTTACAAAACATCATATGTGGGAAATCTTATTACAGACCAAGATTTTGTGCCCATC  
AA

## SEQ ID 106

MNLPFRAMVSDLGGTLLTPEHLVGDLTIDTLRVLEQKGVDIILATGRNHTDMSSILGKIGAERAVMITSNGARVRDLQGNLLYSN  
SLPEELVLELYKTSYVGNLIQTFRFCRHQ

## SEQ ID 107

ATGGAAGAGCAACTTGCCCAAAACGACCAGCGCTGTAACAACTTGTCCGCCGTGTACGGCGCTTGGGCAGAAGGCGGCGCAGGCG  
TTTGGTGACGGGCAATGTGATGGTGGCTGAAAGCGGCAAGGTTGATAAACGATGTGTTGATTTCAGACGACCGCGCCCTTGA  
AATGCTGAAGAAATGGGCGAAAGCCCGCAGCAAAACGACACGCTGCTCATGCAATCAATCATGCGGGCAACAGCTCGCCT  
GCGGTGGTCAATAAAAACCGCTTGACCGAGCGCGCTGCCGCTGGTGGGCATGAATGGCTTTATCAATCCGCGCGCGCAATTGA  
GTGCCGATGAAATCAACGGGCTGATTAGCAATTCGTACAACTGCCAAAATTGCCGAACAGGACGGCTTTTCAGGCGTACAAAT  
TTACGCCGTACACGGTTATCTCATAGCCAATTCCTCTCGCCGACCAACCGCCGCAAGACCAATGGGCGGCGAGTTTGGAA



AACCGTATGCGCTTCCTTTTGGAAACCTACACCGCTATTGCGCGCTGCCGCGGGCAAAGATTTCTTGGTGGGCGTAAACTCAATT  
CGGCAGATTTCCAAAAAGGCGGATTGACGAAAGCGAATCGGTGCAGGTGGTGCAAAACTGTCCGAAATGGGCATTGATTTTAT  
TGAAGTTTCCGGTGGCAACTACGAAAGCCCGCAAATGCTCGCCGCAAAGACAGCACCCGCAAACGCGAAGCCTTCTTCATCGAT  
TACGCCGAAAAAGCCCGTGAGCCAGCCAAGCCCGCTGATTATCACCGGCGGATTCCGTTCCGAAACCGCCATGGAAGATGCCT  
TATCCAGCGGTCACTTTGGATTGGTTCGGCATAGCCCGCCCGTTTCCTTAGTCCCTGATTGGCGAACAAAATGCAAAACAGAAC  
TTACCAACCGGTACAAGCAGACCGCATCCAACTGGCGTAGCATTTGTTGATAAAAAAGCGGGTGCATGTTAGAAATGAAGTGG  
TATATGACGCAAAATGGATTGATCGGACAAGGAAAAACAGTCCAACCTAAAATTGTCGGCGTGGAAAGTATTGCTGAAAACCTTG  
CGGAAAAACGG

## SEQ ID 108

MEEQLAQNDQPSSEKLVRLYGAWAEGGAGVLVTGNVMAESGKGSINDVLSDDRALEMLKKWAKARTQNDTLLIMQINHAGKQSP  
AVVNKTPLAPSAVPLVGMNGFINPPRELSADEINGLIQFVQTAKIAEQAGFSGVQIYAVHGYLISQFLSPHNRRQDQWGSLE  
NRMRFLETTYTAIRAAAGKDFLVGVKLSADFQKGFDESESVQVQKLSEMGIDFIEVSGGNYESPQMLAAKDSTRKREAFFID  
YAEKARAASQAPLIITGGFRSQTAMEDALSSGHLDLVGIARPFALVPLANKMQRNTYQTVQADRIQTGVAFVDKAGAMLEMNW  
YMTQMDLIGQKGQSNPKIVGVESIAENFAGKR

## SEQ ID 109

ATGCCGCAACAAACCATGAATTTAATGCGCGAGTGCATACCCATTTTACCGTATTGAGCGATGAAAACCGCCATCAGATCCTGC  
ATGTATTGTGGAAACACGGTAGGATGAATGTGAATGAGCTGACCGAGCATCTGCATCTGTGCGCCCTGCTGTGTCGCACCATTT  
AAAAATCATGCTGCAAGCCGGAGCGGTGGCGGTGGAGCAGGTCCGCAAGAGCGGTTTTACAGTATTGCCATGGCGGATGCGGTG  
CGGAGATTGAAAACAGCTTGCCGATTGATGGCTCAAAATGCCCCGCTTTCAAAA

## SEQ ID 110

MPQQTMMNLMRECIPIFTVLSDENRHQILHVLWKHGRMNVNELTEHLHLRPAVSHHLKIMLQAGAVAVEQVGKERFYSIAMADAV  
ARLKLADLMAQNCPLSK

## SEQ ID 111

TTGTACAAACAAATATGCGGACTGGAACAGATTATCCTACAATGCGCCAAATTTATGTTGGCAAGGCCGTCCCCAAAGGCTGGCGGC  
AAGCAAGAAATCTGATAATGCGCTAAACCAATCAACCGAAGTGTCCACCGGTGAAAGAACACAGCAGGAGTATTGCCGCTGT  
TTCTGATTTAGATCCTTCCGATTTCATGTGCAGATTCTGTTATCTTTGAAGGTGCCGCTTCTGACATGATAGGCACAAATCGAAGCT  
GCCCTGATTAAATTACACAAACCTCTATGGAACCTCTGTGTGTCGATGTTTCGGAACACAGACCCCGAAAAGGCCGTTACGAAC  
AAGCCAAATCGGATTGGGATGTCTTTCATAGCGGGCGGTTTGGGCAGATAGGCTAAACCGGCATACCGAATAGCTATGATCCAT  
ACTTGAAATATCAACACACATTTAGAGATAATAAAGAGAAAA

## SEQ ID 112

LYKQYADWNRLSYNAPIYVGKAVPKGWRQARNSDNALNQSTELFHLRKEHSRSIAVSDLDPSDFMCRFVIFEGAGSDMIGTIEA  
ALIKLHKPLWNSCVDGFGNHDGPKGRYEQAQSDWDVLHSGRVDADRLNGIPNSYESILENINTHLEIIRK

## SEQ ID 113

ATGAAGTCTTTGGAAATTTTTCGGCGCGGGCGGTTGGCAAAAGGCCTTGAACCTTGCAGGATTCCAACATGCATCTTTTATTG  
AACTCAATAAAGATGCATGCAATCTTTAAGAAGCAACTTTAACCCCAAGCTTGTATTATCAGGGAGATGTGGCAGATTTTGATCT  
TTCCAGTCAAGAAGGCATAGAAGTCATTGACGGCGCTCTCTCTGCCAGCCCTTTTCATTGGGCGGGAACACCTTGCCCATGAA  
GACAGAAGGGATATGTTTCTCATGCGGTGAGATATGTGGAGTATTACCGCCCCAAGCTTTTATCTTTGAGAAATGTAAGGAC  
TTTTAAGAAATCATTGCTGATTATTTGAATATATCTTCTGCTTACTTATCCGAATCTTGGTATTTTGCAGAAATGAAGA  
TTGGAAAGGCCATCTGACACGCGCTGAAAGAAATGAATTCAATTTATATAAAGGAATCAAATATAAGGTTTCATATCAATTTGTG  
AATGCAGCTGATTACGGAGTGCCGCAAAACGCGAAGCGGTGTTATCGTAGGTATCCGGCCGATTGGGATTTGATTGGAAAT  
TCCCAAAAGAACACATTCCGAAGACAGGTGAATTTGGGAAAAGTATGTAACGGGGGAATACTGGGAAAAACACAACGAACCCAA  
AAGATTCAATAAAGATATTGCTGAAAAGTTACAAAAAAATACGGTATATTGGAACAGAAAAAAACCTTGCCAAACGGTAAGG  
GATACCTTGTCCGACATCCCGCATCTTTGGGGAATCATAAAATTACAGGACATGAATATAGGGATGGCGCAAGAAATTTATCCCG  
GACACACAGGAAGCGGATAGACGAACCGTCCAAAACCATTAAGCAGGTGGGCATGGCGTTCGCGCGGAGAAAAATATGATTG  
TTATGATGATGGAACAGTCAGATACTTTACCAGCTATGAAGCAAACTTCTTCAAACATTCCCTGAAGAAATTTGTCATTCTGGA  
GCTTGGGGAAGCAATGCGCAAAATGGCAATGCGGTCTCTGTCAAATTTGCGGAAATTTTAGGCAACATCTGATGGGGGTGT  
TGTCCGAGAAAAGCAGCCTGCACAAC

## SEQ ID 114

MKSLEIFSGAGGLAKGLELAGFQHASFIELNKDACNSLRNPNKLVYQGDVADFDLSSQEGIEVIAGGPPCQPFSLGGKHLAHE  
DRRDMPHVAURYVEYYRPAKIFENVKGLLRKSFADYFEYILLRLTYPNLILQNEWDKHLTRLKEIEFNLYKGIKYKVSQYLL  
NAADYGVPOKRRERVIVGIRADLDIDWKFPRKTHSEDRLNWEKYVTGEYWEKHNEPKRFNKDIAEKLQKKYIGIFEPEKKPWQTVR  
DTLSDIPLPLGNHKITGHEYRDGARIYPGHTGSGIDEPSKTIKAGGHGVPGENMIRYDDGTVRYFTSYEAKLLQTFPEEFVISG  
AWGEAMRQIGNAVPVKLSEILGKHLMGVLSEKSSLHN

## SEQ ID 115

TTGTCCGACATATCGGCTTCGCGGCTGCCTATATGGATGTGCAAAAACAATATCCCTTTGAAACCGTCGCCGTATGCGTGCTGC  
CGAACCATATTCACGCCATTTGGACGCTGCGCCCCGACGATGCGGATTTATCCCTACTCCGCGCGCTGATTAAACCAAATCTCT  
CGCATATCCCCTCATATAAACTTAGGGGCTGTACTAGATTATCCC

## SEQ ID 116

LSDISASRAAYMDVQRQYFFETVAVCVLPNHIHAIWTLPPDDADYSLRLRLIKTKFSAYSPHTNKGAVLDYP

## SEQ ID 117

TTGTTCAAATGGCTTATATTTTGGATTGTTAGAATGAATACTAAAACAGAGTTACAAAACTTTTAGAAGAGGATATATCAACTT  
TAAAGAAACACTAATTCGTGTAGATGCTCTTCCTCCAAGATATGTACSTAGCATTCGAACCTCTATTGTCGCTCGATGGTTAAT  
TGACAAACAATTAATATTTCTCGCAAAAGAAATAGGTTTAACTATAGAATTGCCCATCTTGATACAAGTTTGGTATTTGAAAAA  
TTGTCAACCTTAGAGAATAAAGTTAATTTTTATAGTAGATTAACAAAAATCAGGACAAGCGCGGAGCCGAGACAGTACAAATA  
GTACGGCAAGGCGAGGCAACGCCGTACCGGTT

## SEQ ID 118

LFKWLIFWIVRMNTKTELQKLEEDISTLKETLIRVDALPPRYVRSIATPIVRRWLIDKQLNILAKEIGLTIELPILDTSLVFEK  
LSTLENKVNFSRLTKIRTRRAADSTNSTARRGNAPV

## SEQ ID 119

ATGGCTGGTGGAGTTTATTTAGGCGGAAAAATTATTAGCCCTATATATCATTCATCACAAGAATTTTCTGGTGAACCAATAATCT  
ATGCTGAAACAAATATAATTTTATGCTGCTGAAAAATTTTAACTTTAAACAGAGTTTTCATAATGGAAATATTTTAAATAT  
GAATCAGATAATTACTTTTATCCAATAAACAGGGGGAGTACGTTTTGATAAAAATTACGATAAATATAAACTTGGCAAGTT  
GCTATAGAAAAAGCAGCAAAATTTTAAACCTCGTAATCCATATAAT

## SEQ ID 120

MAGGVYLGKKIISPIYHSSQEFSGEPIIYAETNIILCPAEKFLTLKRVFHNGNIFNMNQIITFLSNKQGGVRFDRNYDKYKTWQV  
AIEKAANFLKLNPNYN

## SEQ ID 121

ATGACAGAAATTACCGTGGATAGCCGAAGCGAGAGGCACATCGGTTTGAAGAATAATCCCGCGCGGAAACACAATCCGACGATTG  
TGCAATGGCTCAAAGAGACGGGCGGCTTCCCGCGCGCGGCAAGTCTTGGTACTTTGAAGACGAAACGCCGTGGTGGCGCTGTT  
TGTCGGATACTGCCTGGGCAAAAGCGGACGCGCGGTATCAGGGACTGGTATCGCGCCAAAGCCTGGTCAATGTCGGGTTTGACG  
AAACTCGAAGCCCCCGCATACGGCTGCATCGCGGTCAAACCGCGCGCGGGCGGCGGACACGTGTTCTTGGTGTGCGGCAAGACG  
CGGAAGGCAGAAATCTTGGGCTTGGGCGGCAATCAGGGCAATATGGTATCCATCATCCCGTTTGACCCTGCGGACATTGACGGCTA  
CTTCTGGCCGTCCAAGCTGATTGGCGGCAAGCCGTGCCTTCGTCCCCCGCGAAGGGCGTTACCGGTTGTCTGGACGTTGCCGCC  
ACGGCGAAACAGGGCGCGGGCGAGGCC

## SEQ ID 122

MTELPWLABARRHIGLKEIPGAHNPTIVQWLKETGGFPGAASWYFEDETFWCGLFVGYCLGKSGRAVIRDWYRAKAWSMSGLT  
KLEAPAYGCIADVPRRGGHVFFVVGKDAEGRILGLGNQGNMVSIIIPFDPADIDGYFWPSKLIIGKAVPSSPAEGRYRLSDVAA  
TAKQGAEGA

## SEQ ID 123

ATGATTGGGGCTTTGCTGAAAAATTGGAAGCCGCTGCTTATTTGTCCGCAATCGCGTTCTTTCGCCGTTTCTTGGCAGCTGGACA  
GGGCGGCGCAATACCGTCCGCGATACGGTGCAGCGGTGTGCGAGGTTTCGGAACGCCCTCAAAGCCGCGCGGTGCAACACGCCGA  
ACACGCCCGCAAATCGTCCGCGGTATCAGGCGCAAAAGCGCGCGCGGAGGAAAAAGAAAGGGTGGCTATGTGCAACGCTT  
AAAATCATTGAAAAACCTGTGTACCGCAATGCCTGTTTGTATGCTGACGGCGTGCAGCAACTCAACGCCCGCTTACGACGCGCG  
GT

## SEQ ID 124

MIGALLKNWKPLLILSALFAFFAVSWQLDRAAQYRRGYGAAVSEVSERLKAAAVEHAHARKSSAAYQAQKAAREEKERVRYVQTL  
KIIKFPVYRNACFDADGVRELNAVDDGG

## SEQ ID 125

GTGCGGCATCGGTTGTTGTCCGGATCGGTACGGCATTTTCATTTCCGCCCATTTATGGTGGCGCTGATAATTTTGTATAACGCC  
CCTTCGCGCAAAACAAACGGCAAAATTTGCCGCGTCCGCCGATATGTAAAAAATCGGGGGGAATGCCGACACTTCCCCCGATG  
CGGCCGCCAACCCGGAACCGACGGTTCGGTTGCAAACTTCCGGTTGACAACTCAATCCGCCGCCAACCGCCGTACCGCGCGCGG  
TGCCCGCGCCCTGCAGTCTGTTATACATACCGGCCCGCTTCAGGGCCACGGCAGCAGTCCGCGCCCGTGTCTCCCTCAAGGTGCG  
GCAGTTTCGGGCAGGGCCGACCAATCGGCGGGCGGCTTAACGCCGCTGTCACAGCGCGCGTTGAGTTTCGCGCACGCCGTGAG  
CATCAAAACAGGCATTGCGGTACACAGGTTTTCATGATTTTAAGCGTTTGCACATAGCGCACCTTCTTTTCTTCGCGCGC  
CGCCTTTTGCCTGTATACGCGCGGACGATTTGCGGGCGTGTTCGCGGTGTTCGACCGCGCGCGCTTTGAGGCGTTCCGAAACC  
TCCGACACCGCGCACCGTATCCGCGACGGTATTGCGCGCCCTGTCCAGCTGCCAAGAAACGGCGAAGAACCGGATTGCGGACA  
AAATAAGCAGCGGCTTCAATTTTTCAGCAAGGCCCAATCATTTACGCTCGCCCGCGCCCTGTTTCGCGGTGGCGGCAACGTC  
CGACAACCGGTAACGCCCTTCGCGGGGGACGAAGGCACGGCTTTGCGGCCAATCAGCTTGGACGGCCAGAAGTAGCCGTCAATG  
TCCGACGGGTCAAACGGGATGATGATACCATATTGCCCTGATTGCCGCCCAAGCCCAAGATTCTGCTTCGCGCTTTGCGCA  
CAACGAAGAACCGTGTCCGCGCGCCCGCGCGGTTTACCGCGATGCAGCGCTATGCGGGGCTTCGAGTTTCGTCAAACCCGA  
CAT

## SEQ ID 126

VRHRLLSGSVRHFHFRPLLVRLLIILYNAPFAQTKRQKFAASARYVKNRGECHFRPCGRQPQGTGDSVANFRLTTQSAPNARTSAP  
CRALQSLYIPAAFRAGHSTSAFVFPSCGSGFQGRKTSAGGLTAVVNGGVEFAHAVSIKTGIAVHRFFNDFKRLHIAHPFFFLAR  
RLRLIRGRFAGVFGVDRGGFEAFRNLRRRTVSATVLRFPVQLPRNGEERDCGQNKQRLPIFQQSPNHLRLRALFRGGNV  
RQFVTFPGGRRHGFANQLGRPEVAVNVRRVKRDDGYHIALIAAQDSAFRVFADNEEHVSAAPARFDRDAVCGGFQTR  
H

## SEQ ID 127

GTGTATGTTAAACATACACCCTTGCTGAAAAAGCCAACGGGCGGACTTTCCGGACATCTCCGGATGTGCTGTTTCCACGAGCAGT  
CGACCAACCTGAAACGTCCGCTACCTCTTCTTGGTGAAGAGAGGCTTTCAAACCTTTCGTGGAGCTTAAATGCAAAACACCAT  
TTCTGTATTTTCTTCAAATCTCAAATGTCCGTACTCAAATCTTGGGGGCTGAACCTTGGTTTTCCTTGGCGATGTTGCGGAA  
ATTCTTCAAATTCAAAATGCCCGTCAGTTGCCATTAAAAGACCAGGCATTCAAAAATCCAGCGTTGCAACAAAAAAGGCAACC  
AAGAATTACTTTTCATCAACGAGCCGAATCTCTACCGAGTCATCTCCGTTACCGCAAAGCCGAAGCCGTCAAATTCGAAGATG  
GATATTTGAAGAGGTTATCCCTCAAATCCGCAAAACAGCGGCTACCAAAATTACTCCCAAAACACCGCGACGACCGTACCGGA  
TTGCGCGGGCGGTTGCGCGGCTTGTGCGGCGCAACAGCATAGGCTACTCTCCGCGTACAGTATGATACCAACCGTTCAACG  
TCGAAGCCGTGGAAGGCATCCCGCGGACAAACTGCCGAAGCCGTGCGCTACGTCCACGCATTGACACTGCACACGGGTTTGGC  
CGGCGAAGTCCCGACCGCGAACCCTTGCCTCGCGCGCAACCCGCCCTGCCCATAGCGGCAACGCTTTGGCGGACATTGCCGCT  
ATGGTTTATTACGCGACACGGATGATCGAATTGGGCAAGACGTTTCCGCGCGCTGAAGCAGCTCGGCTGCAACAGGCGGTTA  
CGATGTGGACGGTTTGGCACGAAACCGTTCAATCTGAAAAGATCCGTGCGAGCCCTCGAAGTGTGCGGGGATATGCGGACAA  
AGACGCCCTCCGCGCGCATAGCCGCATGCTTGAAGGCATTACGGCAAGGCTGCGGCAAGG

## SEQ ID 128

VYVKHTPLLKPTGGLSGHLRMCFFHEQSTNLKRPPTSSWSKRGFQTFVELKMONTISVFSFKSQNVRTQILGAEPWFCLGDVAE  
ILQIQNARQLPLKQGIQKSSVATKKGNOELLF INEPNLYRVIFRSRKAEAVKFDWIFEVPIQIRKTGGYQITPKTTADDRGT  
LRRRAVALVGRKRIGYSSAYSMIHRFNVEAVEGIPADKLPEAVAVYHALTLHTGLAGEVPDREPLPAPQPALPISGNALADIAA  
MYYVGTMIELGKDVSAPLKQLGCKQAVTMWTFVWHETRSLKRSVAALVLRGYADKASGRILAACLEGTYGKAAAR

## SEQ ID 129

GTGTGTACCTTATGCCGGACCTGCATGTTGAAACATAAAGGAAAAATCATGAACCGTCGTCAATTTTGGGCAGCGCCGCTGCC  
GTCTCTTTGGCTTCCGCCGCCCTTTTCGCCGCGTGCCGACGACACGCCGACTACCACCATCATCAGATATGCAGCCTGCCGCCG  
CATCCGCCCTACACCGCGCTCCGCCAAACTGCCGCACACTGTCTGGATGCCGGACAGGTTGCTTGAACCACTGCTGTCCCTGCT  
CACTCAGGGCGACACGTCTATGTCGACTGTGCGGTTCGCCGTGCCGACAGATGCTTGCCTTATGCGGCGCGGTGCACGACCTTGC  
GCACAAAATTCCTCTGACACGCGACGCGGCAAAAGTGTGCCTCGAAGCGTGCAACAGTGTGCCAAAGCCTG

## SEQ ID 130

VCTLCRTCMLKHKGNHEPSSIFGQRRCLFGFRRLFRACARTRLPSSRYAACRRIRLHRRPFCNRTLSCGRTGLPDPLPVA  
HSGRHVYVRLCGCRAPDACLMRRGARPCRTKFPSTDRRGKSVPRSVQTVCSL

## SEQ ID 131

ATGAACCGTCGTCAATTTTGGGCAGCGCCGCTGCCGTCTCTTTGGCTTCCGCCGCCCTTTTCGCCGCTGCGCACGGACACGCCG  
ACTACCACCATCATCAGATATGCAGCCTGCCGCCGATCCGCCCTACACCGCGCTCCGCCAAACTGCCGCACACTGTCTGGATGC  
CGGACAGGTTTGCTTGACCCACTGCTGTCCCTGCTCACTCAGGGCGACAGCTATGTCCGACTGTGCGGTTCGCTGCGCCAG  
ATGCTTGCTTATGCGGCGCGGTGCACGACCTTGCCGCACAAATTCCTCTGACACGCGACGCGGCAAAAGTGTGCTTGAAG  
CGTGCAACAGTGTGCCAAAGCCTGTAAAGAACTCCGCCACCATGCGGAATGCAAGCCTGTACAGTCTGCTCGACTG  
TATCAAGAAATGCGAAAACTCGCCGC

## SEQ ID 132

MNRQFLGSAAVSLASAAAFARAHGADYHHHDMQPAASAYTAVRQTAHCLDAGQVCLTHCLSLLTQGDTSMSCDAVAVRQ  
MLALCGAVHDLAAQNSPLTRDAAKVCLCACKQCAKACKEHSAHAECKACYESCLDCIKECEKLA

## SEQ ID 133

TTGGACTGGCGGGGCAACAAACCGCTTGGGGCGCGGAGCTGGCGGATTTGAAACCGCTTTACAAAGACTTTATGTATTGGGAAC  
GCGGTCTGCACATGTATAAGGCAAGTGCCGTCGTGCCGACCGGATATGTACGGGTGGGAATACCGCGCCGCTGTGCGGCAAGA  
CACGCAGCGGTATGCTCTTTTGGGGCGACGGCTACGACGTGTACCGTCAGTTGAGATGGCGGCAGATACCGGAAAAACAGAGA  
AAGGCATTCAAAAAAGCCGCAAAAGCAAAATACCGTGATGTTTGGCGGACGGGAATACGGCATATCCAAACAGAAATTTAGCG  
ATGTTTGGGATGATTTTGAAGACGCGATGGAATGAAGGCGTTTCCCTGCTGTCTTCGCTGTTTCTGACCAAGTGGCATAAAAA  
TCTATATGAATATCTGGAGGAATATCCGTTTATCACCCGATTGTGTCTGGAACACCGGTGACACCGTGTGATTTCAGCAAT  
ACGCGCATAACCGACCTTTCTGTGATATGACCGCGGTGGAATCGCTTTATTTGAACGAAGGCTTGGACAGCCTGAACCTGAAAG  
GCGAAATCAAGGAAACTGCAAGGTCTGTACCGCGGAAAGGGCGCGGCTGATTTTGAAGTGGGCAAAAGCGTTCCCAAAGT  
GCGGGGTTTGGAAAACTGACCGCGCTCAACGTCTATGGCATTTGCCGATTTCGATATGCAAAACCTGTCCGAAACGTATCCCAAG  
CTCAAAACCATACGGCTGTGGGGCAAAACCGGGCAATATCGCCAAATTTTCCGCCGTATCGGGATTGAGGATTGGAAGTGTTC  
CTGCCGTAGATTGTTTGGTTTGGCGCGGACGACATCCCTCATCCCGACCGCTGCCGAAGCTGCACAGGCTGTGGATGAGCAG  
CCTGCCCGAAGAGGCGGCGAAGGCAGTGAAGAACTTTATAAGAAACGGAAGGAAGACGGGCTGGACCCGTGGATAGAAAAAGCC  
CGAAAAACCGAATGGCTGGCGCAAAATTTGCAACACCCCTTCCCGGATTGGGACGGCGCGGAGCATATCCGAAAAGCCATGCCA  
AAAAAGCGCGGAGCTGTACCGGAAACCGGTGCCGCGGTGGTCAAACTGCTCGGCAATCCCGCTGAAACATAGGGGAGGGGCT  
GGCAGAGGCGGTGAAAGCCTATACCGGAGGTTTCAACAAATGGACAAAAACACTTTATCGACACGCTAGAGCGGGAAGATATT  
GCCGAGCGGTTGGAACGATATTGGACCTGATACCGGATGGGTCTTGTGCCGACAAGGAAAACTGTTTGAATATTGTATAAAA  
ACAGGAATTTT

## SEQ ID 134

LDWRGNRPLGAAELADLKPLYKDFMYWERGLHMYKASAVVPTGYVRVGNAPLCGEDTQRYASFWDGVDYVRQLRWRQIPEKQR  
KAFKKAASKNTVMFAGREYGISQNLSDVWDDFEDAMELKAFCLSSFLTKWHKNLYEYLEEYPFITRLCLENHGTQVLDVFN  
TRITDLSVDMTGVESLYLNEGLDSLNLKGEIKENCKVCTAGKAGLILEVGKSVKVRGLENLTAVNVMGLADFDQNLSETYFK  
LKTIRLWGPNGNIANFSAVSGFEDLEVFTAVDLFGFGADDI.PHPDRLPKLHRLWMSLPEBAKAVKLYKKRKEGDLDPWIEKA  
RKPEWLAQNFDNPRFDWDGAHPIKSHAKAAELYRKTRAGVVKLLGNPPENIGEGLAEAVKAYTGGFNKMDKKHFIDTVEREDI  
AALETILDLIPDGS CADKEKLEIFDKNRNF

## SEQ ID 135

TTGCAAGAGTTTAAATTTATTTTGGACAAGATTTCGGATTGTCTAAAAAAGAGGCTATTTCGGAAAGTGTGAAATGGCTTCCGT  
CCCATTTCAAAATTCACACTGATGGTAGCTCAAGGCATTCAGGGTTTTCATCTTAAAGCTGTATTTTGAAGAATGATAAGAATGA  
ATATTATGCTTTAATCGGTTCTTCAAAATTTGACTCATGCTGCGTTTAAATAGCAATTATGAAGCAAAATTTTACTAAAAATTTCC  
GAGCAGGATTTTATAAAAGTCAAACTCTTGGGCTGATGAAATTGCGATGAAATCTATCCCGGTATCGGAAGATTGGCTTGAGGAGT  
ATCAGGAAGCTGAAATTAATAAGAAATCAACTGTTAGACAATCAGTGTGATAAGTTATTTATGGAGATGCCAAATTATAA  
TCAAGAACTGATTGCCGCACGGAGAAAGCAGATGAGAAACCATCAAACTGTGTATCAATTAATAAAATCTTATTAAGCAATGT  
GCAGCAGGAAAAATAGACAATAATGATTTTATGGGGAATTTAATAAATTATGCTTCTTGGAAAGCGAAAAATAAGGAGAAGGGG  
TAGGCAATCGTTTTCAAGATAAAACGTGGAAGGACGGGTAAAGTCTTCAGATTTAGAAAAATTATGCATTGCCATCCAATCAGT  
TTTTGATGCTCCACTTACTGAGAGAGATAATGTGGTTGCCAAGCAAAATGATTGGCTAAAGAAATGTGGGGTTTCCACTCGTGT  
TCAGTTTTTTCTGAAATGCTTTGTCAAGAAATATCCAGATAGATATCTGTTTTAAATGCTCCCATTAATAAAATTTTGAAGAAA  
ATAAATTTAAGTCTGCAAAAGGAGCAAGCGAAGGCTCCAAATATATTGATTAAAGTATGAAGTTAAGAGCTTTACTAGCTATGCA  
GTCAGAAATAAAGATTGGCTGAATTAGATGTTTTAGTACAGGCAGAAATATCGCAATCGTACAGATATTGATTGGGAA

## SEQ ID 136

LQEFKFIQDFGLSKKEAIRKVLKWLPSHLKFTLMVAQGIQGFHPKAVFWKNDKNEYALIGSSNLTHAFAFNSNYBANILTKIS  
EQDFIKVKSWADEIAMKSI PVSEDWLEEYQAEINYYKSTVRQSVMDKLFMEMPNYNQELIAARRKQMRNHQTVCNQLKNLIKQC  
AAGKIDNNDYGFENKLWSWKSENKGEVGNRFQDKTWKRTGKSSDFRLCIAIQSVFDAPLTERDNVVAQIDWLKECGVSTRG  
SVFSEMLCQBYFPDRYPVLNAPIKKFLEENKFKSAKASEGSKYIDLSMKLRALLAMQSEIKDLAELDVLVQAEYRNRDIDWE

## SEQ ID 137

TTGTCTGAAAAACGGGAAGGGCAATTTGCCGCGACGCCGCCGCTCATTTCCCGGAACCTACATTCCGTCATTCCCACGAAAGTGG  
GAATCCGGAACGCAAAATCTAAAGAAACCGTTTATCCGATAAGTTTCCGCACCGACAGGTCTGGATTCCCGCTTATGCGGGAAT  
GACGGCGCGGGAATCGGCGGATTCGGCGGAGTTGGTGGATTGGCGGGCTGAAGCCCGCCCTGTATATCGGAACCTCCGTTATC  
ATAGCGACAAACGCCCGCGCCGCCACCGCGCCGCCCAAGGCAGACAACCGTTGCG

**SEQ ID 139**

**SEQ ID 140**

**SEQ ID 141**

SEQ ID 142

**SEQ ID 143**

SEQ ID 144

SEQ ID 145

SEQ ID 146

SEQ ID 147

SEQ ID 148

SEQ ID 149

SEQ ID 150

SEQ ID 151

TTGGCAATGGTTTACGGAATCGACTACTGCGCCGATGCCGAATGCTATTTTGAAGATAAAAAATCAAATTAAGGAAGGAATCGGCCA  
ACATCGGCGGCATACAGTTTGCAGAAACCAAAGAGCTGGGCAGGGTCAACCGCATTGATCCGCTCAACATAA CTTATCTGAGAGT  
ACGGGGTATGTGGGGAATCGAAAATCCATGGTTTGTCTTCAACTATATTTACCAACGGAATATGGA AAAAGTTTCAATTTCAATG

GCCATTATCAACGAAGACAAATGGAACAGTTTTTAACAATACAGACAAGCTGCTTGCCATACAGGATTCCAAACCTGGCCATTTCCG  
ACATTAATAATAAAAATCCCAACAACCCGGCGCGATTAAAGAAATGCAAACTCATCACCTACCCTTA

**SEQ ID 152**

LAMVYGIIDYCADAEYLIKIKNIKEGIGNIGGIQFAETKELGRVNRIDPLNITYLVRVGMWGIENPWFVFNYYIQRNMEKSFNFM  
AIINEDKWNFSNNTDKLLAIQDSKLAI SDIKIKNPNPARLRNAKLITYHL

**SEQ ID 153**

ATGCAAAACTCATCACCTACCCTTATAATCCTATGAAAATCATTAGTTTGTGTTAGCGGTTGCGGCGGTTTGGATTGGGTTTCG  
AAAAAGCGGGATTGAAATCCCGCGGCCAACGAATACGATAAAACCATTTGGGCAACCTTCAAGGCAACCATCCAAAGACCCA  
TTTGATAGAAGGCGATATACGCAAGATTAAAGAAGAAGATTTCCCTGAAGAAATCGACGGGATTATCGGCGGCCCACCTGCCAG  
TCTTGGTCTGAAGCGGGAGCTTTGCGCGGCATCGACGATGCGCGCGGACAGTTGTTTTTCTGACTACATCCGTATTTTGAAAAGCA  
AACAGCCAAAATTTCTTTTACGCGAAAACGTACGCGGAATGCTGGCAAAACCGCCACAACGGAGCCGTACAAAACCTGCTGAAAAT  
GTTTGACGGATGCGGATACGACGTAACCTTGACTATGGCCAAACGCAAGACTACGGTGTAGCACAGGAACGCAAAAAGGGTCTTC  
TACATCGGTTTCCGTAAAGACTTGGAATAAAATTTCTTTTCCAAAAGGTTTCGACGGTTCGAAGACAAAGACAAGATTACATTGA  
AAGACGTTATTTGGGATTTCGAGGACACAGCCGTACCTTCCGCCCCGCAAAACAAGACCAACCCCGACGCGAGTCAACAACAACGA  
ATATTTTACCGGCGAGTTTTCCTTATTTTATGAGCCGGAACCGAGTTAAAGCGTGGGATGAACAGGGTTTACCGTCCAAGCT  
TCAGGCGAGGCGAGTCCAACGACCCGCAAGCCCCAAAGATGGAAAAGCAGGGGCAAAACGACTACCGTTTGTCTGCCGCGCAAG  
AAACACTATATCGGAGGATGACGGTACGCGAAGTTGCAAGAATCCAAGGCTTCCCGACAACCTCAAATTCATCTATCAAAATGT  
CAACGACGCATACAAAATGATTGGCAACGCCGTCCCCGTCAACCTTGCTTACGAAATTCAGCGGCAATTAAAAAACCTTAGAA  
AGG

**SEQ ID 154**

MONSSPTTYNPMKIIISLFSGCGGLDLGFEKAGFEIPAANEYDKTIWATFKANHPKTHLIEGDIRKIKEEDFPEEIDGIIIGPPCQ  
SWSEAGALRGIDDARGQLFFDYIRILKSKQPKFFLAENVSGMLANRHNGAVQNLLKMFDDGCGYDVTITMANAKDYGVAQERKRVF  
YIGFRKLEIKFSFPKGSTVEDKDKITLKDVIWDLQDTAVPSAPQNKTNPDVNNNEYFTGSPSPIFMSRNRVKAWDEQGFVQA  
SGRQCQLHPQAPKMEKHGANDYRFAAGKETLYRRMTVREVARIQGF PDNFKFIYQNVNDAYKMI GNAVPVNLAYEIAAAAIKKTLE  
R

**SEQ ID 155**

TTGAAACGTCAATTTAAAAATAAAGAATCAAGGGTTAGCGTGAATTATAAGGAATGCTGTAGTATTTTTCTGATTTTCAGAATGG  
AACCGTATAAAAATGCCGTTAGGAAAGACAAAGCAGCTGAATTGTATTTATGAATTTATCTTTATCAAGAGAACTTTTTTCATGT  
TGTTTCTATATTTGAGATCGTTTAAAGAAACAAAATGTATTTGCTTTCCGCGAGGAGTTAAAGACAGAAACCGGTTATATGAT  
AGCATACAACCACAAACGAATCCTGCAATTGAAATATCAAGGTTGCTTTTAAAGAAATGGTACGAAAGAACTGCGCGAATTAAATCA  
AGGTTGCAATTATCTAAAAATACAAAATAATAGCGGAGGAAAGTTTGACCACAACCAATTGGTTGCGAGGACTAGGATTCGGTTTTTG  
GCGGTATCTGTTTGGCGGAGGAAAGATGCTCAATTTGATGCTGCAGGAAAGATTGATGAAAGTTTTCACAAAAGCCCCAAA  
TCTACACCAAGTGTCAATATAACCAAAAATGGATTTTTCGAGAATTTCCATATTAACAAATTTCCGTAATCGTTTGGCACATC  
ACGAACCGATTTGTTTTAGTTTTAAAGGTGCAATAAAAGATACCGGCTACGCTAGAAATATTCACCAATCTATTTTGAACGTCT  
TAATTACATGGATGTAGATACTGCTTCAGTATTTAGCCATTTTAGCGATCAAGTGATTGCGGCTCTGCGATGAAATCGACAAACTG

**SEQ ID 156**

MERYKNAVRKDKAAELYLLNLSLRELPHVVSIFEIVLRNKIDICFRQEFKDRNRLYDSIQPQTNPAKYQGCFRLNGTKESABL  
IKVALSKIQNNSGGKFDHNQLVAGLGFGFWRYLFAAGKDAQFDAAGKVLKMFPPKPKSTPSVQYNQKWI FREL SNINNFNRNLA  
HHEPICFSFGA IKDTGYARNIHQSIFELLYMDVDTASVFSHFSDQVIAVCDEIDKL

**SEQ ID 157**

ATGAAACGCTTTATTTCTGCCGGTGCTTTTATCCGCAACAACCGCCCCGGCTTCTCCGATTGTGCGGTACATGGCATTGCATCGGCA  
CTGATGAAACCAATTCACAGTGATACAAAGTCAAATATCTTCAGGACGGCAGCTTCCGTGGCGATGCTATACTCAAATCGATGA  
TGACGGCAATATCTTGGCATAACCGTGTGTCGGTGCAGGTAAATGGCGTTTTCGGAACAATGCCCTTAACCTCAAAGCCTAAATCAAG  
TACGGTGAAGTTTACGACAGCACAGCCCCGAAACGCTGGCGTGGTTAGAAAAGTCGGAGGATGCACGACTCTTGGAAAGCATGA  
TGACACCGGATTGTTGCGCGAGATGGACAAACCCGAAAGATGATGTGTATCAACTGGATAAATCAGGCAAATTAGTGTCCGA  
AGACGGAACCTCCCGTGAGGCATGTACGAAAGTGGAG

**SEQ ID 158**

MKRFILPVLISATTAPASPIVGTWHCIGTDENIHSDTKVKYLQDGSFRGDAILKIDDDGNILAYRVVAGKWRFANNALTQSQIK  
YGEVSRQHS PETLAWLEKSEDA RLLESMMYTLGVAQMDKPKDDVYQLDKSGKLVSEDDGTSREACTKVE

**SEQ ID 159**

ATCATCACGCCGAGTAAAATTTGTAATTAATGTTGACGGGGCTTTAAATATCCGTTTCGTGTAACCCGCAACCACTTCAGTCCA  
AGACCGCGCTCTAATATTTTACCGTACCCAACTTACACCATAACGCCGTGAAGCCTGCTCTTTCTCCACAGTATTATCAAACA  
TACCGCTAATACCCCGTACAACCTGCCAAGCCGACATAGCGTAATAGCTGAACGTACCGCTCACCGAAATCGTTTACTGTGTGA  
ACGTTTTGCCCCAAATATTCGTCATGGTATTGTTGCGGCCACTACTGGAAGATTGGGTGCTGCGCCATTTTTCATTACAGACGGCGG  
CTGTAATCCAACACAATACCCGTATTTGCCGTATAACGGTTATTGCCAGCCGGTTTGTGTTGACAAAGGGCCGGAATCCCCACT  
CTAGACGGCTATTCCGATAACGGTAGCCTACTTCGGCATGAAACGCCCTGTTCGCTAAAATCCCGGCATTCCTAATAATGCACACC  
GGAACCGCTGATGCCCTAAGCGGGCAAGTGATTGCTGCGCATGTTAAACATCCGATCAACGCCAGTTCGTACCTTATCCCGTTG  
GCGCGTTTGGGCGAGCTGTCTTCCGATTTTATCCATTTCCGGCCGTTGATGACGATGTCCCGTGAAGGGACGCAATGTTTACAT  
TATCTGTTTGTTCATAGTTTCAATTTGAACGAAGGATGCCACGCTTGACGCTTCCGCTGACGGATATATTCGCGTGAAGCTG  
CCGCATATCGGGCGGCAACACCTCTCGGCCCGGTGCAACTGAACCAATGCCCTCACGATATTGTTTGTCTTCAAACAGCATCACG  
CCCAATCAAACGGGGATAAACAAGATCGGGCTTTTCCGACAACAACCTACGGTATAGATCGGCGCGCTCGAACAT

**SEQ ID 160**

MFEAADLYRELLSERPDIVYPRFDLGVMFLFEDKQYREALVQLHRAEEVLPDMRQLAREYIRQAEAVQAWHPSFNMNNEYEQTDNPN  
NASLSRDIVINGRKWIKSEDSLPRKANGIRYELGVDRMFNMAGNH FARLGISGSGVHYWNARDFSEQAFHAEVGYRYRNSRLEWG  
FRPFVKQNRNLGNNRYTANTGIVLDYSRRLNEKWRSTQSFQYGRKQYHDEYLA KRYNSKTI SVSGTFSYYAMSAWQLYGGISGMFD  
NTVEKEQASRRYGVSLGTVKILDGGGLGLKL GAGYTKRIFKAPATLIYNFTRDD



## SEQ ID 161

TTGTCGGATACGGATAAACAGGCTTTTGTGACTTCTGTGCTCAGCTCAAAGAAGAGGTTAAAAAGTCATTGAACCAAGAAAAGTTA  
CGAAGTGCCCAATCTACACATTCGTCAAAAATGGCAAAGATTGTGGCAACCAACGTTTTTGTGTCGTGATTGTAA  
AAAGTCTTTTGTGAGCAGACAGGCACTATTCTCTACAAACGCAAAAAGACATTGAAGTTTGGGAAAAATACATTCATTGTATG  
ATTGAAAAATACCCACTTCGCAAAATGTGCTGAAATTTGCAAAATCAATCTTGCTACTGCGTTTACTTTGGCGGCACAAATTTTGG  
ACGCACTTCAAACATGATGAATGAAGTTGAGTTAGACGGCATTGTGCAAGCTGATGAACTTATTCGACGATTCTTACAAAGG  
GCACCACAAAATTTTAACTGTCACGCTCTGCTCACAACGAGGAACGAGCAACGAAACGTTGCGATTTCCTCAAGAACAAGTT  
TGTTGCTTGTGGTATCAATTTAGACGGTAAATCTGTTGCTAGAAATTAGCAATTTGGGTAAGCCATCTCTAAAAAATATCAAC

## SEQ ID 162

LSDTDKQAFITSVSSKEQVKVIEPRKVTCKPHCQSTHFVKNKDCGNQRFRCRDKRSFVEQTGTILYNTQKDIENVWEKYIHCN  
IEKYPLRCKAEICKINLATAFTWRHKILDALQNMNEVELDGIQADETYSTISYKGHKNFNLPRPAHKRGTRATKRGISKEQV  
CVPCGINLDGKSVARISNLGKPSLKNIN

## SEQ ID 163

ATGTTTGCTCTTGCCCGCCAGTAATATGATTTTACGCGGAGACGGTAAAGCCAATTTACACCAAAGCAGTTGTTTCATGACTGATT  
TTCAAGGATTTAATCAAAAATCCCAAACTGAAACAGGCTTAAACGCCCAATGTTGGCTTTCTCAATCCACCTTACGCCCAATC  
CAAAGCGATGCCGAATTGCATGAACTTATTTTGTCAAAGAAATGTTGGATATGTTGGCAGAAGGTGGCACAGGCATTGCCATT  
ATTCCAGTCAGTTGCGTGATTCACCAAGCAAAGCCAAAGCGAAATTTGTGAAATATCATCGCTTAAAGCCGCGTATGCTCTATGC  
CGAGCGAAGTGTTTTACCCAGTTGGCAGCGTAACGTCATTGTGCTATTGTAAGCCCATAAACCGCATTTTCAGACAGTCGTGAT  
TGACCCGGACACACAAGAAGAAATCAGCAGCAAAAAAGCCTGTGCAAAACGTTGGTTTGGCTACTGGCGTGATGACGGTTTTGAA  
AAAACCAAACATTGGGACGCAATTGATTATACGACCGCTGGCAGGGCATTAAAGCGCGCTGGTTGGAAACATTATTTAAACAACG  
AAGTTACACAGGAGAATCGGTAACAGCATTGTAACTGATAACGATGAATGGGTGCGGAAGCCTATTGGAAACTGATTATTC  
CAAATTAACCGAGCAGATTTGAGCAAGTCGTGCGTGAATTTGCTTTATTTCAACTACTGGGAGCGGAAGTAGGGCCGACTGAA  
AATTGGATAAATGAAAGCTATGAAGACGATGACAAATACGACTTCGGAGACGATGAA

## SEQ ID 164

MFALAASNMILRGDGKANLHQSSCFMTDFQDLIKNPKEPETGLKRPNVGFLNPPYAQSKSDAELHELYFVKEMLDMLAEGGTGIAI  
IPVSCVIAPSKARSEIVKYHRLKAVMSMPSSELYFVGTVTICIVVFEAHKPHFQTVVIDPDTQEEISTKRACRKTWFGYWRDDGFE  
KTKHLEGRIDLDRWQGIKARWLEHYLNNNEVHTGESVTAFTVDNDEWVAEAYLETDYISKITRADFEQVREFALFQLLGAEEVGPT  
NLDNBSYEDDDNDFGDDE

## SEQ ID 165

ATGGTTGAATTGCAAGAGATTTTGTATGTGAGTTACGGTTCAAATTAGATTTGAATAAAATGAGCAGCTTCAATCCAACAATCA  
ACTTTGTAGGCAGGTCAAGCAAAAATAATGGTGTAACAGCATCTGTGGATTTATGAAAAATACAAAACCTTATCCAGCAGGATT  
ATTAAGTGTGCAATAGGTGTTCTGTTTATCTACTTTTACAAAACAAACCATTTTATACAGCTCAAAATGTTGCTGTTTTTA  
AATCCCAAAACAGAAATGACAGAACAACAAAACCTCTTTATTTGTGCTGCTATTTTGCCAAATGCCTACCGTTTTTCTGCTTGCG  
GTAGGAAGCTAACCGCACGTTACGCAACTGTTTGTGCCATCTTTGGATGAGATCCCAAGCTGGGTTGAAAGCGTGAATTTAAA  
TCCATCTGCGGGTGTAAACCGAACCGAAATTAAGAAGATTCGCTTGATTTGCTGTTGGTTGCGCAATCAAAACGACTTGATGAAAT  
TTTACTATTCAAACCGCATTCGCGCAACCAATTAAGAAGTTTGAACAACGGCAAAAAGACAGGTTGTCTATATCCGTCCTG  
CCAGTACGCAAGCAAGAACGCTACGAAGTTATATCGCTCGTGATAGCGTTGATGAAAAACATATTTTCCATGCCATACGCTTTT  
CACITCTACCAATGGCGAAGGTAGCCATATCTATAGCTATGTTTCAACTTGTGAATTTGTAGCAAATAGTGATGTCGCGGTATTA  
ACACCCATACAGTCCGATATGCCAATAGAAGTAAACTGTATTACGCTAAATGTATTACAGCAACCGCTATCTGTTTCTTATG  
GACGTCACCCCAAGGCGAAAAATTAAGAAGCATTATGTTACCGTATTTTGACCAACAAGAAGATTTTGATTATATCTGCCGTTT  
CATTCACACCTTGCTATTTAGTAACAATTTG

## SEQ ID 166

MVELQEIFDVSYGSKLDLNMSSFNPTINFVGRSGKNNGVTAASVDLLKNTKPYAGLLTVALGGSVLSTFLQNKPFYTAQNVAVL  
NPKTEMTFQOKLFYCAAFANAYRFSACGREANRTLRLQFLVPSLDEIPSWVESVNLNPSAGVTEPKLKESLDLFVVRQSKRLDEI  
FTIQNGIAATKLKEFEQRQKDTVVYIRPASTQARTLSYIARDSVDEKHIFPCHTLFTSTNGEGSHTYSYVSTCEPVANSVAVL  
FTIQSDMPIEVKLYYAKCITANRYLFSYGRKPKGKELKSIMLPYFDQQEDFDYICRFIHTLLFSNNL

## SEQ ID 167

ATGAAGAACTGTACTCCAACCTAACGGCACATGGTTCAAATGGGTGCAACACTCACTGTTGCGGTGGCCGCTGCACAGTATCAA  
CACCTACATCCGCCATCCCCGTACCCACATAAAATGCCTGCGGATTAACGGGCAGATTAAATGCGTCAAACCGGATAAGCCCTAA  
CACTACCCCTGCGCGAGAGCATATTGAGCATGTGCGGAAAAATCCGCGCCGCAAGCAGCGATGGACAGGGCGGCAGCAAGAAAT  
GCCGATAAAATAGCCCTCAAAGCAGGCGGGGAAACATTGTGTCAGCTTAAGGATGAAAAGGGGTTTACCCAGTCCGAATTGGCAA  
CCGCGCAGGATTGCCCTCAACCTATCTGTCCCGCATCGAAAACAGCAAAACAATCCCTGCAAGATAAGACTGTACAAAAAATGGC  
AAACGCATTAGGCGTTTCCCCGCTTGAAGTTGCGCGACGCTTCGAACGGCGGTACGAATATATGGAGCAGGCA

## SEQ ID 168

MKNCTPTNGTWFKMGATLTVAVAACTVSTPTSAIPVTHIKCLRINGQIKVKPISPNTTPAAEHIEHVRKNPRRKAAMDRAAARI  
ADKIALKAGGETFVSLRMKGFTQSELATAAGLPQPYLSRIENSKQSLQDKTVQKLANALGVSPLEVRAAFERRYEYMEQA

## SEQ ID 169

ATGACGGTCCGAAACACGCAACCGGAAACCGTCCGGACGGAAGCCGCGCGCAACAAAGGCGGCAATACCAACCGGGCTATTACA  
AAAACCGCGCTTCGAGTGCGTGGGTTTGGCGCAATACCTCAACTTCAACCTCGGCAACGCTTCAAATACATCTGGCGGCACAA  
GGAAAAAGGCGGGCGGAAGACTTGGAAAAAGCCCTGCGGTACTTGAACGCCAACGCGCGCGCGCGCGGAAGTTCAAGAAACTC  
AAACACCGCGCTATGAAAAAATGTACGCGGTCTGAAAGATTGCGGGTTCGACGCGCGGCACGGAGGCGCGCTGCTTGGCGTCA  
TCTCCGCGCTTATTACATCCGCGACGGCGGAAGACAATTTGCGTGGCGCGCGCTGTGTCGAAGATTGTTTGGAAAAAATGCC  
GCCTGAAGCGGGGCGGGCCCCGACCCGTGAAGCCCGATGCCGCTGAAACGGCGGGCGGAGGCATT

## SEQ ID 170

MTVRNQTETVRTEAAPQGGNTNPGYYKNRAFECVGFQYLNFLNFAFKYIWRHKEKGGREDLEKALRYLERQRAGAPKFKKL  
KHRRYKMYAGLKDCGFDGGTEALLAVISAAYYIRDGEDNFAWAAACVEDLLEKMPPEAGRAPHPESPMPPEAGGGI

## SEQ ID 171

ATGAACGTGAACCAACTCACACAAGAACGATTGAACGTGTAAGTCGGCACAAAGCGGCGCGGCCCTGACAAAGGTTTTTA  
CCCAGCCGGCTAGTTTTTACCGCCGGCCTGCAAACTATGACCTTTCCGCGCCGTCTCAAAAACCTTACCCGGTATTGACCCCGTT  
CGCAACCGTATCCCGCGCGTGGGCGCGCGCCGACCATCGGCTCGAACTGGAAAGCGGTACGAATATCAACGTCGGCAACCAA  
CGCGCCGGTATCGGCGAAGGCAAGCGCGCGCGCGGTATCAATCACGAAACGGTGAACGCAACGCGCAATTCCGCGCCATCGGCT  
TGGAAACCAAGTAACCTTTGAAGCGGATTACGCCGCGCGCGGTTTCGAGGACGTGAAAGCGTTGGCGGTTCGCCCAAACCTTCA  
GGCTACTATGGTTGCGGAAGAAATGATTTTGCTGGGCGGCAACACCAGCCTGAAGGCAGGCGTTACACCTACACCGACCGCGCTC  
GTTTCCGCGGACGCGCGCGGGGAAAATCAGCGTCAGCACCTTGTCTGTAATCTGTGTGGCTTTGGGCTTCAGGCGGTATTGGGACG  
TGGCAGGCGCGAACAACGGTGCAACCGGTCAAAGCCCGAACATTAAGCTGCCCAAGTCCCTGCCAAAATCACACGCGGAAACGC  
GGATGGTACAAACCGATACGTTCCGGCGCGGTTCCGCCGGAATACTGCGCGCGCTTCCGTTTCCGGTATTGAGGCGAGGCAAAAA  
GTAACCGCGGTGATTCCGGCTGTTCCGGCGCGGTTGCTATGCTTGGTACTGGGGTGGCGCGGTTCTGAAAACTGGGCGCGG  
TTACCACTGCCGCCAAAGTGGAAATTTCCGGTGATGCCGAAGGTACCCAGACCGCGCTTCCCTGCCGTCCGAAGACAATTCCAC  
TTCTATTTTGAATTTGACGGCTGTGACCCAAATCGCCCTGCCGTGATTCCGGCGCGTTCTGGTTCGGACAACAAAGCGCGCGG  
CTGACTTCCGACAACGCGCGCGCGGTGTATGAATTTGAAGAGGCGTTTCGCGCATTTCTTTACCCGATACCGCCTGTCCCCGATA  
CCGTCTACGTCAACGCCCGCGATTGGCGCGCGGTGACCAAGCTGATTATCGGAAACAGCGCGCGCGCTTGATTAAGTTGAACGT  
TGACGTGAACAACATCGGCGAATCCGCGCGCGGTGTGCTGCTGCGTTGCTATATGAACAAGATCACCGGCGACGACCTGAACATC  
GTGGTACACCCGAACCTGCGCTGCCGTACTTACCTGTTCTACTCAAGCCGCTGCCCGCTACGTTACAGGCGTTCGGCAATCTGC  
TGCAAGTGCCTACGCGCAAGAGTATTACCAAATCGAATGGCCGCTGCGCACCCGTATGTACGAATACGGCGTCTATGCGGACGA  
GGTGCTGCAAGGTATGTTTCATGCTGCCTTCGGTATGATTACCAACGTGGGT

## SEQ ID 172

MNVNQLTQETIELMKSQAQAGGPPDKGFTQPASFTAGLQTYDL SAPSQKLYPVLTPLENRIPRVGGRTIGSNWKAVTNINVGNQ  
RAGIGEGRRGGVINHETVERNAQFRAIGLENQVTFEADYAARGFEDVKALAVAQTLQATMVAEEMILLGGNTSLKAGVTPPTAV  
VSADAAGKISVSTLSVICVALGLQAYWDVAGANNGATGQSPNIKTAQVPAKITRRNADGTTDTFGGGSARKSAAASVSGIEAGKK  
VTAVIPAVRGAVAYAWYGAAGSEKLGAVTTAAKVEISADAEGTQTAASLPSEDNSTSILEFDGLLTQIALPDGAFWSDNKGGG  
LTS DNAGGVYEFEEAFHFTRYRLSPD TVVNARDLAALTKLIIGNSGAPLIKLVNVDVNTANIRAGVVVGSYMNKITGDDLNI  
VVHPNLPAGTYLFYSSRLPAYVQGVGNLLQVRTRQEYVQIEWPLRTRMYEYGVYADEVLQGMFMPAFGMTNVG

## SEQ ID 173

ATGGCCGCGCCCGGTATCGCTTGAGGAGTTCAAGCAGCGTATCGCGCTTGAACATGACCGCGGGGACGATTTCCTTCTCAGCGTCA  
TTGACGGCGTGTGCGCGCGCGCGGAAGCCTATATCGGGCGCAGCCTCCTGGCCGCGGATTATGTCGGCGCGGTACGACGGCAACGG  
CAAAGACCGCATCGTGTGGACAATTATCCCGTCTGTGCGTGTGCTCGTCAAAATCAACGCGCGGATGCCGCGCGCTGGGAG  
TTTGACAACCTGGCTGCTGATGCGCCCCGAAGGTTTCGCGCGGGGGCTGAAAAATGTCGAGGTATCGTACCGCGCGGTTATGAGC  
GCATGCCCGCGGACATACGCGAAGCGGTGATGATTATCGCGGTGACGCGGTGAACGAAATCGAGGGCAAGGGCGTACGGAGCAA  
GACGCTTGACGGCGAACCCTGCGCTTTTCTACGTTCCGTAATTCGCGCGGTATGCCGCGCTCGCGGTTTGCGTACTCAATGAG  
TACAAACGAAAGGCGTG

## SEQ ID 174

MAAPVSLBEPKQRIQVEHRRDDFFLSVIDGVSAARAYIGRSLLAADYVGRYDNGKDRIVLDNYFVLSVSSVKINGADAGGWE  
FDNWLLMRPEGFARGLKNVEVSRYRAGYERMPADIREAVMI LAVQRVNEIEGKGVRSKTLAGETVAFSTFGNSGGMPPSAFALINE  
YKRRGV

## SEQ ID 175

ATGCAGTTGACGTTTGGCAGCGCGGCAAGTGTTCGCCCAAATGATTACGGATGCTTACGGCAACCGTGTACAGAACGCAACGCCCG  
TGCGGATTATGGGCTTGACAGAAATGTCGTCGATTTGTGCGCGGAATTGAAAGAGTTCTACGGTCAAAACCGTTATCCTTTGGC  
TGTGGCGCAAGGCAAGGTCAAGGTGTGCGGCAAAATGAAAGCGCGGTGATTAAACGGCTGACCCCTCAATACCTGTTTTTCGCT  
ACGGAATATGCAACCGGCACGATGAAGGCGCTTTGGGCGGAAACTACGGGCAAGTCCTCGATGGCGACAATTATCTTACCTTC  
AGGCGAGCGCGCGCGCGCGCGGCAAGTTCGCTGAGGACGCGCGCGGTGATGGGCGGACGCGCATGATCAAGTAGCATC  
CTCCCGCAACCAAGGCCAATATACGGTTTCGGAATCGCGCGGTGATGCTTTTAAACAGCTCGGATAAAGGCAAAACCGTTTATCCG  
AGCTTTACCTATACGCAACGATGCCCGCGGCAAGAAATCGAGCTGACCAATATGGCGACGGGCAACACGCCGACGTTTAAAGA  
TGAGGTACCTGACGAGTTCAAAGGCAAAAGCCCTGTTGGAACGTAAGGCGTAACGCGGCAAAATGGGCTTGTCTCGAC  
TAAAACGACGACTTCTCCGTCCCGCAATCGACTTTACCGCTCAACGACGAGGCGGGCTTAAATCGGTACGCTGTGGATT  
CAGGAG

## SEQ ID 176

MLTFGSGEVFAQMITDAYGNRVQNAFVRIMGLQEMSVDL SAELEKEYGQNRYP LAVAQGVKVS GKMKGAL INGLTLNLTFFG  
TEYATGTMKALWAETTGVLDGDNYSYLQAAAPGGGKFAEDAGVMQDGTAYIKVASSPQOQYTVSESGVYAFNSSDKGRTVYP  
SFTYTQTMPPAKKIELTNMATGNTPTFKMRYLTQFKGKALLELESVTSGLGLFSTKNDDFSVPEIDFTASTDEAGFKIGTLWI  
QE

## SEQ ID 177

ATGGGTGGTAAATCGTCAACCGTTACATCTGCCGAAGAGCGGATTTTATCGTTACAGGTTACGCGGTATCACAGGGCTGACCC  
TGCCCGTCATCTACGGCAGGACGCGCGTGGCGGGCAATTTGATTGGGTACGGCGATTTCTGTCACCATCGAGCATAAGGCCGTGAC  
GCGTCAGGGCGGCAAGGGCGCGCGGTGTGAAACAGGTTCGGTATTTCTTATACCTACGAAGCGCGCTCATGCTTGTGTC  
GAGGGCGAGATTACGGGCTGGGGCGGGTTTGGCGGACAAGGAGAAATTCGATTTCGCCGCGCAGTTGCGCCTGACGCTTATGC  
GCGGCGGCGACGAGCAGCCGTGTGTGACGCACTTCAACAGGCGAAGCACCAGGCCAAGCCTTGAATTTATCGGGCAGCGCTTA  
TTTGTGCAGCCCGAACTACGAACTGACGAAATCGCGCAAAATATATCAGCACAAATTCGAGGTTCATCGGAAATCGGGCTATTCC  
GGCAACATCCCCGATGCAAAACCGCGGCAATCGTATTGGATTGCTGACGCAACCAACGCTACGGCTGCGGTTTCCCGTCCCAA  
ACATCGGCGGATACCGACCGGTACAGCAATTTATGCGCGCGCGGTGATTTTCTTAAGCCCTGCGCTACACGGAACAGGGGAGGC  
GCAACGGAATATTTCCGAACCTGCTGGAGCAGACCAACAGCGCGCGGTATTTTCGCAAGGCCGCTGAAATCATCCCTACGGG  
GACGGCAGCCATTTCGGGGAACGGCGCGGTGTACGTTGCCGACAATAAGGCCGCTACGACCTGACCGATGACGATTTCATCGTTT  
CGGGCGGCAAGACCTGTAAAGGCCGGCGCAAAACCAATGCCGATGCGTTTAAATCAGATTAGGTCGAGTACCTTGACAGGGA  
CAACGACTACAACGTGCGCATCGCCGAAGCGAAAGACGAGCGAATATCGAGCAGTACGGATTGCGCCCGAAAGACGCGGTACAG  
ATGCACGGCATTTGCGATGCGAAGGTGGCGCAAAAGTGGCGCAACAACTGCTGCAACGCGCCCTGTACGTGCGCAACGAATATG

AGTTTAAGCTGGGTTGGAAATACTGCCTGCTTGAGCCGATGGACATCGTAACCTGACCGACGCGGGGCTCGGCCTGAATAAAAC  
GCCCGTCCGAATCACGGAAATCGAAGAAGACGGAGAAGGGGTTTTATCCGTCAAGGCCGAAGACTGCCCGCCGGTGTATTATACC  
GTGTCCGAATATCCGACGACGCGCTCTCGGGTTATTTCGGCCGACTACAACGTTTCGCCGGGCAACGCCCATGTGCGGGTAATTT  
TCGAAGCGCGGTTGCAACTGACGGGCGGCGAACCGCAATCTGGCTGGCAACCGCGGGGGCGGTATGTGGGGCGCGCGAAGT  
GTGGGTATCGGCGGACGCGGACAGCTACACCGCGCTCGGCGCGGTCAACCGCAAGGCGCGTTTCGGCGCGCTGACCGCCGATTG  
CCCGACGCGCGGTTTTTCGACCGCACAAATACATTGGGCGTGAAATTTTCGGCGGGGACGTGACGGGCGGACGGAGCAGGACA  
GCCGCGATTGTGCTGACATTGTGCTACGTGACGGCGAATTTTCGGCATACGCCGACGCCGAACGAAGGGCGTGGGACGCTACAC  
ATTGGGCAACCTGACGCGCGGCGGTACGGCTCCGCCGTCAACGCAACGCGCGGCGGACGCCGTTTCGGCGCATGACGAAGCA  
TTGTTCAAATACGCCGTTCCGCGCAACTGGATTGGCCGACCGGTTTGGGTCAAACCTGGTTTCGTACAACGTTTTCGGCGCGGCA  
TTCAGGATTTCGGCGAAGTGCCGCGCTATTCTACACCATCGAAGGCGCGCGCTCGGTCAAATCCAAAACCTGCGCCTGACATC  
ATCGTGGGCATACGGCAAGAAGCCGTCATCGCTTGGGATAAATTGGACGCGCGGATACCTACGACGTGGAAATCTACGACGGC  
GGCAGCCGACGCGCTCTCGGTGCGGTTGACGGCATCGTTGACAACAGCTACACCTACACTCAGGCGGATATGAAGGCGGACGGCG  
GCCAGGTACGCGGTATTGTCTTCAAGGTTTCGGCGGCGTCCGTTACCGTTAAAACGGGCAATTGGGCGCAATCGCGCGCAAAA  
TCCGCAATTGCAGGCATTGCAGGGCATCTCTATCGACAGCGCGCTGCGCGAGGCGTTTTCCTGCGCAAAAACCTGACGAAGAA  
GACTTTGCAGGGATTATCGTCTGGGTTTCGCAAAACGACGCTGCCCGCGCGGACGCAAAACAGCCTATGACGGCGCGGAAA  
CGTTTATAACCATCGCCAAATGCGGCGGCAACCGCTGGAGAAAGGAAGACCTATTACTTGAGGCGCGCGGTTACGACGTTT  
CGGCAAGATAACCTGAAAATCAGCGCGACATATCGTTTACCGTTTACGACGTATCGGCAACCGACCTGTGCGAAAGCAGTCTG  
AACAAAGCTTTTCGCGGACAAAATCAACCTGATTGACGGCAACGGCGCGGCGAGCGTCAACGAGCGCGTTCGAGGCGTCCGATCGA  
CGGCGGACGGCAATGCGGCGGCGGTTGACACACGCGCCGAAGCATCAACGGCTTGGAGGCGCAATACAGGTCAGGTTGATGC  
AAACGGCAAAAGTGGCGGGCTTCGGCTTGGCGACTACGCCGAAAACGGCACGCCCGAAAGCAAGTTTATCGTGAATGCCGACCGC  
TTCGGCATCGGTGCGGCGCGGAAGGCGGATGTGTTCCCGTTCGTGGTGGACACGACAGAAAACCGGTGGGCATCAACGGCGAAT  
TGGTGGTCAACGGCAAGGCGGTTGTCGATAAGTTGAACGCGGGGATATCCAGGCGGCAAAATCGCGCGGCAACGCTGACGCG  
AAACCGCCTGAAAGCGGAAGCGTTACGCGCGGGAATCGGGCTGCCCGCTTACCGCGATAAAATCGGGGCAAAACGCGGTG  
ACTGCCGATAAAGATTACGTTGCGGATTGAGCGCGGTATCTTCCAATCTCGGAAGCATACGCGGCGGACGCTGAATATCGGCG  
GGGTAATTTTACGGTGTCTTACAGCGCATCTGACGGCGGCAATGCGGTAATACGCGGACGAGTTGAGGCGGATTTCGGGTTA  
TTTCAACGGCACGGTCAGGCTTCGTCCGTGAGGCGGACGTTTGGAGGCGCACAGGCTGCGTTGGACGAGGGTAACGTTTGG  
GTGTTGGATTTCGATAAAGACCCGCTGCGGAGGGTTTGTATTCCGAATTTTATGTGGTTTCGGAACGTTTCGGCAACACAGGG  
TGCAGGCAAAAGTGTCTGTTGAACGGGGTGTGCTTGGCGCGAGGAGTCAAGGAAACCGAGAACTATACCAATTATATTGGCG  
CGGCAAGCTTTTCGGGAGGTACGAAGACCTGCCCGCGGAAAGGGGGGGGGGATTATACCGAACAATCGGCTCAAGGTAC  
AGAACCCGCTCGAGTACGAGATTCAAGTCATCCCGCGGGCAACCCGTCAGCCTGAAGTTGTGCTCGCTTCCACGAATCGG  
TGTTTTTCGCGTTCGTGTGCGTTTCGTATTTCGGCGAATCCGACTACGAATACAAGCAGCTGCTCGGGAGGATGTTTGGCGCAC  
CTTTTCGGGAAAGTTTCGGTACGACAGTAAGAAGCAGATTTATTTCGGCGCGGACCGCGGTGTACACGATTACCAAAATCAGATG  
TATAAACATTGGAATGCTTACGGCGGGCTGCTGCAAGTTCGGCGGACGATATCAGGCGATATCGTTGAGTACCGGCTTTTACCA  
ATGCCGAGTGGAGTACGATGCTTGCCTTTCGCGGTGACCGGTGAGTAAGTTGTAGTGGTTAAGAAATACCGGGGTATCGCGCCCCAACA  
GTATTCTCTGTTTCAGGAGGAGTTTAATACTGCGCTTCCGAAATCCAACTGCTGTTTTTGTGGAACACTGGTGGCAGTATATC  
GAGCTGCGCAATATCAGGGTGTGATTCCGGAATCGCGGAAAACGAGGTTTGGCCCTCCGTC

## SEQ ID 178

MGGKSTVTSAEERILSLQVQRSSQGLTLFVIYGRTRVAGNLIWYGDFVTIEHKAIVTRQGGKGGGKGGVQVQVGI SYTYEAAVMALALC  
EGEIQVGRVVRDKEKFDSPAQLRLTLMRGGDEQPLWTHLQQAQHQQALNYSGTAYLCSNBYELTKSAQIYQHNFEVICKSGYS  
GNIIPDANPREIIVLDLLTNQRYCGFPSONIGDTRYSNYCRAVGFILSPAYTEQGEAQRNISELLEQNTSAAVFSQGRLEKIIFYG  
DGSHSGNGAVYVADNKAAYDLTDDDFIVSGAQDPVKAGRKTNAFNFQIQVEYLRDNDYNVAIAEAKDQANIEQYGLRPFDAVR  
MHGICDAKVAQKVAQQLLQALYVRNEYEFKLWKYCLLEPMDIVTLTDAGLGLNKTFPVRI TEIEEDGEGVLSVKAEDCPAGVYT  
VSEYPTQPSSGYSADYNVSPGNAHVPIFEAPLQLTGGEPIQLWLATAGGGMWGGAEVWVSADGDSYTRVGAVNRKARFGALTADL  
PDGAVFDRNTLTGVEISAGQLTGGTEQDSRDLTLCLYVDGEFLAYADAELKGVGRYTLGNLTRGAYGSVNAHAAGSRFARIDEA  
LFKYAVPRNWRIGTVWVKLVSYNVFGGQIDLAEPVAYSRTIEAGTGTQIQNLRLTSSWAYGKEAVIAWDLKDADYDVEIYAG  
GSRRLRAVDGIVDINSYTYTQADMKADGGQVRGIVFVKRYGTAETKGNQWQAQIAAQNPQLQALQGISIDSLRQAFFTCQKPDDE  
DFAGIIVWCENACPAADANKAYDGAETFIITAKCGGKPLEKGTYYLRAAGYDSFGKDNLKISGISISFTVYDV SATDLSSESL  
NKALRDKINLIDNGAGSVNERVEAVRSTADGNAAVQTHARSINGLEAQYTVKVDANGKVAGFGLATTPKNGTPESKFIYNADR  
FGIGAAGKADVPFVVDTPQKNRVGINGELVVNGKAVVDKLNAGDIHGGKIAADTL DANRLKAGSVTAREIGAAAVTADKIGANAV  
TADKIQVADLSAVSSNLGSI TGGSLNIGGGNFTVSSDGI LADNAVIRGRIEADSGYFNGTVRASSVGBDVLRAHLRLWRTEGNVW  
VLDLKDPLPRVLI PNFYVVS ETFGNRRVQAKLLNLGGVLAPREVRETENYTNYIWRGRTFGRYEDLPPRARGGGDYTEQSGSRY  
RTRLEYQIQVIPAGKPVSLKLSLASHESVFSFFVSYSYLAQSDYEQQLGRMVWRTFAESFRYDSKKQIYLGDRRVHDYQNM  
YKHNWAYGGLLQLPDDIYGISFEYRPFTNADWSTMLAFDRSDKFVVVKYRGHAPQOYSLFQREFNTAVPKSNLLFFVEHWWQYI  
ELRNIRVLI PESRENEVWPSV

## SEQ ID 179

ATGAGCGATTTCGAAGCCAAAGTCAGGATAACGGTAGAAAACCATACGAAGCAGGGTTTTGATTTCGGCCGCGCGCGATGCTGATA  
AGCGCGCGGAAAGATGCGCAGCAGCGGCGATAATGCCGCAAGGGCTTTAAAGCTGCAATCGACAGTATGCACGAGACCATGCG  
CAATTTGCACGCGGATGTGAAGCGGGATTTCGAAGCGGCGGCAATCAGCGCAACAGGCGCTCTGAAAAGGTTAGGGCCGAAGTG  
GGTAAAATCGGCTCAGGCTTATCGGGGCTGACCAAACCTGCTGGCAGGATTAGCAACCGCAGACTTCGCCAAATCGGTGCTTGATA  
CCGCCGATGCGATGCACTGATAAACAGCCAAAGTCCGACAAGTCACGTGCTGTAACCGGAGTATCTGGCCGTGACGACGAGCT  
TCTCGATACGGCAAACCGTACCCGTGCATCGCTTGAATCAACGGCAAACTGTACGTTTCCACAAGCCGCGGCTTGAAGACTAC  
GGCTACACCGCAGCAGGAAATTTTAAATTCACCGAGGCGGCAACAACCGCATGACCATCGGCGGCTTGGCGCGCAACAACAGG  
CCGCCCGCTGATGCACTTATCGCAGGCTTTGGGCGAGCGCGTATTCAGGCGCATGAATTTAAATCCATTTCCGAGGCGGCGACC  
TATTTTCTGCTGATACCATTCGCGGAATATATGGGCAAACTCCCGCAGCAAAATCAAAAGCTGGGCGAGGAAAGGAAATTGACGGCG  
GATGTGATTTCGAAGCCATTTCGGCGCGCTCGGAGAAGTTCGGGGAGCAGGCGGCAAAATGCCCGTACGATGGGGCAGGCTT  
TGACGGTGTCTCGAACAACCTGGCAAAGCATGTTTCAAACTGCTGAACGACAGCGGCACAATGTGGGGATTCCCGCCGTTAT  
TAACTGATTTCGGGATAACCTTAATTTGGTTGTTCCGATCGTCGAGGTTTTGCGGTTGCCGTTGCCCGCGCGCTTGCACCGACA  
CTGGCTTTGAATCTTCGACTGCTGGCAAACCCGTTCCGGATTATTGCGGTGCGAATCGGCACGGTTGTCGGGCTGATTGCGAAAT



TCGGCGATGAAATCGATGTTTTTCGGCGCGCGCTGGTCAATCTTTCCGATGTGATTCGGGCGGTTTGGCAAATCATCACGGAAAC  
CGTCGGGGAAGCGGTGGGAACCGTCAAACTCGTGGTTTGACGGGCTGACAGGCGGCTGAACGAGGGCGCGGGCGGCTGGCCGTGCG  
TTGTTTCGGGCGCGTGTAGCGCTCATCTCAAGCCCAATCGGCGCGTATGTGAACGTTTATATCAACATATTCGCAACCGGCTGGA  
TGCTGATTAAAGAACCGCAACGATATGCCGAATTTCTTCGCAATCTCGGCAAGGCCATAGGCAACGTTTATTTCCGCGAT  
CGAACGGATGATAACAAAGCGGTAGGCATGATTAACAGCATGATTGACTTTGCCAACAAGCCGCGTTCGATGGCCGGGATATCG  
GGCATTGGAAGCTGAACAAGGTTTCGGATGGGGCGGATGGACGACGGCGGCTTGGCGAGCGTATTCATGACAGCTTGACGAAAG  
ACCGCGCGCGCAATGGCAATGCCGTTCGCGAACGGGCGCGGATATTCACGAAGCCGATGCCCTCAAGGACCGCGCGCGCGG  
AGGACACGCCAAAAACCGCCCGAAAAAGCCGGGCGCAATCAGGGCGCGCAAAAGGGGGCAAAATCCCGTTTCGGGCGGTCGGGCG  
GCGGCCAAAGACCCGATGCGAGGCTTGGGAAGGGGAAATCAAAGCCGAAAACTCGCACACCGCGAAATGACAGCGCAAAACGCTCG  
CACACCAAGAATGGGATTTGGCGCGTGGGCGGAATATTGGCGGGCGAAGCTGGCAACGGTGGACGCCAACGGCAAAACGGGCGT  
GAAATCCGCGAAAAATCTGATGCTTGAAGACCAATTATCGAAGCAGTCAACCGAAGCCAAAAATGAATCAGGCGGCGCAATGG  
GAGAAATTGGACAAGCACAAGCTGGAGATGGAGAAAGACGCGCGCAGACCAAGCCCTGGCAGACGGACGTATTTCCGCAACTCGAAC  
GCCTGGACTTGGAAATCGAGTTTGAACACCGACGTTTACCGGATTGCTTATGACGATTGACGAAACGGATCGCACTTGGCGGAACA  
AGACCCGGCATACAGTCAGGCGGCAATCGGCAAGCTCAAGGCCCAATGGGCGGAATTGGGGCGGGGCGACGAGCGGACGCGAGGCG  
AAGAACGAGGGCAACCGGAAAAACCAACGCGCAAGACGCGCCCAACGTCATGAAATGCTGCAAGACGGCGCGCAGGAACGCTTT  
GGCAGGAAGCAGCAGCAGCAGATGGGGCAGGCGTTTACCGCCATGCTGGCGAGGGCGCAGAAATTCAGGCGAGGCGATGAACGCTT  
TTTCAAGAGTATGGGGCAACCTTTATTCAAGAAATGGTTACGAAACCTTTGACGGGCTTGATGCGGCGCATGGTTTCAGGAATCG  
GCCATTTACAAGATGATTTTCGGAACTAAGGAAACGCTGGAGACAGCGGCGCGCAGCCAGACGGCGGCAACTAAGGCAACCGAGA  
CAACGGCGGTTGTCTAGTAGTAATGCTGTTCAAGCGGCTTACGGCGCGGCGGCTTCCAGGCGCATATCCCATATGTCGCGCGGAT  
TCTTGGCGTTGCGGCAATGGCGGCAATGATGTCGGCAGTGTGCGGCTTGGGCTTGATGGGCGGGCGGCGGCTTCTCAAACGACCAACC  
ACGACGCGCATTCCTTCGGCGCGCAGGCGGCTGGGACATCCCGGCGAGGATCAACCGCTGACCCAACTGCACGAAAAACGAGATGG  
TCTTACCGCGCAGAACACGCCCAACCATCCGTGAAATGGCGGATCAGCAGGAGGCGGCGCAGCAGCGTCATCATCAATTCGACAGG  
AGGCGATTTCATCCATAAAATGACTTGGCGAAGCTCTTGAAGCAGATGAAACGGGACTTTAAATTTGTC

## SEQ ID 180

MSDLEAKVRITVENHTKQGFDSAAADADKAAEKMRSSGDNAAGFKAAIDSMHETMRNLHADVKAGFEAAGNQAQQAASEKVRAEV  
GKIGSGLSGLTKLLAGLATADFAKSVLDTADAMQSIINSQVRQVTSSETEYLAVQQQLDNTANRTRASLESTANLYVSTSRALKDY  
GYTQOEILKFTTEAANNAMTIGGVGAQQQAAALMQLSQLGSGVLQDEFKSISEAAPILLDTIAEYMGKSRDEIKKLGSSEKLT  
DVIFKAI SGA SEKFGEQA AKMPVTMGQALTVF SNNWQSMVSKLLNDSGTMSGIAAVIKLIADNLLNVPIVAGFAVAVAAVAPT  
LALNLALLANPFGIIA VAIGTVVGLIAKFGDEIDVFGGWSNLSVIRAVWQIITETVGEAVGTVKS WFDGLTGR LNEGAGGWPS  
LFGVRMSVSSAIGAYVNVYINIFATGWMLIKEAANDMPQFFANLGAIGNVFI SAIERMINKAVGMINSMIDFANKAASMGAGIS  
GIGKLNKVRMGRMDGGLGERIHDSITKDRAGAMANAVREARAADIHEADALKRGGGGHAKTARKKPGANQGGGKGGKSRSGPG  
AAKDPMQAWESEIKARKLAHREMQRRETLAHQEWDLAREAYWRAKLATVDANGKTGVKIREKILMLEDQLSKQSTEAKMNQAAEW  
EKLDKHKLEMEKDAADQALADGRISQLERLDLEIEFENRRYRIAYDALQERIALAEQDPAYSQA AIGKLAQMGE LGRGHERTQA  
KNEGKRENQRRKDA PNVMEMLQDGG RNVWQEAQQQMGQAF TAMLARAQNFRQAMNGFFKSMGQTF IQEMVTKPLTGLMRMVQES  
AIYKMI FGTKETLE TAAAKTAATKATETTAVVSSNAVQAASGAAASQAHIPYVGPILAVAAMAAMMSAVMGLMGGGGSGVTTTT  
TTRIPSAAGWDIPAGINPLTQLHENEMVLP AEHAQTIREMADQGGGSTVIINSTGGDF IHKNDLAKLLKQMKRDFK FV

## SEQ ID 181

ATGGCAACCATCACTCAACGTAACGGCAAAATGGCGGTACAAATCCGTATGAAAGGCGTTTCCCGTTCCGCCACATTTGAGCGGG  
CATCAGACGCGAAGGCGTGGGCGGCGCAATAGAGTCGCAAAATTATGGACGGCATCCAAGGCAATGCCCGCGGAAATACATATCTT  
TGCCGACCTTATCCGGCGGTATTTATCCGAGGTACACCATCAAAGCGGGGCGCACGGGAAGAATCATACCGCATTTGACGCGCA  
CTAAAAACACCTTTGGCAAAGGTGCGGCTTGCCGACCTGCGCCCTCAAGACTTCGCGGATTGGCGAGATCAACGGTTGACGAGG  
TATCCCCCACCAGCGTCGAGCGCAATTAACCACTTTATCCGCGCTTCGCGCAACACGCCATGAAAGAGTGGGGACTTCTTCGCGA  
AAACCTGTACGCAAAATCAGCAAGCGGAAAAAAGCCGGGCAAGGACAAGACGGCAACCGAGCAGGAAATGCGGATATTTGC  
GCCGCCCTCTATACCGGCTAATGAGAAACCGAAAAATGGCGGTGCAACGGGTGCGGTTGCGGCTCTATTTGCCATCGAAACCG  
CCATGCGGGCAGGCGAAATCTGCGGCTTAAATGGGCAGATGTGAATATGCGGCGTCTGATTGCCCACTCCCAATAACTAAAAA  
CGGCGACAGCGGTGACGTGCCATTATCTTTCGAGCGCGCGGAACTAATAGAGCAACTGCGCGGAATTGATGACACATGGGTGTTT  
AGCCTGGATGCCAAAGCCTTGATGTATTATTCAGGCGAGCGCGGATAATTGCGGCATACAAGGCTGCAATTTTACACGACCCC  
GCCGCGAAGCCCTCACGCGCTATCAAAAAAGTGCCTGTGGAGGCTTTGGCAAAAAATCAGCGGGCATCGGGATTTAAGGATTTT  
ACTCAATGTTTACTACCGCCCCGACATGGCGGATATTGCAAAATGTTGGAT

## SEQ ID 182

MATITQRNGKWRVQIRMKGVSR SATFERASDAKAWAARIESQIMDGIQGNAPRNTIFADLIRRYLSEVTPSKRGAREESYRIGRA  
LKTPLAKVRLADLRPD FADWRDQRLQEV SPTSVGRELTTLSAVCEHAMKEWGLLREN PVRKISKPKKSRRARTRPTEQEIADIC  
AALLYRPNEKPKMAVQ R VAVAVLFAIETAMRAGEICGLKWADVNMRRRIALHPITKNGDSRDVPLSLRAAE LIEQLRGIDDTWVF  
SLDAKSLDLVFRARDNCGIQGLHFDTRREALTRL SKKVPVEVLAKISGHRDLRILLNVYRPMADI AKMLD

## SEQ ID 183

ATGACATATTTAAAAGTAATAGCAATTAGTATAGTTTTATACATTTTATTATGCAAAATTAATCTTAAATGTTAGAAAAAGGA  
TTGATTTCTTAGTAGAAAAATATAGATAAATATTACAGCAATATGGATCTTACCCAAATATTTTGATTTTATATCAACTAAAC  
TGATTTTACCACGTAATCATATTGTGATTTTGGGATAAAAAATATTGCAGGATATGGTAATTGTTACTTCGTAAAGAAATGATAAA  
GACTATACTATTTTAGTCATGGGTTTCTCATCGAAAAATACTATTTTCATCTCAATAAAATAAAGAAATCAATTCAAATAAAT  
ATGAT

## SEQ ID 184

MTYLVKVIASIVLYILLQLINLKMLEKRIDFLVENIDKYYQYQSYSPNNFDFISTKTDFTTESYCDFWDKNLAGYGNCFVKNDK  
DYTILVMGFSSKILFSSHNKIKEFNSNKYD

## SEQ ID 185

TTGATGACCCATTACGTTACGTTTATGTCCCAACCCACAACGAAATTTCCCGCGTCAAAATCCCCGCGTTTTGACCTGATGC  
GCTTGGGCTATGATTATCTTTTCGCTAAAAAATGCAAAATGGGACAGACAAACCAATATCTTTCCCGAAATCTTTGTAGACAGCCT  
CTGCCGATCAATCCGATTTGCGCGCGGATGATGACGCGCGCTGCTTGGCGACATACGCTTAGAGCTGGATAACGAAGATTTG  
GGGCAAAATTTTACGAACGCCCTACCAATCAATCCGGCGTAAGAAGCTGATCGATTTCCAAATTTTGACAACAACAGTTTCC

ACGTTGTAAGTGAAGTTCGCTTGTATCAACGGCGACGAAGCATTCCGCCCGGACATTGCCCTGTTGGTAAACGGCATGCCTTTGGT  
 CTTTATCGAAGTCAAAAAGCCCAACAATAAAGGGCGCATCGGCCGAGAGCGGAGCGCATGGGCAACGTCGCAAAAATCCCAAA  
 TTCCGCCGTTTATCAACATCACCAATTATGATTTTTCACCAACATGGAATACGACGACGGCGCAACCGCGCAAG  
 GCGCGTTTACGCCCTCGTCTGCTTGGCGCAAGCCCGTATTCAACTACTTCCCGGAAGAGCATAAATTAAACCTTACCGAATTATT  
 GGACACGCTTTAGACGACCTTGAAAACAACGTTCTACAGACCAACCTGCCCGTTATCAACACAGCCCGAATTATCAGC  
 AATAAATCGCCCGATACGCGACCAACCGCATCTGACTTTCGCTGCTTTGCCGCAACGCTTTCTTTCTTCTGCAACACGGGC  
 TGACTTACGTCAAAGCAAGTCAAGGCTTGGTGCAAAAACACATCATGCGGTATCCGCAGCTATTGGCCACCTTGGCATTGAAAA  
 ACATTGGGCAACGGCGGCAAAAAGGCGTGATTGGCACACCCAGGCTCTGGCAAAACCGCGCTTGCCTATTACAACACCCGC  
 TACCTGACCCACTATTATGCCAAACAGGGCATCGTCCGGAATTCTATTTCATCGTGGACAGGCTTGATTATTGAAACAGGCGC  
 AGCGCGAATTACTGCCCGCGATTAGTCTGTCATACATCGACAGCGCGAAGCCTTTGCTGCCGACATCAAATCCGCCCAAC  
 TTGCAACACACGCGAGCAAGCGGAAATCACTGTTGTTAATATCCAAAATTCGAAGACGACCCGATGTCGTGCGCCGTAAC  
 GACTACGACCTCGCCATTACGCGCTTATTTTCTGACGAGTACACCGCAGCTACAACCCCAAGGCTCATTTCTTGCCAACC  
 TTAATCAGTCCGATTAACCGCGTCAAAATCGGGCTGACCGGCACGCGCTTATCGGCGTAACCGCAGGCAACGTCAACACCCG  
 CGAATCTTTCGCGACTACATCCACAAATACTATTACAACGCTTCCATTGCCGACGCTACACCTGCGCCTGATACGCGAAGAA  
 ATCGGCAGCCGATACAAGCGCAATTACAAGAAGCACTGGCGCAACTTGAAATCGAAAAGGCGAGCTTTGACCGCAAGAAATCT  
 ACGCCCATCCGCATCTCGTCCACCCGATGCTTGACTACATCTTGGACGACTTCGCCAAATTAGAAAACCAACCAAGCAGAG  
 CCTCGGTGCCATGGTCTGTTGCGACAGCGCAGAACAGGCACGCCAGCTTTTGGAGCATTTTCAGACGCGCTCAGACCACAATTC  
 ACCGCGCGTTGATATTGACGACGTCGCGCACTAAGGAAGAAGCAGCAATGGGTTAAAGATTTCAGAGCGGCAAAATCGACA  
 TCTTGTGTTGTGTAACAACATGCTTTTGACCGGCTTTGACGCGCGCGCTGAAAAGCTCTATTGTTGGCAGACTGATAAAGCCCA  
 TAACCTTTTACAAACCTGACCGCGTCAACCGCACCTACAATCTTACCGCTACGGCTATGTCGTGCTGATTTTGGCGATATCGAA  
 CGCGAATTGACAAAACCAACCGCGCTTATTGGGACGAATTTCCAACGAATTGGGCGACGAAATCGGCAGTTACAGCCAGTAT  
 TCAAAACCGCGCAAGAAATCGAACAGGAATTCAGACATTAATAACCGCCTGTTGATTTCGATACCGAAACCGCGCAAGATT  
 TTGCAGCCAAATTAGCCAAATAGAAGCAAAAAACAGCTTACGCTTAAAAAAGCCCTGCAACCGCCAAAGAGTTGTACAAC  
 ATCTTGCCTGCAAGGCGAGCCAGCAATTTCTTGGCGACTCTGAGCTTAAAAAAGCCCTGCAACCGCCAAAGAGTTGTACAAC  
 GCGAATTCGACCAAGACGACCCGAATACATCAGCTTGGCGAAGAGCTGGAACGCATCTTCAAGAAAAGAGCTTGGCGAAG  
 TCGGGCAAGAAGAAATGCGGCAACATCGCCCACTTCAACCGCTCTATACCAAAATCAAGAGCGCAACCGCAACCAACGACCT  
 CTTGCGGCACAAATACGGCGCGGACGCCAAATACGCAAGGCGACACCGCCCTTGTCTCAATGAAGCGCTGGAAGAGCTTTACTT  
 TCAATTCGTCAAATCGGCGAGGCGGAATCAAATTCGCGACGATTGAAAGACATCATGCGCAAGTCCGCGAAGGCTTGGCG  
 GGCAATTCGACCAAGACGACCCGAATACATCAGCTTGGCGAAGAGCTGGAACGCATCTTCAAGAAAAGAGCTTGGCGAAG  
 TCGGGCAAGAAGAAATGCGGCAACATCGCCCACTTCAACCGCTCTATACCAAAATCAAGAGCGCAACCGCAACCAACGACCT  
 CTTGCGGCACAAATACGGCGCGGACGCCAAATACGCAAGGCGACACCGCCCTTGTCTCAATGAAGCGCTGGAAGAGCTTTACTT  
 CTCAAAGTCTTTAACCGGCTAAGCGGTGTAAGAACCGATGCGGACCAAAAGTGCTGGATATGGAGCAGATTTTGGACAACCAAA  
 ATTACTTTGAAAAACAAATGCAAGGCATCGTATTAAACGCTTTAGAACGGAACAGCAATTCCTGTTACGCTGACAGCATCCA  
 AGCCATCAACCGCTGTTGGTGGCGGAATATTAAAAAGAAAGCGGCGGATT

## SEQ ID 186

LMTHYVTFMSQTHNENSrvKIPAVLHLMRLGYDYLKLNANWDRQTNIPPEIFVDSLRLINPDLPPDDARRLLADIRLELDNEDL  
 GQKFYERLTQSGGKKLIDFQNFNNFHVTELPCINGDEAFRDPDIALLVNGMPLVFIEVKKPNKGGIGEERERMGKRAKNPK  
 FRFRINITQFMIFSNMYYDDGATEPAQGFYASSACGKPVFNYPFREEHKLNLTELLDLSDDLNNVLQDNNLPVIXHSPFIS  
 NKSPDPTPTNRLTSLLCRERLSFLLQHLTYVKASQGLVQKHIMRYPQLFATLAEKHLANGGKRGVWHTQSGKLTALAYNTR  
 YLTHYAKQGIIVPKFYFIVDRLLKQAQREFRTARDLVHTIDSREFAADIKSAQTLHNHAGKAEITVNNIQKFQDDPDDVYVARN  
 DYDLAIQIRVYFLDEVHRSYNPKGSFLANLNQSDVNAVIGLGTPLIGVTAGNVNTRRELFGDYIHKYYNANASIDGYNTLRLIREE  
 IGSRYKAQLQELALQLEIEKGSFDRKEIYAPHFVHPMLDYILDDFAKFRKTNQDESLGAMVVCDSAEQARQLPEHFQTASDNHF  
 TAALILHDVGTKEERDQWVKDFKAGKIDILFVYNMLLTGFDAPRLKLYLGRLLKAHNLQTLTRVNRYKSYRYGYVDFADIE  
 REFQKTNRAYWDELSENLDEIGSYSQLFKTAERIEQEIADIKNALFDFDTENAEFCQSISQIEDKQLLALKKALQTAKELYN  
 ILRLQGSHEFLAHLDFDKLNLRYRETAARLDTLNLAEKLQGGDTAHLLENELEDVYFQVKIGEAELKLADDLKDIMRKVREGLA  
 GNFDQDDPEYISLREELERIFKKKNLAEVGQEEQMNIATLQTVYTKIEPNRQNDLLRHKGGDYAKYRIHKLRLMENAALYGDK  
 LKVFNALSGVKTADQKVLDMQILDNQNYFEKQMGIVLKRFRTEQQFPVQPADIQAINRLLVREYLKESGRI

## SEQ ID 187

ATGAATCATTTTAAAGAAACAACAATTCAAAATATTGCTGATTTTAAATCCGAGAGAGCAACTAGCCAAGGGAGCATTTGGCAAAAA  
 GTGTTCCGATGCAATGTTGAAAGAATTTCACGACAAATTACGGGTTACGAAATCAAGGCATTTAACCGTGGAGCTAAGTTTCG  
 CAATGGTGATACCTTATTAGCTAAGATTACCCCGTGTGGAAGAAATGGGAAACCGCTTTTGTAGATATTTTAGATGATGGAGAA  
 GTGGCTTTCGGTCTACCGAATTTATCGTGTAAAGAGCAAAAAATGAAACCAATCCCGAATTTCTCTATTATTTTGCATCAGTC  
 CCGATTTTAGAAAACGAGCGATTGAATGTATGGAAGGAATTCGGCGCAACGTCAGTGAATAATGCAATTAATAACACTGGA  
 GTTGCTTATCCAGAACCTCAAATCCAACATCCATCGCCCGCTCTATCCGCTTTGGACAAAAAATCGCCCTGAACAAACAA  
 ATCAACGCGCGCTGGAAGAGATGGCGAAAACCTGTACGACTACTGGTTTGTGAGTTCGATTTCGCCGACGCAACGGCAAGC  
 CCTACAAATCTCAGGCGCGGACATGGTGTGTTGACGAAACCTTGAAACGGGAAATTCCGAAGGGGTGGGGAAGTATAGAATTACA  
 ATCTTGCTTAGCAAAAATCCCAATACACAAAATATTAAATAAGATATTAAAGGATTTTGGAATAATCTCTGTTGTTGACCAA  
 AGTCAAGATTTTATTGTTGATTTACCAATGATGAAAATCTATATTAAACCCACAAGATGCTCATATTATTTTGGTGATCATA  
 CAAGAATTGTTAAGTTAGTTAATTTTCAATATGCGCGGGGAGCAGATGGTACACAAGTAATATTAAAGCAATGAACGAATGCC  
 AAATATTGTTTACCAATCATAAATCAAATAGATTATCAAGTTATGTTTATGCTAGACATTTTAAATCTTAAAGAAATTT  
 AAAATAATTTTGCTAGTAAAGATATTTCTCAAAAATATAATGAAATAGCAAAATCTTTCTTTGTTAAAGTTGCAAAATATCTAA  
 ACAAACCCACCTGACCCAACTACGCGATTTCTACTACCCATGCTGATGAACGGGCGAGTATCCGTAAGATGTAGCGGAGC  
 AAGAGATGGA

## SEQ ID 188

MNHFKKQIQNIADFNPREQLARGALAKSVPMAMLKRFQRIQITGYEIKAFNGGAKFRNGDTLLAKITPCLENGKTAFFVDILDDGE  
 VAFGSTFIVLRAKNETNPEFLYFAISPDRKRAIECMBSGSRQVRNENALKTLELPIPEPQIQQSIAAVLSALDKKIALNKQ  
 INARLEEMAKTLYDYWFVQDFDPDANGKPYKSSGDMVFDLTKREIPKGWGSIELQSLAKIPNTTKILNKDIDFGKYFVVDQ  
 SQDFICGFTNDEKSIINPDQDAHIIFGDHTRIVKLVNPOYARGADGTQVILSNNERMPNYLFYQIINQIDLSSVGYARHFKFLKEP  
 KIILPSKDISOKYNEIANTFFVKVRNNLKQNHHLTQLRDFLLPMLMNGQVSVRCSGARDG

## SEQ ID 189

ATGGATAAACTATTTAAATATTTATTAATATAAGTAGTACATCTTTGCTGTTATCAATATATTTTATTAATCGCAATATTATA  
TATTAGACCTTACTTGGTTTTATCGTGTAAATTTCAAATCATTTGGATAGAACTATTTCTAAGTTAAGTCTACTTTTTTATTTTCT  
AATACCATTATCGCAACCGCTACTGCTTTATGGCTAAGCAAATCTTGGGGAAGGATGAATTCAGCAAGGAGAGGTGAAAGAA  
TTAGAATATGTTAACGATAATTTCTTACCTAGCTATCTTGGTTATTTTTTGTGCTCTAAGCATACCCGATAATAATCTTTTTT  
TGCTATTTGTTATGTATGGAATTTTCTTACTAGTTTCATGCTCTAAGTCATTTTATTTTAACCCGTTTTTTCTTATTTG  
CTATCGATTTTATCAAGCAAACTGAATCAGGGTTATTTAGTCTGATTAGTAAACAGGAATTTAGAACGCCACAAAGTGTA  
AGTTCGATTGCTGTATATCGAATTAATAATTTTACTTTCTTAGAAAAA

## SEQ ID 190

MDKLFKILLNISSTSLLSIYFIKSQYYILDLTWYFVRVISNHWIEPIKSLSLFYFLIPIFIATATVWLWLSKYLKDEPKQGEVKE  
LEYVNDNFLPSYLGFFVALSIPDNNLFLFVYGIIFLLVSCSKSFYFNPVFFLFYGRFYQAKTESGLLLVLISKQEFRTPOSV  
SSIAVYRINNFTFLEK

## SEQ ID 191

ATGAATTTTGTGTTTAGCTAAAATTACTTGCAGAAAGATTTAGTAAAAATATTATCTGATGATCATATTTTCCCTGACTTTTCTT  
ACGAGAATTTAAATTTTATAACATATAACTATGATTACAATCTTGTATGATGATACTTGGTTTCAAATTTGAAAATTTAAAGAAATCA  
AGATTTTGTCTTAAGTTTGTGGATAACTCAAATTTATTTGATTCAAAAATGTTTAGTGAAATAAAAAAGGAAGAAATAAATATA  
GAGAACTAAAGTATTTAGTATCTTGTACTAATGATGCATTTCTTCCAGAAAATCACAAGTTCATTATTACTCAAAAAGAAGC  
ACTTGCTAACTATATGCGGAAATGGTGCAGAACTATGCGAACCACAAGACTTATTTGGTTATTAAAGATATTCTGATGCTGTTTA  
TATAATAAAGGATGATAAATTAATATTAGAACCCTTCTTCTATTTCAAAATATATTAAAGGGATTGAAGATTTGTATCGAGAA  
GCTACAAATCTGAAGTACAGCAATCTTAGAAAGCGATTATTGATTAAAAGAAGATTTTAAAGTGAAGAAGTATCTATTTC  
CCAATAGGAAAAGAAATAGCTTTAGTTCAAGATAGATTGAATAATATGACGCTAGATCAAAGACAAGAACTATTAAATTACCTTGC  
TGAATATAATAATAATATCTTGAAATTTAACGCAGATGGCTCTCGTGTAGAAAATTTCTACTGATGTACAGCTGAAACATTTGTTA  
TATGGTATTGATGAACGTTATTACACAACAGCATTAGGAAAAGAGAAAAGGTTGGCAAATAGTGTCAACCTATT

## SEQ ID 192

MNFVLAKITCKKDLVKILSDDHIFPDFSYENLNFITVNYDYNLDDTWFQIENLKNQDFCPKFLDNSNLFDSKMFSEIKKEEINI  
EKLKYLVSCTNDALDFQKITSSLLLLKKHLLTICNGAKLCBPQDLLVIKDIIDAVYIIKDDKLIPIRFLSSISNIFKGIEDLYRE  
ATNTEVQQFLESDFIDLKEDFLSEKVSIPNRKRIALVQDRNLNMTLDQRQELLNLYLAEYNNNLIKFNADGSRVEISTDVQLKHL  
YGIDERYTTALGKEKRLANSVQPI

## SEQ ID 193

ATGGGAAACAGCCGATTAAGCCAACTCCCGCGCCCGCCGATCGAAGAAACCGACTTTGAGGGCATCTTCGCGCGCAAAAAAG  
CCGCCCCACCGCCCTATGTCCCGAAAGCATCCCGCGAAACCGTCGCCAAACCTCGAATTAGAATCAGAACCCCTAACCATCGA  
CCTGCAACAGCAAGCCTATCAAGAGCTGCTCGTCCGCAACCGCATCAACGAAGCCGTCAAAGCCAACTCTTGGCATACGCACAA  
GGCAGCGACCTCGACCACATCGCCGCCCAATACGGACTTTTACGCAAAAACCATCCGCGCCGCGGACCCCGACGCGCAACCCGCGG  
TTGCGCCCGAATACGAAACCGACGCAATTCGCGCCCGCGTCCAGCCCATCCCGAAAAATACGCGCCGCGGCGCGCACCCGC  
ATACGAAGCCACGCCATCGACGCAACCCCAATCACACAGCCCGCGCGCTGCGCCGCGCGCGCGGACCGGTGGAGGTTTACA  
TCAAAACCCAAAGCGGCACGCCGACGAAACCATTT

## SEQ ID 194

MGNRSLSQLPAPAAIEETDFEGIFARKKAALTALCPESIRETVAQTLELESEPLTIDLQQQAYQELLVRNRINEAVKANLLAYAQ  
GSDLHDIAAQYGLSRKTIIRAADPDANPPVAAEYETDDAFRVRVQAHPEKYAAGPRATAYEBAHAIDAPPKSHTPAPCAAPPARWRF  
SKPKAARPTKPF

## SEQ ID 195

ATGAATCCGCTTTTACCACGAACCGCAGGATTTCCATAAGAAATATTGGATGGCAATATTCTTGCAACCAACAATAGAGCGG  
TAGTCAGCAATGCGGATGGGAGCAATACCCGAAGTTTCAATATAGCCAAGGGGATTGCCGACTTACTGCAATTCGGAACCGTTTC  
GGAAGATTACCCGGTCAGACATCGGGAATGCTTTTGAAGCAATATGCAGTGAGTTTGTCCAATCTGCTTTTGAATAATGTCAG  
CATATCAGACCCCGGACGCAATGTTAAGCAGGTCGGTTCTCGCAACCGCTCGGAAATCGCACGTTATCAGCAATACGCACATC  
TGACAGCCTTAGCCAAGGCTGCCGAAGAAAACCCGAATTGGCTGCGCCCTTGGGCAGTGATTACACCATTTACTCCCGATATTAT  
CGTTACCAGAAATTTGATTGCAGATGCGAAATCAACCGTAATGAATTTTATGTTGATGAAAATATTGCCACATATGCCAGTTTG  
CGTGCAGGTAATGGCAATATGCCGCTGCTCCACGCCAGTATCTCTGTAATGAGCAGATTGCGCAGGACGAGGCTCAAAATGCC  
GTTCTGAAGGATTGAATTTGGTTAGAAACAGAAAAGGCAGACTGCCGCACATTTGTTGCTAAGCGCAGAACCAACGCCAAGCCG  
CATTTTCATCTATTGCTTGGGTACAGGGGAAATAGATTGCGTTTACCATTTTGCCTTATATGAGCTGGAACAAATTTTACAATCA  
TTGAATTATGAAGACGCTTTGGATTGTTTTACATCATGGTCAATGGTATACGATTAAAGATATTTCGACCTTCCCTTAGATT  
TGGCATTT

## SEQ ID 196

MNPLFTQERRIFHKLLDGNILATNNRGVVSADGSNTRSFNIAKGIADLLHSETVSRPLPGQTSNFAFCAICSEFVQSAFEKLQ  
HIRPGDWNVKQVGSRRNLEIARYQOYALHTALAKAAEENPELAALGSDYITPDIIIVTRNLIAEINRNEFLVDENIATYASL  
RAGNGNMLLHASISCKWTIRSDRAQNARSEGLNLVRNRKRLPHIVVVTAEPTPSRISSIALGTGEIDCVYHFALYELEQILQS  
LNYEDALDLFYIMVNGIRLKDIDSLPLDLAF

## SEQ ID 197

ATGACCACCGAAGTCAACAGCGGACAAGTGCGCGGCCCGGTGCAACTGGCGTTTGCCCAATCCATCGATCCGATTGTGCCGCCG  
AAGTTTCCATCACACGCATGGCGGTAACCAATGAAAAAGACTTGGAAAAAGAACGCACCATGGGGCGCAATACATCGTCCCTTA  
CGTGGTCTACCGCGTCATGGCTTTATCTCCGCCAACCTTGCCGCCAAACCGGTTTTTCAGACGACGACTTAGCCAACTCTGG  
CAAGCCCTGACGTTGATGTTTGAACACGACCGCTACCGCCCGGTGGAGAAATGGCGGCACGCAAACTGGTTGTTTTCAAACACG  
ACAGCGCACTTGGCAGCCAGCCTGCACATAAACTGTTTACGCCGTGAAAGTCGAACGCGTAACGCGCAATCAGGTACGCCCGC  
AAGCGGTTTTGGCGATTACAAATCAGCGTGGTTTACAGCGGGCTAAATGGCGTGAGTGTGAAGAGTATTTG

## SEQ ID 198

MTTEVNSGQVRGPFVQLAFAQSIDPIVPPEVSITRMAVTNEKDLEKERTMGRKYIVPYVVYRVHGFISANLAARTGFSDDDLAKLW  
QALTLMEFHDRSAARGEMAARKLVVFKHDSALGSQPAHLKLFDAVKVERVNGESGTPASGFGDYKISVVSGLNGVSVEEYL

## SEQ ID 199

ATGAATGCTGTCCAAGTTTAAACTTTCAACAAAACCTCCGTCCTACTGTTGCCGATAACAAAGCGAGTTGTGGTTTTTGGCAA  
ACGATGTTTTCGAGATTTTAGGCTACACCAACCCCTCGCCGAACGGTTGACCTGCCTGCAAAAGCAGGGCGCTAACAAAACGGTA  
CACCCCACCACCAGCGCGAACAGGAGATGACCTATATTAACGAGCCGAATCTCTACCGCTTGATTATCAAAATCCCGCAAGCCT  
GCCGAGAAAGCGTTTGAAGAATGGGTAATGGAACCGTCTGCCCGCCATCCGCAAAACAGGCGGCTGCCAAGTCGGACCAAAAA  
CCACCGCCGACGACCGTACCGGATTGCGCCAAGCTGTTGCCGCGCTTGTCCGACGCAAAAGGTATAGACTACTCTCCCGCTACAG  
TATGATACACCAACGCTTCAACGTCGAATCCATCGAAGACCTCCCTGCCGGAAGCTGCCGAAGCGCTCGCCTACGTCCACGCA  
TTGACACTGCACAGGGCTTGACAGGCGAAGTGTGGACGCAACGCCCAAGCCGAGCCGAAATGCCCATCGACGGCAACTCTT  
TAGCCGACATTGCCGCTATGGTTTATTACGGCACATGGATGATTGAATCGGGCAAGACATCTCCGCGCGCTGAAGCAGCTCGG  
CTGACAGGCGCGGTTACGATGTGGACGGTTTGGCAGCAAAACCGTCCAATCTGAAAAGATCCGCGCGCGCCCTCGAAGTGTG  
CGGGATATGCGGACAAAGACGCTCCGACCGCATAGCCGATGTCTTGAAGGCATTTACGGCAAGGCTACGGTAAGG

## SEQ ID 200

MNAVQVLNFQNSVRVTVADNKGELWFLANDVCEILGYTNPRRTVDLHCKSRGVTKRYTPPTSSEQEMTYINEPNLYRLIIKSRKP  
AAEAFBFWMETVLPAIRKTGGCQVGPKTADDRTGLRQAVAAALVGRKIDYSSAYSMIHQRFNVESIEDLPAGKLPEAVAYVHA  
LTLFTGLTGEVLDAPPKAEPLPIDGNSLADIAAMVYYGTWMIESGKDISAPLKQLGCRQAVTMTWTVWHETRPILKRSAAALEVL  
RGYADKDASDRIAACLEGIYKATVR

## SEQ ID 201

ATGGCACAAGACGAATACGGCCTACGGCGACCCGAGCGCATGATGAAGCAGGCGGCGGGCTGTTTGCATGTCATATGCAGC  
GCAACAGTACGCTGAACCGTTTGGCGGGCAAGATGCTTCCGGTACCGCGGTGCGGAGGCGACTTTGCGCAACAGACGACCCA  
GCATATGCCGGTCTGCGCTGTGAGGATTGACGCGCGGCGATGGGTGACGAATCCGTTTCAATTGGTCAACCTGTTTCCGCC  
CTGCCGATTATGGCGGACAAACACGGCGGAAGGCGGCGTGGGGATGAGCCTGTCCGAGCGCGGTTTGGCTGTGAATCAGGCGC  
GTTTCCCCGTTGACGGCGGCGGACGATGACGAATCAGCGCAGCCCTGCCGATTATCGCGCGCTGATTGCTCGGCGGCGGCAAG  
CCTGATGGACGTTATGCCGACAGACGCTGTTGGTGCATATGGCGGGCGCGCGGTTTTCATGACAAATATCGAATGGGCGTG  
CCTTTGGCGGGCGACCCGAAATTCATGATTATGCCGTCAATCCGTCAAAGCCCCGTCAAAAACCCCATTTTACGGCTTCGG  
GCGATGCCGTACCGGGCGTTGGGGACACGGCGGCGGAGTTGAAGATTGCCCTCTACCGATTGTTTACGATGGATACGGTGGACAG  
TATCGTACCGTGCTCGACCAGATTCCGCTGCCGCGCGGATTGTGAAGTTGAGGGCGACAAGGCGGCGGTTGATTGCCCTTTG  
CGCGTGTGGCTGCTTTCCCGCGCGCAGTACAAACCGTTTGGCGCGGATCCGAAATTCGCGCAGCTTCGCGCAATCGCGC  
GCGCTCCCAGGCAAAATCAAATCCGCTGTTTGGGCGATGCGGGTTGTGGAACGGCTTTATCTGTTGAAAATGCCGCGCCC  
CATCGTTTCTATGCCGGCGATGAGATGAAGTATTGCCCGGATAAGTTTCAGCGAGGCGGAATCGGGCTTGAATAACCGCGCTTCG  
TTTGGCGACAAGTTTGGCGTCGACCGTTTCGTTATTTGGGCGGCGAGGCGGTGTTGGAGGCGTTTGGCAATACCGGCAACACG  
GCGGTATGCCCTTCTTTTGGTCTGAGAAGGAGCTTGACCACGGCAACCGTGTGGAACCGCTCGTCCGTACGATACCGGCTGTGGC  
GAAAACCGCTTTCGCGTGGATGTCGGCGGGGTGCGAAGGAAATTACCGACTACGGCGTAACGTTTGTGGATACGGTGTCTCT  
TTGCACGGCGGTATCCG

## SEQ ID 202

MAQKTNNTAYGDPQAMMKQAAGLFAMHMQNSTLNRLAGKMPAGTAGAEATLRKQTTQHPVVRCDLTRGMGDEIRFNLVNPVSA  
LPIMGDNTEAGRGVMSLSEAGLRVNQARFPVDGGGTMTNQRSPADYRALIRPAAQSLMDRYADQTLVHMAGARGPHDNIEWGV  
FLAGDPKFNDYAVNPFVKAPSKNRHFTASGDAVTGVGDNNGELKIASDFTMDTVDMSRMTVLDQIPLPPPVIKFEKGKAAGDSPL  
RVWLLSPAQYNRFADPKFRQLQASALARASQANQNPFLFDAGLWNGFPIVVKMPRPIRFYAGDEMKYCADKXSEAESGLKIPAS  
FADKFAVDRSVILGGQAVLEAFANTKGHGMPPFFWSEKELDHGNNRVETLVGTIRGVAKTRFAVDVGGGAKEITDYGVTVVDTVVP  
LHGGIR

## SEQ ID 203

ATGACAGTCCGAAACACGCAAAACCGAAACCGTCCGGACGGAAGCCGCGCCGCAACAAGCGGCAATACCAACCCGGGCTATTACA  
AAAACCGCGCTTCGAGTGCCTGGGTTTGGCGCAATACCTCAACTTCAACCTCGGCAACGCTTCAAAATACATCTGGCGGCACAA  
GGAAAAGGCGGCGCGAAGACTTGGAAAAGCCCTGCGGTACTTGAACGCCAAGCGCGCGCGCGCGGCAAGTTCAAGAAACTC  
AAACACCGCGCTATGAAAAATGTACGCCGCTGTAAGATTGCGGGTTTCAGCGGCGGACGAGGCGCGCTGCTTCCGCTCA  
TCTCCGCGCTTATTACATCCGCGACGCGCAAGACAATTTGCGTGGCGCGCGCTGTGTGGAAGATTGTTGGAATAAATGCC  
GCCTGAAGCGGGCGGGCCCCGACCCCTGAAGCCCGATGCCGCTGAAACGGCGGGCGGAGGCATT

## SEQ ID 204

MTVRNTQTETVRTEAAPQGGNTNPGYKNAFECVGFQYLYLNFNLGNAFKYIWRHKEKGGREDLEKALRYLERQAGAPKFKKL  
KHRRYKMYAGLKDCCGFDGGTEALLAVISAAYYIRDGEDNFAWAAACVEDLLEKMPPEAGRAPHPESPMPPETAGGGI

## SEQ ID 205

ATGAACCGAATCGAGGAAACGGAAGCCGTCATCTAGCCAGCGTAGGGGCGGAACAGAACATTTTGGCGGCGCATCTTGATTG  
AACCGACGGCGATTGCGCGGTGCGCAATCTTGACCCCTGAAAAGTTTACCAGGCGCAACACAGGATTATTTCCGCGCTCTGCT  
GGATATGGCGCGGCAACAGAGCTATCGACATCATCAGCTGGAACGACAAGCTGGAAGCGCGCGGCGAGGCGGAAAACGCGGGT  
GGCTTGGCTTACTGTAGACCTGAACCAAAACACCCGAGCGGAAGATATCAGCCGTTACGTTGGGATTGTGAACGACAGGT  
TTGTTCGAGCTTGCCTGCTGAAGGCTTCGCGCGGATGGAATAATCCGCGTTTCCAAAGACGCGGGACGCTCGCAGAAAAGCT  
GTCTAAGGCGGCGGATGAATTGGCGGCGAGTCCGCAAGACGCGGTAAGCGTGAACCAAGACATTGCGCCAGACCGTTGAGGAT  
TTGATTGGCGGTTTGGACAAAAGGCTTGACGGCGTGCCTTTCGATTGCTTACCGCTTGATGAAGCTTGACGGGATGACCGGCG  
GTTTGGCGGATGGAACCTGATTGTGATTGCGGCGGCTCCGTCTATGGGTAAACCGTTTGGCGGAAAACATTGCGCGATTTCG  
GCTGAAGCAGGGCAAGGCAGTTTCAATTTCCAAAGCTACGAAATGAGCGCGGTAGAGCTGGCAAGGCGCGGATGGCGGCTGAGTGC  
AATATCCCCATGCAAACTGAAAACCGGCAATCTGACGCAAGACGATTACGCCAATATGCCGATTACGTGACGCAAGCGAAAG  
AGTGGAAAGTTTGGCTGAACTGCGACCTGCTCAACGTTGACGAGCTTTCCTTTTGGCTAAGGAGAAAACACTCACTACCGGCTT  
GGATTGTTGTTGTCGATCACCTTTCATCATGCCAAGGGCAGGGAGGACGAGTGGCGGAGTTGGGGAATATATCGCGCGCT  
TTGAAAACCTTGGCGGCGAGGCTGAATACCCCGTCTGCTTGGTTGCCAGTTGAACAGGGGAAACACAAAGCAGGCAGACAAAC  
GCCCGAATATGGCAGACATTGCGGCGAGCGCGCGATTGAGCAAGACGCAACATCATCATGCGCGACCGCGAAGGCTACTA  
CGACGGAAACGAGAATCCGAGCATTCCGAGCTGATTATCGCCAAGAACCGGGACGGCGAAATGGGAACGGTGGTTTGGCGCTG  
AAAGGCAATTTATGAAGTTTCGAGGAAGAGCTGATTGGCATGGCAAGCCCCCAACATGATGAATATGACCCTTACAGTGTCT



## SEQ ID 206

MNRIEETEAVQSLASVGAEQNILGGILIEPTAIARCAITPEKFYQAOHRIIFRALLDMAAANEPIIDIITLNDKLEARGEAEANAG  
GLAYLIDLNQNTPSAKNISRYVGIIVNDRFVERGLLKASAAIEKIAVSKDGGTVAEKLKSKADELAAGKDAVKRETKTFGQTVED  
LIGGLDKRLDGVRFGLPTGLMKLDGMTGGLPDGNLIVIAARPSMGKTVLAENIARFALKQKAVHFQSYEMSAVELARRGMAAEC  
NIPMQNLKLTGNLTQSDYANMPIYVSQAKWKFDVNCDDLNVDELCLFLAKEKLLTTGLDLLVVDHLHIMPRAGRDEVAELGNISRR  
LKNLAAELNTPVVLVAQLNRGNTKQADKRPNMADIRGSAIEQDANIIIMPHRESYDGNENPSIAELIIAKNRDGMGTVVCGW  
KGQFMKFEEDPLAWQAPKHDEYDPSV

## SEQ ID 207

ATGACCGCCCTCACACTCTACCGGTGCGCGGCAGACGTACAGCGCGGGCTGGATTACTACTTTGACAGCGAAACCGAGCGCGAAG  
ACACGCTGGAAGCGCTTATCGGGCAGTTCGAGGTCAAAGCGCAATCCGTTATCGCTTATATTAACCAAGAAATCACGGAATA  
AATGCTTGAAGGGCACATCAGGCAGATGACCGGGAAGCTCAAGCGCGCAAAAGCGCGGAATCAAAGCCTGAAAGACTACTTGGCG  
CGCAATATGCAGCGCGCGGCATTACCGAATCAAAGCGGATGACGGCATTTTAAAGCCTCGTTCGCGCAATCCGAAGCCGTCG  
TGATCTTAGCAGAAGCACAAATCCCCGCCGAATTTATGCGTGAGGCGGTCAAACCGCAACCGGACAAAACCGCCATCAGAAAAGC  
GATTGAAAGCGGTGCGCAAGTAGCAGGCGCAAGATTGAAGGGCGGAAGATTTCAGATTAGA

## SEQ ID 208

MTALTLYRCAADVQAGLDYFFDSETEREDTLEAVIGQFEVKAQSVIAYIKNOBITEKMLEGHIRQMTGKLKAARKNQSLKDYLA  
RNMQAAGITEIKADDGTFKASFRKSEAVVILDEAQIPAEFMREAVKTEPDKTAIRKAIESGRQVAGAKIEGRKNLQIR

## SEQ ID 209

ATGTTGTCTGCGCGCAAAGGTATCGGAAGACGAAGCCCTGACGTGCGGCATCATGATGCGGCTGTCCCTGCAGGATATGCGCTATG  
CCTGCAATCAGGAATTAATCAACTTCGCCGAACATATCGTCAAACAGGTGCAACGCTTGGGCTGTACTGCAACACTGACGACCC  
CGCAACGGGGAAAGCGTACTGTTGCTTGCCTGCCGGAAGCATCGCAGGCGCTCGCTCAATGGACTAAAGATTTTGACAATTTAAGC  
CCGAATCAGCGCCAACCTGCTGCTGCTCCGCTGTCAAATCTCTTCGCGCGGTACGAAGAATTTCTGAAAGACGCGCTGCACGGC  
TGATAGCCGAAGTATCGGCATACTCATTTGGCCGTGCGGGTTGCCAAGAAAGCCATGGCGTTTTTAGAGCTTGACGGCGGTTTGAT  
TTCCGGCGTTGGCAAAGTCGTCAACGCGCGGATTTCGCGCGCGGAAGCCCGCGCTTAAATGCCGTACGCGGAATTTACAGGC  
CGGATCCTACACGCCCGCAACCTGCTTTACGATGTGGGCATTTCAGGCGGACAAGGAGCTTTTCGCGCATGTACGCGCAAGCCGCTGA  
ATCCCGTGGCGCCCCGACGGATAAGCGACGTGCGCGCGCGCATGATGAAATGCTTGTGTGCGGACAAAGCGCGCGCTTGGTCCG  
GGCCGTAAAAGACTCGGAAGACGTCAATCCGGCATTTCGACAAACGCGCGCGCTTCAGCTGCTTCAACTGGACCGAACATTTCAAA  
CGGACGGCAAACCTGATCAGCCTCATGCACAGGAAGCGCGCGCA

## SEQ ID 210

MLSGAKVSEDEALTCGIMMRLSLQDMRYACNQELINFAEHIVKQVQRLGLYCNTPDPANGESVLFACREASQVAQWTKDFDNLS  
PNQRQLVLRPLSNLFAAYEEFLKDAAPARLIAEVSAYSLAVRVARKAMAFLELDGGLISAVGVVNGADSRARRLKMPYAEFTG  
RILHAANLLYDVGIQADKELSAMYGKPLNFPVRPRRISDVRRPMMKMLVADKGGALVRAVKDSEDVIRHCDNGAGFSCFNWTEHFK  
RTANLISLMHREAAA

## SEQ ID 211

ATGAACAACAAAGACAGTTCAGTGCATCTTACTTGGCTTCGCGCGCGCTTCTATGCACGCGCAAGGGGCGGCGCTGCAACA  
CGCGAAGCATAGAGAGACAGACAAATACACCTCGTCTCGCAACAAAGGCAAGAGAACAACTATACCTTAAATGGCGGAAC  
CGAAGTCAAACCTTAAATTCCTTCATCATTTGCCGCCAAGCGCGGTACGAACAACATTACGATAAAAGGCAATTTGGCAGACGGT  
CCTGCCGATGCCCCGCGGACGATTGACAATAACTCGATTGAAAGAAATAAATAAAAACGGTTACACGTACGATGGCAGAATTT  
GGAGCGCGCGGTGATGTTGGTGATCAAAGCTATGAGGGAGAAATAAGGTTACTTTTGAAGAACGTAACCATAGCCGCCATAA  
CGCGCTTCCCGGCAATTTGTCTGATGATAGGCATAAATCCAGTAGCTTGGCGCGCGCGATGCTTGCCTTTAAAGGGCGCAATACC  
ATCAATATGGACGCGGACTCAAATGCCAATCTAGTAACGAAGGTATCCTATTGCTTAATAATGGTGAAATAATGGGAGAATATC  
GTCTTGTCTCCGAAGAAGGCTCGACGCTGAATATCAACATCAAATCAGGAAAGATAAAGGACAGGGCATTACCGCCAACCACTA  
TGGTAACCTCAGACATCAACTTCAACAGGCTTCTCCAAACATCACCACAATGGAGTTCAAGGGCGATGTAAACATTAATTCGAT  
AGGAACGGACAGGAAGAGCGGAAAGCAACGGTTTGGCTTCTATTCAAGCCGCAATTAGGCAATAAGAACGAGATTCCGGAAG  
GTTCTAAGATGGAAGCGATTTTCCGTGGGAACGTGATATCTGTTGCAACGCGCGTTTATGACGAGCAAGGCAGGCCAAAAGCAT  
AGGCAGCGCTTTCGATGACGGGAATAACAGCAAGTCGAGGTTGTGCGCGGGGAAGGCAAGGTTGTCAAATCAAAGCGCAT  
ATTTTCGCCTACAAACGCGCGCAGCGTGAGCGTGAACCTTGCCAAACAAAGACTCTTATTTGAAGGGGAAGCCCATATCGGAAAA  
GGAGCTTTGCCAAAGGGAAGATATGTTTGCCTTAACCGTGGATGCGGACGGATATGAATTAACCCCGGATACAAAGTCGATTGA  
AAAGAAAAGAAAGAGCTGAATGTTAGGGGCTGTACTAGATTATCCCTAAATTCACACCGATCCCGCAGGATTTT

## SEQ ID 212

MRQKRTVQCILLGFAAASMHQAQGAANAASGTIEKTDKYTLVLAKQOENNYTLNGGTEVKPLNSLIIAANGGTWNITIKGLADG  
PADAPPTIDNNSIERNINKGYTYAWQNWGAVMLVDQSYEGENKVTFFENVTLAAHNAPAGILSDDRHKSSSLAPAMLAFFKGRNT  
INMDADSNANSNNEGILLNNGEKMGEYRLVSEEGSTLNINIKSGKDRGQGITANHYGNSDINFNKASPNITTEFRKGDVNIKID  
RNGQEEAESNGFGFYSSRKLGNKKQIPEGSKMEAIFRGNVDIVATPVYDEQGRPKSIGSAFAIDGKYSKVEVVGGBGKVVKIGKD  
IFAYNGGSVSVNLANKDSYFEGEAHIGKRSFAKGDMAFALTVADGYELTPDTKSIKKKKELNVRGCTRLSLNSTPIPDQF

## SEQ ID 213

ATGAAGCGCGCGCAAAAGAACTGATTGGCCTGCTGCACGCGCGCGACGAGTTTCAGATGGCGGATTTGTACACCATTACGCTTT  
CGGGCGGCGGGTGCTGCGGCATACCGGCGCGGATATGCCCGTCTGTTGGGACGGTCAGGCCTACGGGGCGCACGAGCTGGTTAT  
CAAGCGCGGCGGCAACCCGTACCGCGTGGATTGGAAGTGATTCACACCCCTGCAGATTTCAGCCGCGCCGATTACAGGCTT  
GAGGGCTGCAATGGGCGGAGCGCGCCCTGGGCGGCGTATTGGACGCGCGCGGGTCAAATAGACCGGTGTGTTTTTGTATGCCG  
GACTGCGCCCCGTGGTGCGGTGAATATTTTTCAGGGCGCGTGTGCGACGATACGGGCGCGAGGTCGTCGTTGAGGACGCTCTATGACGACGCG  
GAAATCCGACATCGAGCTTTTGAACGTTTTCAGCCCGCGCAACATTTATCAGGCGGGCTGCATGAGGACGCTCTATGACGACGCGC  
TGCAAGGTCAACCGTGAGAAATTCAGGTAACCGGCGGTAACCGGAAACAGCCGACGCGGAACCGTGTGAAGCACAACTCTGA  
CGCAGCCTGACGGCTGGTTTTTCGAGGGCGTGATTAAGTTTTCGGGCGGGCGCAACGCGGGTTTGTAGCAGGACGCTCAAGGCACA  
CGCGCGCAACACGTTTCAACTTGCCTTCCGCTGCCCTACCCGCGCAGCGCGGGGATGCGTTCAAGGTTTATCCGGGCTGCGAC  
AAGCGGCGGATACCTGCAAGGATAAGTTTGACAATATCGTGCATTTTCGCGGCTTCCCGTTATCCCTTCCGCAGATACGGTGG

TG

## SEQ ID 214

MKAATKELIGLLHGGDEFQMDLYTITLSSGRVLRHTGADMPVVDGQAYGAHELVIKRGATRTAVGLEVDSENTLQISAAPDYRL  
EGLQWABAALGGVLDGARVKIDRVFFDAGLRPVGAVNIFSGRVSDVSGGRSSVKVDVKSDELLNVSSPRNIYQAGCMRTLYDDG  
CKVNREKFTVNGRVNTENSRTGTVLKHNLTQPDGWFSGQVIKFAGGRNAGLSRTVKAHGGNTFELALRLPYPPQAGDAFKVYPGCD  
KRRDTCCKDFDNIVHFRGFFIPFIPADTVV

## SEQ ID 215

ATGTCGGTTCAACCAAGCGTTTCGGAACAACTGAAAGACAATGCAAATGTTGATGCGAAAGATGAAAAAGTTATTGAATATCTGA  
AGAAATCATCATTAAGAGATGTACCAAAAGAATTGCAAGCCAAAGTATTAAAGGTTAAAGGTGATGAATATACAGGAGTGCGAAA  
ACAATATGCAGGTAAAGCTCGGTAGGGTGAATCTGTCAAGGCAATGCTATTCTAGACGGCGAAGAGCCGTTTAGTAAGGAACAA  
CTTCAGAAAGATGGATGTATATGTTAATGGTAAAAAATACGAAGGTAGTAAGGGGGGGGAACCTAGATGTTCTCCCAAGGTTTGA  
GTGAGCAAAAGATTGAGTTTACGGTGGGATAAAGAACAGAATTATGCGCTATTAAAAACTTGGGTTTATGAGCAACCGTATTC  
TGTGGTTAGAGGCTATTTTGGCTACAGTCGAAAAGACGGTAATCCTATAGAAGGGGATGGACAAAATCCTGAAGAGATTCTTTT  
GACTTGTATCTGGGCGACATTAGAGGCGTGGCAACAGATGAAGACAAATTACCCAAAGGCTGGGAGCTTTCAATATGAAGGTGCGG  
CATTGGCGGTAATGGGTTTATCCAAAGAATCGTTAGATAAACCATAATGGCGTATTTAGATACACAATTGATTTTGTATCGTAG  
AAAAGGCTCTGGCTCAATTGAAGGAATGGAACAATATGGAAGATCAATAGAGAAGCTGCTATTAGAGAATCCCTTATCGA  
GAGTCCCGCTCAGCTTGGGGTTGAAAGACCGGGTTTCTATTTCGGCGTGAACGAAGGGGTGCTATTGTAGAGAAGGAATATG  
AGATTAAGAAAGTATCATTTGGGTATTTTCGGCGAAGCGGCTAATGAAGTAGCAGGTGCTGTAAGCCAAGAGCATAAACATCAAGC  
TGTTATCGGTTTCGGCGCGGAGAGAAA

## SEQ ID 216

MSVQPSVSEQLKDNANVDAKDEKVIKSLKSDVPKELQAKVLKVKGD EYTGVRKQYAGKLGKGSVKAMLFLLDGEPPFSKEQ  
LQKMDVYVNGKKYEGSKGGLDVLPLKGLSEQKIEFYGADKEQNYALLKTVWVEQPYSVVRGYFGYSRKDGNIIEGDQNPBEIPF  
DLYLGDIRGVATDEKLPKAGSFQYEGRAFGNGVLKESLNDNHNGVFRYTTIDFDRRKSGSIEGMBQYGIKLEBAIERIPYR  
ESGSSLLGLKDRVSYPGVNEGVMLEKDNEIKKYHLGIFGEAANEVAGAVSQEHKHQAVIGFGEKK

## SEQ ID 217

ATGGCCGGCTGCCTGACCGACTTGGAAGAACTGTCTGGAAGAAATACCTCGAACAGTTCGGGCGCGGTATCGGAAAGTATCGAAGCCT  
GTACCGCCAACTGCAGGAGCAACCGTCGTTCTTCAACAGGCTGATGAAGCCAACGACAAGCTCAACAGGCAGATTGACGTGTT  
GCAGAAACAGTCCGGCAGCCATCCACAACGAAGCCTATATCGAAATGAACACGCTGCTTTACCGCCATCGCGAAGTAGTTTCCATC  
CAACACCGCAAAGCAGATTATGCGGAAAAGGGCAAAGAGCGGATTGCGCTGTTCCCGCGCGGTTTGAACGGCATCACCAAGCTGC  
CTGCCCGCGTCTGTTGCCCGAGCGTCCCTACCATTGATATGAAGGAGGTTCTGTATATATTTCTCCGAATACCGAGA

## SEQ ID 218

MAGCLTDLENCKEYLEQFGPVSEIEACTAKLQEQSPFFNRLMKANDKLNRIQIDVLQKQSAIHNEAYIEMNTLLYRHRREVSI  
HNRKADYAEKGERIALFPRLNGITKLPAVLLPERPHYFDMKEVLYIFSRIPR

## SEQ ID 219

ATGGGAATACACATATTTGAAATAACAGAAAAGCGGGGGCAAACCCGCCGCTGCATCTGTGCTGTACATCCCTGCTGTCGGA  
CTTACCGCTTCAACTTCGCAAACGCATCCGCCATCGCCGAATTGGTTGGGACACGCTCGTTGCGTGTGCTTTGCGGCCGGCTGT  
CCGTTGCGGCTGCGGTTTTCAGCTCGGACAGAATGTCAGAAATGGTCGGCAGTCCGAAGTGTTCGTGCGGTGAAGTCGGACCC  
TTTGATTGCTTACGCGCTCGCGGTTAACTGCCTAAATATGAAATCTTGGTCTTCTTG

## SEQ ID 220

MGIHIFEITEKAGAKPAAASVAVHPCRTYRFNFANASIAELVGRSLRCLRPVRSRLRFFQLGQNVQNGRQSEVFGVEVGR  
FDLLHALAVNCLNMKFLVFL

## SEQ ID 221

ATGGGATTATAGAACCGTTTTTATCAAGCTATACACCTTTATCACGAGATTATGTACAAGCTCGTACTAACCGAAAAACGACAAA  
CCCTACTTTCCAAAATCGTATATACGCACCTCGGCTTTACGCGTTTCAGTAACTGAAAACCTCTAATATTCGACAAATAAATTTCTT  
GATTAAGCGTGGTTCGAGCATCCACAAGGCAAGCTAAATAAAAAAGAAATTCGCCCATGATGTTAGTAGACTTAATAAACCTTT  
CAACAAGATTATCTAACCGAAACAGAATTGAATGATTATTTTCAACAGGGAATAGAATCAGGATTATTGAACGAAAATACAATC  
AAATAAGTTATTTATGGAACCTATTAGACAAATTAGACGACTTAAACAGAGTAGGTGATGACTTATATTTTGTGAGGATGCCCA  
ACGTATTTTGGTAAATTGGATGAAATTACTGTAAGGAAACGCGACCCCTTATTTACATCGCCTATACAAAAACCACTTCAAGAA  
GAAAGTGAAGAACATTACGGTAATGTGAAATGTATGCTGGAAAACTTGCCATCTGTATTGATTGCCAGTCATATTAAGCCTT  
TCATCTGTGCGGATGATACCGAAGCATACGACCCAAATAACGGCTTGCTATTAAGTCGTACCTTGGATAGCCTATTGATTGAA  
ATATATTTGCTTTGATGATGAAGGAAATATGTTGAAATTAAGCGGTTATCGAGGTTTGGCGACGCTTGGTGTGATGATGTAAG  
CTAGATAACAATCTGCTCAACGACAAACGTAATCTTACTTGGCATATCATCGAGAACTTATGCTACAAGAAGACCAAGAATTC  
ATATT

## SEQ ID 222

MGFIEPFLSSYTPLSRDYVQARTNRKQTLISKIVYTHSGFQRSVTENSNIQINFLIKTLVEHPQGLNKKEIAAMMLVDLKTFF  
QQDYLTETELNDYFQQGIESGFIERKYNQISYLNWLLDKLDDLKRVGDDLYFAEDAQRIFGNLDEITVRKRDPLYHRLYKNQLQE  
ESEHYGNVCKMLEKLAYPVLIAHSIKPFLSDDTEAYDPNGLLLSRTLDSLFDLKYISFDDEGNMVKSKRLSDDVWRRWCDDVK  
LDNNLLNDKRKSYLAYHRELMQEDQEFHI

## SEQ ID 223

ATGACGCTGAAGAACAACAAGCCAAAGAAGCATTGGACGGCATTATCAAAAAATCCCGTGTCCACCTTTATAAACCCATTCAAA  
TTGCAGAAATTTTATATCATGACCGTTGTATAAAACAGTTGGATTTTTTAAATTTAGATACTTACCGCAACCAATCTAAACGCTG  
GAGGGATGAAATCTGCCGTCGGTTTTTAGGGCGGATTCTACTTCATCTGCAAAATCCCAAGATAATCTGTTTGAAAAAATGCA  
ATACCGCTCGAAAAAC TAGCGGTATTGGGAACATTAAACAGACAGCTCGGACGGCGGGGTAGAATCGTACATTTATAACAGTTT  
TCAATCGTTTTCCTCAATGAGCGAAGCATTGGCTTATGTGCGCAATACAGACAGATACTCCTTCAACTGTCTGAATTTCTAAA  
TTTATTTTGGCTCGAGCCGGGATTGAAAAGAAGTATAGACAAGATATATGAAATCGTTGTTTATGCGTGTGTTGATGCATTGGTT  
TCAGAATTAGGCATAACGTTTCAATTGATTTTCTAAGGAAAACCTGTTTATGGGAGGAATATCAAGATTTTGGCGAAAAAA  
TCATCACTATGCCGAAAAATGAGCATTAAAACCTTCTGCAAAAAATCCATCGTGTAGGCGTAACCAATGCTGCCGATAGAGGGTT  
GGATATGTGGTCTAATTCGGATTGGCCATACAGGTCAAACATCTCTCTTTAGACGAAGAGTTGGCAGAAGATATTGTATCTCTC  
ATTAGCGCAGATAGAATTGTCATTGTCTGCAAAAAGGCAGAACAAATCGGTGATTGTTTCACTTACTGACGCAATAGGCTGGA



GCCGAATTCAAACATCGTAACTGAGGATGATTGATAAGTTGGTACGAAAAAGCATTGAGAGGCCAATATCCGATTGCAGAAGC  
GTTGTTGGAAAATATTAACCTGAAATTATGCGTGAATTTCTGCCGTAAATGAAGCCAATGAATTTTATAGATTTCCGCCAAAAT  
CGCGGATATGACATTACTGTTACTCATTTT

## SEQ ID 224

MTLEEQQAKEALDGIKKSRVHLYKPIQIABILYHDCIRQLDFLNLDTYRNQSKRWRDEICRRFLGRISTSSAKFQDNLFEKNA  
IPPEKLAVLGLTLNRQSDGGVESYIYKQFFNRESQMSALAYVGNTRYDFQLSEFLNLFWLEPGLKRSIDKIYEIVVYALFDALV  
SELGITVTSIDFPKENLFLWEEYQDFABKIIITMPKNEHLKLPKIHVRVGTNAADRGLDMWSNPLAIQVKHLSLDEELAEIVSS  
ISADRIIVVCKKAEQSVIVSLLTQIGWKSRIQNIIVTEDDLISWYEKALRGQYPIAEALLENIKTEIMREFPAVNEANEFLDFAQN  
RGYDITVTHF

## SEQ ID 225

ATGAACTGGCCTTATTTAATCGATGCCGTACCCAAATTCGCCGATGCCGCAAAGCTGACGCTGGAATTGTCCGTTTACGGCGTTG  
TTTTGTCGTTGCTGTTCCGCCCTGCCCGTCCCGTGGTAACGGCATACCGCATCCGCCCTTCTACGCATTGGCGCGCGCTATAT  
CGAGCTGTCGCGCAATACGCCCTGCTGATCCAATTGTTTTCCTATATTACGCTGTCGCCGAAATGGGCATCAAATGGGACGGT  
TTCACCTGCCGCGTAAATCGCGCTGGTTTTCTTGGGCGCAAGCTATATGGCGGAAGCTGTCCGCCCGGCATCCTCGCGCTCCCA  
AAGGGCAGGTCGGAGCGGGCAAGCAATCGGTTTGAGCCGCTTCAAGTGTTCCGCTATGTGAATTGCCGAGGTTTGGGCGGT  
CGCCGTTCCCGCCATCGCGCAATATATTGTTTTTAATGAAAGAAACATCCGTCGTCAGCACGGTCGGCATTCGGGAATTGTTA  
TTTGTTACAAAGACGTCATCGGTATGGACTACAAACCAATGAAGCCTTGTTCCTGCTGTTTGGCGCTTATTTGATTATCCTGC  
TGCCTGTTTCTTGTGTTGGCGCGCGGATTGAAAACCGGTACGGAGTCCGAAATATGGCGTT

## SEQ ID 226

MNWPYLIDAVPKFADAAKLTLLELSVYGVVLSLLFGLPVAVVTAYRIRPFYALARAYIELSRNTPLLIQLFFLYYGLPKMGIKWDG  
FTCGVIALVFLGASYMAEAVRAGILAVPKQVQVAGKAIGLSRFQVFRYVLEPQVWAVVPAIGANILFLMKETSVVSTVGIAELL  
FVTKDVIQMDYRTNEALFLLFAAYLIILLFVSLARRIENRVSARKYV

## SEQ ID 227

TTGGGCGAAGGCCTGCTCTTAACGGCACAATTTCTTTAATCTCTGTTGCGGCTTCTTGCCTATTGGGCACGCTGTTCCGCTTGG  
TTTTGCGTTCCGCGCAACCGGCTTGTCCGCTTTGTCCGACGGTTTATCTCGAAACCATCCGAATCGTCCGATTTTGGTGTGGCT  
GTTCCGCCCTGTATTTCCGCCCTATCCGTCTGGACAGGCATCCACATCGCGCGATTGTTGGGTCTGCGTCTGGGTATTTCCCTGTGG  
GGCGTTGCCGAAATGGGCGACTTGGTGCGCGCGCGCACTGGAATCGATTGAAAAACACAGGTGCAATCGGGTCTTGGCGCCGGCT  
TGAGCCGGGGCGAGGTATTCGCTGTCATCGAGCTGCCGCAAGCATCCGCCGCGTATGCCCCGGCGCGGTCAACCTGTTACGCG  
CATGATCAAAACAGCTCGCTCGCTTGGCTTATCGCGCTGATCGAAGTCGTCAAAGTCGGGCAGCAAATTATTGAAAACTCGTTG  
CTGACGCAGCCCAATGCTTCATTTTGGGTTTACGGCCTGATTTTATGCTGATTTCTTCTGTTGCTGGCCGCTATCTCTACTGG  
CGGCAAACTTGAACAAAATGGGAACAC

## SEQ ID 228

LGEGLLLTAQISLISVAASCVLGTLFGLVLRNRNLVRVFRFYLETIRIVPILVWLFGLYFGLSVWTGIHIGGFVWVWVSLW  
GVAEMGDLVRGALESIEKHQVESGLAPGLSRGQVFRCIELPQSIRRVLPGAVNLFTRMIKTSSLANLIGVIEVVVKVQQIISNL  
LTQPNASFVWYGLIFMLYFFCCWPLSLLAAKLEBQKWEH

## SEQ ID 229

ATGAAATTGAACGCCAACTCAAAGCCCTTTTGGCTTCCGCCGCCATCGCCGTCGGTCTGACCGCCTGCGGGGGCGGCTCCGGCG  
ATGCCCAATCTTCAAAAGCAGCGGTGCGGCAACCGTTGCGGCCATCAAAGAAAAGCGTTATCCGCATCGCGGTATTTCCGCGA  
CAAACCCCGTTCCGCTATGTTGACGCAACCGGCAAAACCAAGCGCTTTGACGTTGAAATCGCACAAGACCTGGCCAAAGACCTG  
CTCGGCAGCCCGCAAAAGTCGAATTCTGCTGACCGAGGCGCAAAACCGCGTCAATACGTCGGTTCCGGCAAAGTCGACCTCA  
TCCTCGCCAACTTTACCCAAACCCCGAACGCGCCGAAGCGCTCGATTTCGCCGATCCTTACATGAAAGTGGCGTTGGCGGTGGT  
TTCCCCCAAAACAAACCGATTACCGACATGGCGCAATTGAAAGACCAACCTGCTGGTCAACAAAGGCACCACCGCCGACGCT  
TTCTTACCAAAAGCCATCCCGAAGTCAAGCTGTTGAAATTCGACCAAAACACTGAAACCTTCGACGCGCTGAAAGACGGTCCGG  
GCGTAGCACTCGCGCACGACAACGCCCTGCTGTGGCGCTGCGCGGAAAGAAAACCCGAACCTTGAAGTCCGCATCGCAATCTCGG  
TCCTGCCGAATTTATCGCCCCCGCGTTCAAAAGGCAAGCACTCCGTAAGTGGGTCAACGGCGGAATCGCCGCCATGAAA  
AAGACGGCCGCTCGAAGCGCCTATGAAAAACCTCTTGCCCGTGTATGGCGAGAAAGTCAAACCGGAAGCATTTGTTGGCCG  
AA

## SEQ ID 230

MKLNALKLALLASAAIAVGLTACGGGSGDAQSSQSSGAATVAAIKEKGVIRIGVFGDKPPFGYVDANGKNQGFVLEIAKDLAKDL  
LGSPDKVEFVLTEANRVEYVRSKVDLILANFTQTERABAVDFADPYMKVALGVVSPKNKPIDMAQLKDQTLVKNKGTADA  
FFTKSHPEVKLLKFDQNTETFDALKDGRGVALAHNALLWAWAKENPNFEVAIGNLGPAREFLAPAVQKGNADLLNWNNGEIAAMK  
KDGRLLKAAAYEKTLLPVYGEKVKPEALLAE

## SEQ ID 231

ATGAGATTAAACGAAATATCCTTATAACTCCATAAGAGAGTTAGAAGACTATTTAATAACACCTATCAAAAATATATTATTCTAC  
AAGAGGGAGGAAAAGAGATTTATCGATGTTTTATCTTTCTTTTATAAAGAATTCAATATAGGTATTGGATTAGCTGTTTCTTG  
CATAAGTATTTCCCAAAAGTATTATGCTTGATGATAAAATATTTTATCGGATTTGATTCAGTCGTTTTTGTATTCTTCTATA  
CAAAATTCAAAAGTTAACATACTAATAAGTAAATTTTATGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT  
ATGAGTTGGGTGCAATTATTACAGATAAAATTTAATAAGAGAGAATTCAGTATCTACCGATATAATATCAGACTGGGAAATAGA  
TAAAGTTAATAAGTTAATCATATTAAAGAGTTAGACTCTGAAAAATAATTTCTCTAAATTATGAT

## SEQ ID 232

MRLTKYPYNSIRELEDYLINTYQKYIILQEGGKEYRCFILSFYKEFNIGIGLAVSCISIPPKVLMDDKNIFIGFDSVVFCSIS  
QNSKVNILNIDGIVFDIYLLDNQKICIIHELGAIIIDKNLIRENSVSTDIISDWEIDKVNKLIILKELDSEKIIISLNYD

## SEQ ID 233

ATGGTTGCGCTATGCTTTCTTATTTTGTGTTGTAACGCGCGCGGTGCTGCTGATTGTCAGGTCGCACTACCGCTGGACGTATTTTT  
TCGCGTCGGCGCTGTTTGTCTTTTGGCGGGCGGTATGCTGATGTTGACGGCGCAGTGGCAGCGCGCTTGAATTTCCGTTCCGT  
CTGGTTTGTGGTGTGATACTGTTCCACAGGCTGAAAATCCATTATACAAACAGCCGCTGTTGATTTCGCACTTTTTGCTGATT  
GCCGACTGGCGGAATTGGGAAACGCTGTTTCATTATAAGGAAGCGGTTATCGGTATGGCGGGGCTGCTGGCTTTGGCGGGGATG  
CGGTTTTCGGCTGGAGCGGTGCGGATTCCTTGGGTATGCCGTGGCGTTGGGCGGGCGCGGTTCTGTTTGGCGGGCGGTTCCGTGTC



GGTCCGGCATTTTTC AAGCACCCCGCGCGGTAAAGACGTGGCTGGATTTCGCTGCCGGACGACGGGCGCGACGTGTTTTTGAAC  
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AAACCCGCGCGTACGGCATGTCGGATGAAAAAGCCGATATTGTCTGTTACCTGATGGAATCGACGCTCGATCCGCACTGTTTCGA  
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TTTATTCGGTCTGATCCGCATTTG CAGACCGGTTTTGTCCGCAACCTGCGCGAACACGGTTATTTTTCGCTGGCGCTCTCGCCGTT  
TACCAAGGGCAACTACAATGCCAAGGCAGCATATGACCATTTCCGGCTTTAATCTGATGTTCCAGCCGCAAGATTGGGCTATCCC  
GCGCCGATGGGCAAAACCTGTGGCACATTTCCAGTGAGGAAATGATGCAGTATGCGCGGATGATTCTCGAAAAACGCCATCCCG  
ATTTGGAAAAACGTGCGGCAGCCGATGTTTCGTATATGTCTGACCATGAAGGAGCACGGGCCGTATCGGACGGATACCGACAATGT  
GTTTGATTTGGATGCGCCCGATTGGAATGCCAAAACCGTATCCGCGCTTAACGACTACATCGGGCGCATTGCCGATTGGACAAA  
GCGGTGGAAGTTTCGACCGTTATCTGCACGAACGCGCAAAACCTTTGTTTTCGGTTATTTTCGGCGATCATCAGGTACCGTTTG  
AGGGCGTGTCCGTCAGGAAGAAATGGGATTACGCTCAGCCGGATTATGTAACGCAGTTTGCCGTCAGGAGCAATATTGCCGGCGG  
ATTCGTACAGCGCGCAGGATTTCCTCGACCTTGCCTTTGCAGGCGCGCTACTGATGGAGGCGGCTGGTTTGAAGCCAAAGACGGC  
TTCATGCGTGCGGAATATGGCGATGCGCGGTTTGTGCGCGGAGGGTTGGAAGACTGCCCGAACCGGAGTTGGTCGGAAATTACC  
GCAACTATCTGTACGACGTTTTGAAAAATTGCCCGT

## SEQ ID 234

MVAYAFLEFLVTAAVLLIVRSHRWTFYFASALFVFLAGGMLMLTAQWQALNFAVSVFVVLILFHLRLKIHYKQPLLI SDFLLI  
ADWRNWETLPHYKEAVIGMAGLLALAGYAVFGWSGADSLGMPWRWAGAVLFAAAFVSVRHF SKHPGAVKTWLDSL PDDGRDVF LN  
LPMSCRAVFFQVVFEGDGEAFARQMPSETRPYGMSDEKPDIVVTLMBSTLDPHCDFDFAAKI PDLKMFGRQEDTVFSS PLRVHT  
FGGATWKSEFAFLAGVPSTDFGALASGVFYSVVPHLQTGFVRNLRHGYFCVALSPFTKGNYNAAAYDHF GFNLMPQODLGY  
APMGKNLWHISSEMMQYARMILEKRHPDLNVRQPMFVYVLTMKHBGPYRTDTDNVFDLADPDLNARTVSNALNDYIGRIADLDK  
AVESFDRLYHERGKPFVFGYFGDHQVFPFEGVSVRKKWDYAQPDYVTQFAVRSNIAGGFVQRQDFDLDAFAGGVLM EAAGLEAKDG  
FMRANMAMRGLCGGLEDPCPNRELVGNYRNYLYDVLKIAR

## SEQ ID 235

ATGAAGCACGCTCCGATTATCCTCCTGCTTACCGCTTCGTCCGCGCCCTACTTTCGGCGGGCTGCACCGCCCTTCCCTCTGACC  
GGCGCGCGCTTCGCACCCCTGCCGAAAAGCGCGCCCATCAACCCGCCAACCCATACAGCCGGCCGCTTCAGGCACGCGCGACGG  
CGCATTCAGCACCCGCGCCTCAAACGGGCGCGTCTTGAAAAGCATCGTCAAAAACGGCGGTTCGACCGCTTTGTCTGATTTTAC  
CATCCAAACGGCAACTGCATTGCGCACACGCGGTTGAAAACGGCGTGGCGCAAGGCTATACCGAACAGGGCATATTGCGGACGG  
GCATCCTGTACCGGACGGGCATATCGTCCGAGCGCAAACTTTGGATCGCTCGGGCAAGGTGAACCGCAATGGCAGCCG

## SEQ ID 236

MKHAPIILLLTASSAALLSAGCTALPSDRPPLRTLPKSAPIQANFYSRPPSGTDPGAFSTRASNGRVLSIVKNGVDFDRFVDIY  
HPNGKLHSHTPVENGVAQGYTEQGILRTRILYRDGHIVRAQTL DASGKVEREWQP

## SEQ ID 237

GTGTCCATCCCCACCGCCACGCCGCTGCCCGCGCGGAGGTAACGTTATCAAGCGATAACGGCAATATCGAAAAATCAACACCG  
CCGGCGCGGAAGCGCATCCGACGCGCGGAGCCGACGAGCGCTCGTCTGATGCCGCCCGCAAAACACATCCGGCATTTCCAT  
TCGGCAGCGGGAAGTAGAAAAAGACTATTTCGGCTATAAATCAAAAGAAACATCATTCATCTTCAAAACACCCGGCGCGCGCAA  
TACGCCCTTTCATCTACGCCGACCCCATAAACGTCAGCTACTCTCCCCCGATTTCAAAATTTCCGACCGCCACGCGAGGCGAGC  
GGCTCGCCGACGGCAGCCGCATCTTTATCTGCTGCAGCGACTCCGGGGCTACTTCTGATGCGGAAATTACCAAAACAGATTATAT  
GAAATTCGGGCGGTGATAGGTCTTAACGGCGAAATCGACCTCTTCGCGCGCGGCTTCCCGTCCGCAAAACGCGCCTCTGCG  
TTCTCTACGGCAGCAGCAGCCCGAAACCGCATTTGTCAAAGGTAATAATCACTTATCAGGTTTGGGGCATCCGCGTCAGAAACG  
GGCAATTTGTTACTTCTCTTATACGCCCGCGAAAAGCGGTTCTTATTATGGGACACTTGCCAAATACCCCGCTCTCTTCTTTAT  
CACCGCAATTTTCAACAGCAACACACTGGCAGGCAAAATCCTCGGCAACAGCGATTACGGGCGGGATGTGGATATTCAAACGCA  
ACGATTACCGGTCCGACCTTTTCCGGCGATGCCACGTCGGCGGGGAAAACGGCAAAATGGAAGGCAAGTTTTTGGCAAGTTTCG  
CCAGCACCCGACGAGCGAAGTCAGCATAGGCGCGCAAAATCACTTTTGAAGCGGACCGCTCCCTCGATACCGTATTTCGGCGGTGT  
GAGTTATGAAAAAAACTTGATGACACCAGTCAAGATACCAACCCTTACTAAACAA

## SEQ ID 238

VSIPTATPLPAGEVTLSSDNGNIENINTAGAGSASDAPSRSRSLDAAPQNTSGISIRQREVEKDYFYKSKETSFIKTPGGAQ  
YALSSYADPITVSYSSPDFKIPDRHAGQRLADGSRIFCCSDSGATSYAETKQDYMKGAWIGPNGEIDL FAGGFVPGKTPPPA  
FSYGSSTPETALSKGKITVQVWGI RVRNGQFVTSSTYPKSGSYGTLANTFVLSFITANFNSNTLAGKILGNSDYGPDPVDIQNA  
TITGPTTFSGDATSGGKSGKLEBGFKGFASTRSEVSIGGKITFDGDRSLDTVFVGGVSYEKKLDDTSQDTHLTKQ

## SEQ ID 239

TTGCCGCCAATTTGCGGGGGGGGGGGGGTAATATCCGCTTTATAGACGTAAACCCCGAAGATTTCGCGCGCTTCCCTTAAACA  
TCAGGCACATTTCCATTACGACTTATGCCCGCCTGAAATTTGGGCGAATACATTGCCGATGCGACAAAGTCCGTATCTGGATAC  
GGACGATTTGGTCAGGACCGGCTGAAGCCCTTATGGGATACCGATTGGGCGGTAAGTGGGTCGGCGGTGCATCGATTGTTT  
GTCGAAAGGCAGGAAGGATACAAACAAAAATCGGTATGGCGGACGGAGAATATTATTTCAATCCGCGCTATTCGTATCAACC  
TGAAAAAGTGGCGGCGCACGATATTTTCAAAATGTCCTGCGAATGGGTGGAACAATACAAAGGACGTGATGCAATATCAGGATCA  
GGACATTTTGAACCGGCTGTTTAAAGCGGGGTGTGTTATGCGAACAGCCGTTTCAACTTTATGCCGACCAATATGCCTTTATG  
GCGAACGGGTTTTCGTCCCGCCATACCGACCCGCTTTACCTCGACCGTACCAATACGGCGATGCCCGTCGCGCTCAGCCATTATT  
GCGGCTCGGCAAGCCGTGGCACAGGACTGCACCGTTTGGGGTCCGGAACGTTTACAGAGTTGGCCGCGCAGCTGACGACCGT  
TCCCGAAGAAATGGCGCGGCAAACTTGGCGTCCCGCGGCAAAAGCGTATGCTTCAAAGATGGCGCAAAAGCTGTCTGCCAGATT  
TTACGCAAGATTAT

## SEQ ID 240

LPPICGGGGNNIRFIDVNPEDFAGFPLNIRHISITTYARLKLGEYIADC DKVLYLDTDLVLRDGLKPLWDTDLGGNWWGACIDLF  
VERQEGYKQKIGMADGEYFNAGVLLINLKKWRRHIDFKMSCEWVEQYKQVMDQDQDILNGLFKGGVCYANSRNFNFMPTNYAFM  
ANGFASRHTDPLYLDRNTAMPVAVSHYCGSAKPWHRDCTVWGAERFTELAGSLTTVPEWRGKLAVPPTKRMLQRWRKLSARF  
LRKIY

## SEQ ID 241

ATGATTTTTCGCAGACCCGCTTACTTTCTTCCAATGACGGTTTCAGTTGTCAAAACGGGCAAATGGTTTCCGTCAATAAGGGCA  
ACTGGGATAAATCCAAAGGAATGGCGGCAGATTGGAATTTTACGAAGAATGGCTCCGACTGTGTACGCCCTTATTAACCAAA  
CGGCACAATTTGGGTTTGCAGCATTTCATAATATCTATTTAATCGGCTACCTGATGCAAACCGCTCGGCTACCATATTTGAAC  
AATATTACTTGGGAAAAACCAATCCTCCCCCTAATTTGTCTCGCGTTCTTTACCCATTCGACAGAAACAATCTTATGGGCAA  
AGAAAAATAAAAGCCAAACATACGTTTCATTATGAAATGATGAAAGCACAAAATAATGGCAAACAGATGAAATGTGTTGGAC  
ATTCGCACCTCCAAATAAAACCGAAAAACATTTCGGCAAACATCCGACACAAAAACCCTCCCTTACTTGAACGCTGCATACTA  
TCGGCTTCAAATATCGGAGATTAAATTTTGACCTTTTATGGGAGCGGCACAACAGGCGTTGCCGCTTAAACATGGTCGGA  
GATTTTTCGGTTTGCAGACTGGAAGAAGATTTTGAAT

## SEQ ID 242

MIFADPPYFLSNDGFSQNGQMVSVNKGWDRSKGMAADLEFYEEWLRLCYALLKPNGTIWVCGTFHNTYLYGYLMQTVGYHILN  
NITWEKPNPPNLSRFFTHSTETILWAKKNKAKHTFHYEMMKQNNGRQMKCVWTFAPPNKTEKTFGKHPTQKPLPFLERICIL  
SASNIGDLIFDPMGSGTTGVAALKHGRRCGCELEEDFLN

## SEQ ID 243

ATGAAATACACAGCCGCACTCTGACTTTTCTTTAACTGCCTGCATGAACCCGAACGATGCGTTTTCACAAAACCGGCGTTATC  
AAATGCCGAGGCGCAATTGAACGGTTCAAACGCCGTTTTCATTACGGTTATTCACAAAATCCCGATCATGATTTATTTGGTCGA  
CCAAGTCCGCGTCCCGACCGGTACAGGGCTTCATTTCGCGGGGATGGATAGCGAAGGAGCAAGGTTACCGCAAAAACGACTGC  
GTACTGGAAAAAGCGGAAAGCGGGGTGTGACGTACTACACCTCGCATGCGGAAAAAGGATTCACGGGCACACGTTTCGTCATCT  
ATGTCGTGAATATGAAAAACGACAAAGGCTACGTCAAAGTTTACCGGGCATGAATAAGCCGAATCAGGAAGAGTTAACCAAATT  
GTTGCCGATTTGAATAAGTTTACCCT

## SEQ ID 244

MKYTAALLTFLLTACMNPNDAFFQNRRYQMPAQNGSNVAFHYGYSQNPDHDLVDQVRVPDAYRASFARDWIAKEQGYRKNDK  
VLEKAESEGGVTTYTCDAEKGFNGTRFVIYVNMKNKDGIVKVYRGMNKPNEELTKLVADLNKFPY

## SEQ ID 245

ATGGAAAGCAACCTGCAGAAAACCGAGCGTTTGATCCGCGAAATCAACCGCTGCACGCACAATATTTCGAGGATTATTTTGAAA  
CCGGCAAAGTGCAGAAAATCAATTTGAGCCACAGCTCAAAAACGTTCCGACCGAACATATTTGTCTTATCGCCTTAATTTGCA  
CGAAGCAGTTAACGATTATTTAGCCTTTGCCGATACGCGCGCATAGACTTTTCTACCGCGTGAAAACCGCAGAAAGCATACAT  
GATAAATCAACCGCTATCTGGCAGCGCGCACCAATATCCGACCAACAACATCTGAACGATATTTTCGGCGCGCGGCTGATTT  
GGCGCTCTGAAACAGTCCGCGGATTTTAGAAAACTTGACGGCTGGAAAACAGAAATACGGCTTGAAAAACGGTATTTGCCGGA  
TGCCGCGGCTATATCGGCATACACATTTATTTCAAAAACAGCAGCAATTTCTACTATCCGTGGGAATTCAGGTTTGGGATGAA  
AAAGATGCCAAAGCCAATATTGAAAACCATATGGCGTACAAACGGAATTTCTGTGCGT

## SEQ ID 246

MESNLQKTERLIREINRLHAQYSQDYFETGKVRKINLSHTLKNVPTZHLISYRLNLHEAVNDYLAFAADTRGIDFFYRVKTAESIH  
DKINRYLARGTQYPTNNILNDIFGARLIWSETVAGILEKLDGWKTEYGLKNWYLRDAGGYIGIHIFKNSSNFYYPWELQVWDE  
KDAKANIEHNMAYKRNFR

## SEQ ID 247

ATGCGTAACACCGTAGGATTGGACATATCCAAGCTGACATTTGACGCAACGGCCATGGTCCGCAAAACGGAGCATTTCGGCAAAGT  
TTGACAAACGATTCAAAGGTTTAGATCAGTTTTCGGACCGGTTGAAAAGCTTGGGATATCAGAACTGTCATATCTGCATGGAGGC  
AACCGGCAGTTATTTAGAGAAGTTGCCGACTACTTCGCGCAGTATTACAGCGTTTACGTAGTGAACCCGCTGAAAATAAGCAAG  
TATGCAGAAAGCAGGTTCAAGCGAACCAAAACAGACAAACAGGATGCAAAACTGATAGCGCAGTATTGCCGCGTCCGCGCAGGAAA  
CGGAGCTTGTAAGAGGCAGAGCCTACCGACGAGCAATACAGGCTTTCACGGATGACCGCAGCATACCGGCAATCAAAGCGA  
ATGCGCGGCAATGAAAACCGTCATCACGCGGCAAAAGATGAAGAAGCGGCCAAAGCATATGCGGAAATCATCAAAGCCATGAAT  
GAACAGCTTGAAGTTTAAAGGAGAAGATAAAAGAGCAGACGGAGAACCTTAACGCAAGGAAGCGGTGAAGCGCTTTGAAACCA  
TACCGGCAATAGGCAGAAATGACCGCAGCGTATTGTTTCATCATCTAACATCTTCGAAATTTGAAACATCAAACAAATTTGCAGC  
ATTTCGAGGCTTAAGCCGCAACAAAAGAATCCGGGACAAGCGTAAGGGGAAAAGGCAAACTGACCAAGTTTGGCAACAGGAAA  
TTACGCGCCGCTCTGTTTATGCCGCGCATGTCGCATACCGGATAAGGGCATTTCGCCGACTTCATCAAAGGCTGGAAGAAAAGA  
AGAAGCCTAAAAAGTCATCATCGCAGCATTTGATGCGTAAACTCGCGCTTATTGCGTATCACGTACATAAGAAAGGCGGAGATTA  
CGATCCATCGCGTTACAAATCGGCG

## SEQ ID 248

MRNTVGLDLSKLTFDATAMVGKTEHSAKFNDNSKGLDQFSDRLKSLGYQLNHICMEATGSYYEEVADYFAQYYSVYVNVNPLKISK  
YAESRFRKTKTDKQDAKLIQYCRSAQSESELVKRQKPTDEQYRLSRMTAAYAQIKSECAAMKNRHHAAKDEEAAKAYAEI IKAMN  
EQLEVLKEKIKEQTEKPNCKEGVKRLETIPAIGRMTAAVLPHHLTSSKFETSNKFAAFAGLSPQOKESGTSVRGKGLTKFGNKR  
LRAVLFPAMVAYRIRAFPDFIKRLEKKKPKKVI IALMRKLAVIAYHVHKKGGDYDPSRYKSA

## SEQ ID 249

ATGTTGCGAACCTACTTGAACCAATTGACCCCTCCCGAATTAGCTGATTCTGTTAAAAATACCGTTGATGGTTTATGGAATAAT  
TGTCACAAACCGAGCCGAAAATCGCCCAAAATGTTTTATTTGCTGGGCAATGTTCAAAGTGGCAAACCGGCACAGGTTTGGGTGT  
ATTAAGTGGCTGGCTGATGATGGCGACCACAAAGTTTTTTTGTATCTTACTACTGACAGCGTAGATTTACAGGATCAAACAGTC  
AAACGAGCCAAAGCCAATCTGAAAACTTTATCGTATTGTCGTAAGCTGACGACCGAAGTTTATGGAAGTAATGAAGGCAGAGA  
ACCCCATCTTGGTCGTGATTAAAAAGAATGCCCGTGTATTGAAACGTTGGCGTAATTTGTTTGCCAGTCAAAGTAGCCTGAAAGG  
CTATCCTTTGTTTATTGTGGACGATGAAGCCGATGCTGCCAGCCTAAATACTAATTTCTGATAAGCCGGCTAAAGATGCCAGTACT  
ATCAATAACTGCTAAACGACATCAAAAATCTGTTGTCAAAGCCGTTTATCCAGTTGATGCTCCAGCCTCAATCGCTTTTAT  
TACAACATGAAGAATCTGATTGGCAACCTGAATTTATCCACTTCTTTGAAGCAGGCGAAAAATACATCGGCGGCAACTTTGTCTT  
TTCTGATCCACCAAGCTATATAGTTTCGTTTTATTGATAGCGAATTGGATGATATGAAAGACGAGAGTGGTGAATTTGCCGAAGGA  
GCAAAACAGGCATTGCTTAGTTTCTAATAACCTGTGCAGAAATTCGGCTATGTGATAAGGCTAACGTAATTTTGCACTACATC  
CAAGCTATAAAATTCAAGATCATCAAGCCTTTTCAAAGAAGATCCAAGCCTTTTAAATGACTTAGTGCAAGCAGTCAATAATAG  
GGAAGACCTTGCAAGTAGCTTTAAAGAAAGTTATTTGGATTGCAAAAGACCAAGCCGATATTCACTACTTTGATGAAATATAC  
GAAAAATTGACAGCACTTTTAGAGAATAAAACAAATCTCTACTCTTGTGCTTAACTCGCAGACAGAAACAGATTTTGACTTAGAAA  
AAGGTTTCAACATCATTTATGGTGGTAATGTGATTGGTTCGTTGACTATTCCGAAACTACAAACGGTTTATTATAGTCGCAC

TGCCAAAAAACCGAATGCAGATACTTTCTGGCAACATTCGCGTATTTTGGATATGACCGCGATAAATCATTATTACGGCTTTAT  
 ATTCGGTTCGATGTCATTACTTCTTTGTACAACTCAATCAAGCAAATACTGATTATTGGGCAGGCAAAAAATTCAGGCGGCA  
 ATATTCAGGTATTATTCGGAATAATCAATCAACTCGAAAAATGTATTGAAATTCGATAGTATCAATCAAATTTGGGTGG  
 TGTGAATTATTTCCTCACTCCACCAACGAAGATAAATTTATCGGAGATTAAACAAAATTTGCTTCTATTTTGAAAGATGAAAT  
 CAATCTGATTATATCAATAGATATAGAAGATTTATCTTGGTCTAGATAAATGGGTGCTTATGTTCCAGATGACTGGAATA  
 AGGAAAAATTTATTGCTGGTGTAGAAGCATTAAAGCACAACGTCGAAGTTTAAACCTATGTTTGGATCAAAACCGGACGTA  
 ACTTCTCGAGCAACCGGCACAATGCTTTGGAAGACGACCGTAAATAGGAGAAAAATATCCCAATGATTTATCTTACGCTT  
 TATCAAGTAGTAGGAAATAAGACAAAGTTGGCAGGGAAGATTTTGGTTACCCAATATCAAGCTACCACACAATGGCTTGG  
 TGTACCAAAGTGCAAAA

## SEQ ID 250

MLRTYLNQLTPPELADSVKNTVDGFMKLSQTEPKIAQNVLLGNVQSGKTAQVLGVLSALADDGDHVKVFLYLTDSVDLQDQTV  
 KRAKANLKNFIVLSEADDRSFMEVMKAENPILVVIKKNARVLKRWNLASFQSSLRGYPLVIVDDEADAASLNTNSDKPAKDA  
 INKLLNDIKNSCCQSLFIQLTATPQSLLLQHEESDWQPEFIHFPEAGEKYIGGNFVFSDFPSYIVRFIDSELDDMKDESSEI  
 AKQALLSFLITCAEFALCDKANCNFALHPYKIQDHQAFSKKIQAFLNDLVQAVMNGEDLAGSFKESYLDLQKTKPDIIHFDE  
 EKLTALENKQISTLVNSQTETDFDLERGFNIIGGNVIGRGLTIPKLOTVYYSRTAKPNADTFWQHSRIFGYDRDKSLRLY  
 IPFDVYVFFVQLNQANNLIIGQAKNSGGNIQVIYPKNINPTRKNVLPKFSINQIVGGVNYFPLHPNEDNLSEINKILPSILKDE  
 QSDLYQIDIEDLFLVLDKLGRYVPDDWNKEKFIAGVEALKAQRPSPKTYVLIKTGRKLSRATGTMLESDDRKLGKEYPNDLFL  
 YQVVGKDKGWQKDFWLPNIKLPNGLVYQSAK

## SEQ ID 251

ATGAATACAGTTTTCCTCAATATCGCCAATGCCAAATCACTGAAAAATCTCTTAATGCGGTTTGGATGGATTATTTAAATCAG  
 CGGATGAAGTGTGTATGGCGACAGGTTATGTATCTAATGACGAGTGGTTGAGTTACATAAAATTTGGAGCTAAACGATCATAT  
 TCAAAAAATAGATTATTTGGTTCGGAATGCATTATTTGGAGGTTTATAGCCATTATCAATATGACAGCTTATGTAACATAATGAT  
 TTTTTCGCGACATGAGAAAAGAGGAGCGCTATGTTTCCCTTTTGTGAAATTTACGCGCAAAATGTATCTCTTAAATATATC  
 AAAAAATCAATGATTAAATGGTCTGCTAACTTAACGTGTTTTGGGATAGCACGGAACGTACTTATGAACTATGTTGCATTT  
 GAACGGTAAGCCTGCACAGATTTTGCAGGCAGATATTCAAGTACTATTCATAAGCTAGGCAAAATATCCAAGAAGTTGAAAGA  
 CCAAGTAAATTTATTGAACATAATAGCCATTAGAAAATTTGTTGGGTGTTTCAAGAAATGACACGAGAACAGATTCCGCAATAT  
 TGGCCCAACGTCAGAAATATCATTTCTCAATTCAGCTAAACCGAAGAAAAAGTAATTTGAATGATTATTTGGAGAGGTCG  
 ACGAGATAAACGAGGTTTGTCAAAACGACGCTTGGTATGAAGTAGAGTTGATTGTATCCAAAGACATCACTTCACAAGAAGGG  
 TATCCGGTCTCGAAGTCTTTTACAGTTATTACCGATGATGTTGGCAATTTCAATGCAAGACATCGGGGATTACTCCAAAACT  
 TCCGCTCAGAAAATGATTAAAGACACTTGGTAAATGGATTAAAGGTCGTTTGGAAAGTCATGGCTGCCTGCAAAATAACGAGAA  
 GATTACGCAAGAAACCTACGCGAATACGGTAACGATCATTTGAGTTACGTTCAACCGATAATCCTGATGTTTGGCTGCTCTCA  
 TTTAAGGGGAAAAAC

## SEQ ID 252

MNTVFSNIAKITEKSLNAVWMDLFSKSADEVLMATGYVSNDAVVELHKLIELNDHIQKIDLLVGMHYLEGFSLQYDSLCKLND  
 FLRHEKRGAVVSPFVKFHGKMSYFNKYQKINGLIGSANLTCFWDSTERTYETMLHLNGKPAQILQADIQSTIHLKGNIEVER  
 PSKFIENSHLENCLGVQKIAPEQIRQLFAQTSEYHFSIPAKTEESNLNVFFEGEGRDRKRGFVKPRFWYEVLELIVSKDITSQEG  
 YPVLKSFTVITDDGWQFQCKTSGDYSKNFRSENDLKLTKWIKGRLESHGCLQNNKITHETLREYGNDFELRSTNDPVDVWLLS  
 FKGN

## SEQ ID 253

ATGACAACAGAAAATAACGCTTTTGAACACGCCAAACACATCGACGAAACAGGCAATGAATATTGGTCGGCGCGCACCTTGCAGC  
 AAATCTTGAATATTCCGAATGGCGCAATTTCAAACGGGCCATTGATAAGCCATAACCGCTTGCAGAACATCAGGAAATGACAA  
 AAATCATCATTTGTTGAAACCAACAAATGATAGCCCTTGGGAAAGGCGGCGAGCGCGAAGTGGCGGATTACCGCTTTCCCGC  
 TATGCCTGCTACCTGATTGTGCAAAACGCGCATCCGTCCAAAGCGTCAATTGCGCGAGGGCAACCTACTTTGCGGTGCAAGCCC  
 GCCGCAAGAGCTGCAAGACGAGGCGAGCATTAGAGTTTGGGCGAAGACAAACACGCTGCTGCTTCGAGGCAGCTGCGCGA  
 ACACAATACCGACCTTGGCGCGCGAGCAGGATCGAGGCTAGAAAACCCGTTGAGTACGCGCTTCCAAAACCGGCTAT  
 CGGGGCTATACGAGGACTGGACAAGCAGGCGATACACAGCCGCAAGGCTTGAAGAAAAGCCAGAGAATCTAGACCACATGA  
 ACGCCAGCGAACCGGCTGCCAATCTGTTTCGCGCCACGCAAAACCGAAGAAAACCTACGCCGCAAAACATCCAGGCAAAACACA  
 GGCAACCGGCTGCATTTCGAAGTCGGACAAAAGTGCGCCAAACCATTTGAAGAACTGGCGGCATCATGCCTGAAAACAGCCC  
 GTACCCGAGAAAAGCATCAACAGCTTGAGAACGAAGAACAGAAAAGGCTTGGCGCAACCGAACAGCATCAAAACCGCAAAAAA

## SEQ ID 254

MTTENNAFENAKHIDETGNEYWSARTLQOILEYSEWRNFQRAIDKAITACETSGNDKNHVFETNKMIALGKGGQREVADYRLSR  
 YACYLIVQNGDPSKSVIAAGQTYFAVQARRQELQDEAAFRSLGEDKQRLLLRRQLREHNTDLAAAKDAGVEKPFVEYAVFQNHGY  
 RGLYGGLDKQGIHSRKLKKSQRILDHMNASEPAANLFRATQTEELRRKNIQKQTQANRVHFEVQKVRQTIEELGGIMPENQF  
 VPEKSIKQLENEEQKRLAATEQHONGKK

## SEQ ID 255

ATGAAAGATTTATTGTCGTCCTCCCATCATTCCTGCTGTTTTCTGTATGCTTGGCGTTACCTGCCCTACCGGTTAATCGGCTTTT  
 TCGCACTGCGTAACCGAACCTTAAGCCGCGCGCCAAACCGTTATGGAAGCCGCGCGGCTGCGTCTCATTTCCGTCATTGCG  
 CCCCTATTTTGTATCCGACAAGCCGACGAACTTATGCCATCGCGTTAACCGCTTGGCGGCTGCGGTTTTCTATGTTGTTT  
 ACCGTATTGATAGGGGTCGGCTCGTCAGGCATCTCGGATGTTGATGGCA

## SEQ ID 256

MKDLLSSPSFLLFSCMLAVTCPTRLIGFFALRNRLSRRQAQTVMEAAPGCVLISVIAPYFVSDKPHELIALTAFACRFSMLP  
 TVLIGVSGSIGWLMA

## SEQ ID 257

ATGGATAAAGAGAAAGTCTTAGACAAAATCAAGAAATGTTTGGCTTTGGGTGCGTTCGTAATGAACATGAAGCCGCACAGGCGT  
 TAAGCGAGGCGCAGGCTTTAATGAAAAGTACAAAGTAAATGCCGAGGATATCGCCTTATCAAAAGTCTCCGAACAGAAAGCCGA  
 TCGGAAAATGGCTTTTAAATGGCAGGCTGCAATGGGCGTTGCAATATGATTGCCGATATATTCGGGTGCAATCTTACCAA  
 CGCGGAAAACAAATGATGTTTACGGCATTTGGAATCGAGCGGAACCTCAGCCTATGCCTTTGATGTAGTCTATCGTCAGATTT  
 CCGCCGACCGCCGCAATTTTGAACCTGCGCGGCGGGAAGCCCTCGCACAGAACTTATCTTGGCGACCGATTTTGGCGCGG

TTGGATTGCGAGCGCTTGGGAAACAGTCAAAAAATTTGAGATGTCAGATGAAGAAAAAGCCATTATGGACGGATACAAAAAGAAA  
GAATATCCGGATATGGCCGAAGCAAGGACAAGAGATGCGAAATCGTCAATCCTACAAGGGTCAAAAAATGGAATATGAGGCATTAA  
CCCGAGGAATGGAATCGGGTAAGCAAGTGAAGTTACACTATGCCGTGAACGGTACGGGCTTCGTAAAACAAATCGGAGGGCAAAC  
A

## SEQ ID 258

MDREKVLDRKIKKCLALGRSVNEHEAAQALRQAQALMEKYKVNEDIALSKVSEQKADRKMAFKLAGWQGVANMIADIFGCKSYQ  
RGKTMMFYGIGNRAET SAYAFDVYRQISADRRKFLKTCRAGKPSHRTYLAADRFCGGWIASAWETVKKFEMSDEEKAIMDGYKKK  
EYPDMAEARTDRDAKSSILQSGKMEYEALTRGMESGKQVKLHYAVNGTGFVKQIGGQT

## SEQ ID 259

ATGGAAGCAAAATAAATTTGAAGTGAAAAGTTTGTGACACCTTATAAAAAGTCTTTGCAGGCATTGCTGCCGATTTCGAAGCGGCAA  
TGGGTGTAAAACCGCGCCGACATTTCACCGAATTTGACGAACCGCAACATGAGCCGCAACCGCCGGTAACAGTTGCCGAGCAAAA  
AGGTATCAACGACTTTGCCATCGGCAAGGAAGTCATCATCCGCACTTATTCGGCAGGCGTTTGGTTTGGTGTGTTGAAACAAAA  
GCAGGCAATGAAGTGATTCTGACAAAAGCGCGCCGAATGTACAGCTGGTGGGCAAAGGAATCAATCAGCTGTGAGGTGTCGCAC  
GACACGGCATCAGGCAAGACGGCAGCCAAATTTGCGCGGAGCTTGATTCCGTATGGCTCGAGGCGATTGAGATTATCCAGTAAC  
AGGCGGCGCGGCTGAATCAATCCGCACCGCGCTGGAGGTGCGCCAGTCA

## SEQ ID 260

MEANKFEVKSLSDLIKVFAGIAADF EAAMGVKRA DISTEFDEPQHPQPPVTVAEQKGINDFAIKKEVIIRTYSAGVWFVGLKQK  
AGNEVILTKARMYSWWAKESISLSGVARHGIRQDGSQICGELDSVWLEAIEIIPVTGGAABSIRTALEVAQS

## SEQ ID 261

ATGATTCACTTAAATGTCCACTATTGCGATGAAATTATCCGCCATGCGGAAAATGACAAATACAGCCTGATAGGTATATTCCCCG  
ATATATGCCATATTCGACACCGCAGGCCATTCTAGGCCGCTGTGCCTGTCTGTTTCATTTTCGCGCGAAGGCATGGATATACA  
GACTATGAAAACCGGTCAAATTTTCTGGAAATCGTCCGCAACGATGATGTAATCTCTGCACCTTGAGATTCCATCATATGACGGC  
AGTGATACAGAAGAAAACGTGTCTATTCATGTACACCAAACAATCAGCGGACTACCCGTTTCAGACAACGACCGCATTTATGTAA  
GAATGACAACACACAACCATATCTCTCCGAGAGCGCTCTTTGTCTTTTCTTGGCTTCCTTACCCTCA

## SEQ ID 262

MIHLNVHYCDEIIRHAENDKYSLIGIFPDICHIPTPQAILGRLCLSVSFSABGMDIQTMKTGQIFLEIVRNDVISALEIPSYDG  
SDTEENVSFMLHQITISGLPVSDNDRIYVRMTTHNHILSESRPLSFSWLPYHS

## SEQ ID 263

ATGGAGCTGACCGTCCACTTTAACGCCGAGCAGGATTTAGACCGCCTCTTTGAAAAAGACGAAGAAGCGGTTCGTTATCTCGAGA  
ATGTCATTGCGATGATTACAGCGGACTCTGCTATTTTGTACGGCTTATACAAAACAGATACCTCAGGGAATATGGCGAACCCTAT  
AGGCCCGATTGACTTGGAAGTGAAACCCATATTTGTCTATTTGGGGAAGACATCAAAGTTTACCGCTCCGATTGACAGCGAA  
GAAGCCGCCGATACAGAATAATTTACGCACCATGCCATGAAAACAGCCAAACGGCACGTATATCCGCCCATAGATATATTTGG  
CTGTTGTAAACAAGAAGACAGACGAATTTGACTATCAGGCAGAACCCCAATCACAAAACGGATTATCAAAGACTATGAAGAAT  
GTACTCCAAC

## SEQ ID 264

MELTVHFNAEQDLRLFEKDEEAVGYLENVIAMIQADSAIFDGLYKNRYFREYGEPIGPIDLEVKPIILSLWGKDIKVLVRVDFSE  
EAAGYRIIYAPCHEKQPNGTYIRRIDILAVVNKRTDEFDQAEHPITKRIKDYEELYSN

## SEQ ID 265

ATGAATCAACAAGAATTTGAATTTATGAACGACTTGGCGCGTGCTTTTGAGCGTCGTTACCGTGATACGCGCAGCCTAAATAGAT  
GTTTCAGTATCGAAGGCCGTTATATGGGGAGGAAGCTTGCCCGCATAAGCCTGAAATCGGCTTGAGATACGGCGAAGATGCCAT  
GTTTCTTACTTTACAGGCATGGCGGAAGGTGGATGCGCCGCAACAAGAGCCGTCCTGTTTTCGTTCCGCATCGGTGCGAAGTCG  
CAGGCAGCTACGAGGAACGTTTGCAGGCTGAAATCAGGCGCGCGCGGAGGGGCCCTGCAATTTGCAGACGGATTGTTGGGCTTGG  
CCGCGTGGTATAGGGCGATACGGCAGGCGGCAGGGAATGATTTTGATTGCTGTTTGAGAAGGTT

## SEQ ID 266

MNQEFEFMNDLARAFFERRYDRTRSLNRCFSIEGRYMGEACPHKPEIGLRYGEDAMFLTLQAWAKVDAPOQAEVRIISFGIGAKS  
QAAEERLQAEIRRRGEGPLHLQTDLGLAAWYRAIRQAAGNDFDLLEK

## SEQ ID 267

ATGAGTAAAGCTATTAAACAAGTTAAATGAAAAGGAAAAGGAAAAAATACGCCTGCTTTTCGCACAAAGAGAAAAATTTATCGTA  
TCTTGGAAAATCCGGAACAGGGATTACTCTCTCTACCGCTCTTTTAAAAAGTGCGGAACTTGTTTTGTATTGATTATGTTAA  
TATGGGCGAGGTGTTACTGAGAGGTCAGAACCTATACAGGGACACGTTTAAAACTTGGCTCCACACCGGTTTATTTAGGGGGC  
GGGAAATCCGTAGCAAATGAAAAACAGAAGAATGTTGCGTACGGAGAGTTGGTATTGACGAATTTACGTTGATTTTTGTAGGGA  
ATATGAGAAGTATAGATTGCGCGTGGATAAAATAAACAGCGTGAATGTTTCAAAGCAGCATCCGAATCAGCCAAAGCGGCAA  
AAACAAACCGATTTCCTTAAATACCGTTTAAATCCGCAGTTATGGAAGAGGCTATATTGGTACTTTCCGATAAGAAG

## SEQ ID 268

MSKAINKLEKEKEKIRLLFAQREKFYRILENPEQGFTPTTALLKSGETCFLLIDYVNMGEVVTERVRYTGTRLKLGSTPVYLGG  
GKSVANEKQKNVAYGELVLTNFRLLIFVGNMRSIDLPLDKINSVECFQSSIRISQSGKNKPIFFNTVFNPQLWKEAILVLSDKK

## SEQ ID 269

ATGAGCGGCACGAAACGCAAATTAGGCCGTCCGACAGATTACACGAAAGACATGGCCGATAAGATATCGGAAAAATCGCAAATG  
GCAGAAGCCTACGTTCAATATGCGCCGAAGATGGTGTGCGCCCAATGAAACTATTTACCGTTGGTTGGAAGCTAATGAAGAATT  
TCGCCACCAATACGCGCGCGGAGAGAAAAGCAGCGGACTATTTGCTGAGAAATCATCCGAGATTGCCGATAGTGCACAAGCA  
GAGAGCGCGCGGTTTCAAAGGCGAAATGACAGATAGATGCCCGAAAGTGGGCGGCTTCCAAGATTGCGCCGAAGAAATACGGCG  
ACAAATCGGAGCTTGACGTTAAATCGGGCGATGGGAGCATGAGGGCGGCTGTACGGCTTGATGCTGAGGAATATCGCAAGATAGC  
GGAAGATGTGTTGCGTAGGTT

## SEQ ID 270

MSGTKRKLGRPTDYTKDMADKICEKLIANGSLRSICAEDGVPPMKTIYRWLEANEFEFRHQYARAREKQADYFAEEIIBIADSAQA  
ESAAVSKALQIDARKWAASKIAPKKYGDKSEL DVKSGDGSMAAVRLDAEEYRKIAEDVLRV

## SEQ ID 271

ATGGGCAATGCGGTTTCCCGGAGTTCCCGGCTTGAAGTGGGGGCGGAAGAAACGCGCGGTATGGAGTACGGGGACGCAGAAAT  
CGGCAAGCGGCGGTGAGTTCCGAACCGCTACTACACCTACCGCAATGGCGGTTTTCGCTGTCTCGAGGTATTGCGGACAAA  
AGCGTCCGTAAACGAGTTGGAAAACTGGCGGGATTCTTCAACGCCCGCAAGGCAGCTTTGAAAGTTTCCTTTACGAAGACCCG  
GCCGACAAACGCGTAAACGACACGCTGTGCGAAACCGGTGACGGGCGTTGCGCGTTATCAGCTTGTCCGTTTCGATGGGCGGAT  
TTATCAGACCTGTGTGCGGCGTCAAGGAACGCGCCCGCTCAAGGTGCGGCGCACGGCGTTGGCGTACGGGCGCGATTACACCGT  
TACCGACAAGGGCGTTTGGTTTCAACACGCGCAACCGCGGGCCCGCGATTACATGGACGGGCGGCTTTTATTTCCGCGTG  
AGGTTTACGTCTGACACGGTGGATTTTGAAACGTTTGGGCAGCTTGTGGCGGCCAAAAGATTGAGTTTACGAGTGTGAAAC  
TA

## SEQ ID 272

MGNVFPPEFPGLKWGRKKTAVWSTGTQKSASGREFRYAYTYPQWRP SLSFEVLRTRKASVNELEKLAGFFNARKGSPESFLYEDP  
ADNAVTDQFVGNVTQGVARYQLVRSMMGGFIEFVSAVKERP AVKVGGTALAYGRDYTVTDKGVLFVNTQPPGRPIWTGGFYFRV  
RFTSDTVDFENVLGS LWAAKIEFTSVKL

## SEQ ID 273

ATGCCGTCCGAAACGATTGAGGGCGCGGATCGTCGAAGAGGCGCGGTCTGGCTTGGCACGCCGTACCATCATCATGCAATGG  
TCAAGGGCGCGGTTGATTGCGCGATGCTCCTGGTCGCCGTCTACGGGGCGGTGCGACTGCTTCCGAAGGGTTCGACCCGCG  
CCCTTACCCTCAAGATTGGCATCTGCACCGGATTGCGAGCGTTATTTGGGGTTCGTCACGCAATTTGCGCGTGAAACGGAATCG  
CCGACGGCGGGCGACATTGCAGTATGGCGTTTGGGGCGGTGCTTTTCGCACGGCGGCATATTGGCGGGCGGGCGCAAGGTTATTC  
ACAGCTACATCGGGCGCGGCGTGGTGTGCGACGACATCGGCCAAGCCGAACCTATCGGGCGCGGGTTCGGTTTATCATTTTC  
ATTT

## SEQ ID 274

MPSETDLRARIVEEARSWLGTPTYHHAMVKGAGVDCAMLLVAVYGAUGLLPEGFDP RPYPQDWHLHRDCERYLGFTVQFCRETES  
PQAGDIAVWRFRSFSHGGILAGGGKVIHSYIGRGVVSDDIGQAE LIGRGVRFFTFPSF

## SEQ ID 275

ATGCCTCGTTTCCCCCGCACTTTACCCCGCCTGACCGCTGTCTGCTGTTGGCCTGTACCGCTTTCTCCGCCGCCGCACACGGCA  
ATCACACCCATTGGGGCTATACCGGACACGACTCTCCCGAAAGCTGGGGCAATCTGTGAGAGAATTCGGTTTGTGCTCCACCGG  
CAAAAACCAATCTCCGGTAAACATTACCGAAACCGTTTCCGGCAAACTGCCGCCCATCAAAGTCAATTACAAACCGAGTATGGTT  
GACGTGGAAAAACAACGCCACACCATTCAGGTCAATTATCCCGAAGCGCGCAATACCTGACCGTGAACGGCCGCACCTATACCC  
TGAAACAGTTCCACTTCCACGTGCGGAGCGAAAAACAAATCAAAGCGCCGCACTTTCCCGATGGAAGCTCACTTCGTCCACTTAGA  
CGAAAAACAAACAGCCTTTAGTATTAGCCGTGCTGTATGAAGCCGGCAAAACCAACGGCCCGCTGTCTTCCATCTGGAACGTCATG  
CCGATGACCGCAGGAAAAAGTGAACCTCAACCAACCGTTGACGCGATCCACCTACTGCCGAAACGGTTGAAATACTACCGCTTTG  
CCGGTTCGTGACCACGCCCGCGTGCACAGAGGGCGTATCATGGTTGGTGTGAAAACTTATGACCACATCGACCAAGCGCAAGC  
GGAAAAATTCACCCGCGCGCTCGGTTTCGGAACAAACCGCCCCGTACAGCCTCTGAATGCACGTGTAGTTATTGAA

## SEQ ID 276

MPRFPRTLRLTAVLLLLACTAFSAAAHGNHWHGYTGHDSFESWGNLSEEFRLCSTGKNQSPVNITETVSGKLPAIKVNYKPSMV  
DVENNGHTIQVNYPEGNTLTVNGRTYTLKQPHFHPVSENQIKGRTPMEAHFVHLDENKQPLVLAVLYEAGKTNGRLSSIWNVM  
PMTAGKVKLNQPFDASTLLPKRLKYRFAGSLTTPCTEGVSWLVLRKYDHDIDQAQAEKFTRAVGSENNRPVQPLNARVVIE

## SEQ ID 277

TTGAAGACTGATACTGCCAGAATGAACAATCTGATTCCCGAACATTAGCCGCCTATGCACATAGTGATAACCTGCAAATTGAAG  
GCGGGCATCGTTGCTTTTTCATTATCCTGCCAAGGTAGAGATACTTTCCACATCCGTTACTATGGAGAGCCTTTTGATGGATTGAT  
TACCGATACTGATAAGGCGCCGGTAAAAATGTGGCGGTAGAAGCTGTAAGCGCGGATGAAATCGTATGTTTGTATGGGGCGGAA  
CATGGCTATAACGCTATGTTCTGCGACAAATATAGCCAAATCAAAAGCAAAACAGAACGTTAACTGATTGGATGAATATACCT  
ACCGAGTTCCGATTCACTTTTATTAACAATATAGACTACGAAGATGAATATGAAGATTTCGTCAATTCTGAAGGACAAGTCCCTT  
AATTGATGGCCGCATCATTAGTTTGTACTCATTAACGAAATGGCTTTGATGCAATCAGCATTGATCTAATTGATGAAAAACAC  
TCTGTTCTGTAATTATTGAATGAAGAATTAAGC

## SEQ ID 278

LKTD TARMNNLIPEHLAAYAHSDNLQIEGHRCSLSCQGRDFTFHIRY YGEPFDGLITDTRKAPVKIVAVEAVSGDEIVLFDGAE  
HGYNAMFC DKYSQNKQNR LTLDLDEYTYRVPIHL YYNIDYEDEYDFVNSEGQVPLIDGRIISFDSLKRNGFDAISIDLIDEKH  
SVRELLNEELS

## SEQ ID 279

ATGCTCGAGAATCTGCCCTATTTCCAGCGACATCTGCCCTGAAGACCTTGCCAAAGTCAATGAAGTCATCAACCGTGCGGTGCAAT  
CCGATGTCGCACTGATTTTCGCAATCGGTACATATATCATCAGCGCGGGCGGCAACGCCTGCGTCCGATTATGACGATTTTGGC  
GGGTAAGGCGGTGCGTTATGATGACGAGAACTGTATTGCTGGCAGCGATGGTCGAGTTTATCCACACTTCCACACTCTGCGAC  
GACGATGTCGTGATGAAAGCGATTTCGCGCGTGGGCGGGCAACGGCAAAACATCTGTTCCGGCAATGCGCGCGCAGTGTGGTTG  
GCGACTTTTATATACCCGTGCATTCAACTGATGGTTGCTCGGGCAGTATGCGCGTTTGGGAAGTGAATGGCGGATGCGACCAA  
CATCATTTGCCGAGGAGAGGTATGACAGTCATGCAACATCGGCAATACGGACATTACCGAAGAACATATATCCGAGTCCCTCAA  
TATAAAACGGCAAAATTTGTTGAAGCTGCCGCTCAAGTCGCGCAATTTTGGGCAAAAGCTTCCCGGGCACGAACAGGCCTTGA  
AAGACTACGGTATGTACGTGCGGTACGGCATTCAGATTATTGACGATGTGCTGGATTATTCCGGGGAAACCGAAGAAACAGGTAA  
AAACGTGCGCGACGATTTGGCGGAAGGAAACCGACCTGCTTTGATTATCTGATGCGTCAGGGTCCGAACAGGTTGCGAAC  
GATGTGCGTACTGCTTTGGAAAAATGAGATCGCGGCTATTTGAAAAAATCCCGGATATGTGCTCCGTTCCGATGCTTTGGCAT  
ATTTCGATAGGCGAGGCGCGCAAGCAGTCGATTGTGCCGTTGCCGCGTTGGATGCCCTGTCCGACAGCGAAGTGAAGGATGCTAT  
GATTACGATGGCGAAGGAATCTTTGGTCAGGGTGTGCG

## SEQ ID 280

LMQVRVLSVNDKAFVTADLDYELPQAYYVDDPKAPPVEISAPVEAVPAAASDTASDGI AEDASAENGVSQNLWKQIWKAKQGQIV  
VVGIALTILLVLFQDWIVRYEKYDRFRFAFLTFTLFYIGWYAQAQLSVVNTLTLSAILTEPHWFFLMDPIVFIWLWFTAA  
TMLLWNRGTFPGWLPFGSLQELTNRIAKKLGVKQITVPHMLHTRLNVIKYLILFGLAISLYDLGTAEKFAEVEPFRKTAIILKF  
MCDWFWFAFAVALLIAGLFIERFFCRYLCPLGAGIALPGRFRVFDWLRRYKMGCPQIC THECPVQALAEPEGDIHPNEC IQCLH  
CQVMYHHDTRCPQVVAENKKKQKQAAAKSGELENVSKQPQEQVVRVFKPETAQSEK



## SEQ ID 281

ATGAAAAAATTGAAAAATATTTCCGTTGTTGCTGTGTGTGCCGTTTTCGTTGCTGCCGCTTCTGAAAAATTCGTAGCCAACT  
ATGCTATCGGCGACGATTCCGCCGTAATCAAGGCTGGTCGTAACCGTGCCGAAGCGGAATTAGCCGTGCGGAACCTGGCGCAACA  
CCGCCGTCAACGTAAAAATGTTTCTGAGGAGTTGGCTTTGGAACGTGAAAAACGTGCCAATAAGCATGACGCAATCCGTCAAGGT  
ATGGGTACGGCTGCCGGTGGTCTGATGCTGCTGAACGGTGTGGTTGGTACCCTGGGTGTAATGAAAAACGGTGTTC

## SEQ ID 282

MKNLKNISVVAVCAVLLAACASENSVANYAIGDDSAVIKAGRNRAEARI.SRAELAQHRRQRKNVSEELALEREKRANKHDAIRQG  
MGTAAAGGLMLLNGVVGTVGVMSVF

## SEQ ID 283

ATGAAAAAAGCACTGCTTGCACTGACTATTGCCGCCATCTCCGGTACTGCTATGGCCAGTTGCCCGACTTTCGGGTAAAGGCG  
AATATACCGTCCGTACAGACATCTCCAAACAAACGCTGAAAAATGCCGATTGAAAGAAAAACACAAAGTACAAAAAACATCGG  
TTTCCGTGCCGATATGCCGTTTGACGATATTACCCACGGCATGCGTTTCGAAGTATCACACAGCCGAGACAAAAAGACATGTAC  
GTTGTGACCGAAAGTACTACTAAACCATTCGGCAAAGACGTTGAAGAAAAACGCACCGACGTGTATGCCGGTTACACCTACACTC  
AACCGATCAGTGAAGCCACCAACTGCCGTTTAGGTTTGGGCTATGAAAAATACAAAGATGCCGTAGCTAATGAGAAAGG  
AACAGTCAGCACCAGCGCGAAGCCTTCTATACCAAAGCGCACGCCACCTGACTTCCGATTGGGCGCGCGGTGGTATCTGAAT  
CCTTGGGCAGAGGTTAAGGTTGACCTGGACGCCAAATTGAAACACAACGCAACTGTAGCCGGTGTCTCAGCCGACATTAACGCAA  
AAACACGCGGATGGGGCGTGGCGGTAGGTGCGAATATCGGCAACAAATTACCGATACCGTCGGCATCGAAGCCGCGCCGTTCTA  
CAAACACCGTCACTTCAAAGCATCCGGCAGCTTCGTTTATAGACGCGGGAACATCCGAGTCGATCCTACCAAAATCAACGAATAC  
GGTGTTCGTGTCCGCGTGAAATTC

## SEQ ID 284

MKKALLALTIAAISGTAMAQLPDFLGKGEYTVRTDISKQTLKNADLKEKHVKQKNIGFRADMPFDDIHHGMRFEVSHSRDKKDMY  
VVTESTTKPFKGDVBEKRTDVYAGYTYTQPISEATKLRLAGLGLYEKYKDAVANEKGTVSTEREAFYTKAHADLTSDLGGGWYLN  
PWAEVKVDLDAKLKHNATVAGVSADINAKTRGWGVGVGANIGKQITDTVGIEAGFPYKHRHFKASGSFVLDGGNIRVDPTKINEY  
GVRVGVKF

## SEQ ID 285

ATGTTCAAACGACCTGAAGAAATCATCGTCTGATACTTGCCGCTCTCTGGATTGCCGGTACGTATTTCTCGCCGCCCTGTTTG  
GAGCGGATGCTTATACCGTGTAAAAATCACTGCCCTTACCCTGCTTTGGTCTGCCGCATCATTCCTCCTTTGGCAAAAAAAC  
TCAGCCGGCATATCTGCCGCTGCTGCTCGGCTGCCGTGACCACCTGTTGGTGGCCGTATCTGAATCAATCGGTGCGACCCGGTTC  
TTTACCTTGGCATGCATCATGACGTTCAAACCATCTTAGCCCTGATTCCCGCAACCGCAGGTTATCTGTT

## SEQ ID 286

MFKRPEEIIVLILAVLWLAGTYFLAALFGADAYTVLKITALTLLWSAASFLLWQKPPAYLAAAARLPDHLVAVSESIGRTRF  
FTLACIMDVQNHLSPDSRNRLSV

## SEQ ID 287

GTGATGATTTTGTCTGGACACGAATGTGATTTCGAACCTTTGCCGCCACAACCCAATGAACGTGTGGTGGCATGGTTGGATAGTT  
TGATATTGGAAGATGTGTATTGTCTGCCATTACTGTGCAGAAATTGCGTTTGGGTGTGGCGTTGTTGCTCAATGGCAAGAAAAA  
GAATGTGCTGCACGAACGTTTGGAAACAATCCATTTTGCCCTTTATTGCGGGGCGGATTCTGCCTTTTGATGAACCGGTTGCCGCA  
ATCTATGCGCAAAATCGTTCCATGCCCCAACACATGGCAAAGAGATTGCTGCCGAGACGGCTATATTGCCGCCACTGCAAAAC  
AGCACAGTTTGACAGTTGCTACGCGTGATACCGGCTCATTTTTTGCAGCCGATGTCGCGGTGTTCAATCCGTGGCACGAT

## SEQ ID 288

VMILLDTNVISEPLRPQPNERNVVAWLDSLILEDVYLSAITVAELRLGVALLNGKKKNVHERLEQSSILPLFAGRILPFDEPVAA  
IYAQIRSYAKTHGKEIAAADGYIAATAKQHS�TVATRDTSFFAADVAVFNPWHD

## SEQ ID 289

TTGAAAAAGCGTGGTGCCAAGGGGGCAGGGGATTCAATTATGAGGTGCTTTATGTTTTCGACTGTGATTACTGCTGCTGTTTAT  
ATATTGCTACAGCAGTAGATTGTTGGTAATACTATTAAATTTTTTGTCTAGAGCAAATACTAGAAAAGATATCGAGATATTTA  
TATCGGACAATATTTAGGTTCTGTAATTTTAATATTAGTTAGTTTATTTCTAGCTTTTGTGTTTGAATTATGTTCCGGAATAATG  
GTGTTGGGTTTATTAGGTTTAAATACCGATTACTTAGGTATTAAAGTTGCTATTACGACGATTGTGAGGGCGAAAAAGAGCTA  
AAAAAGAATTGGATGAAAAAGGGTTGTCAAATATTAGTCGGTATTGTTGCTTTGGTTACAGTTGCTAGTTGTTGGTGCAGATAATAT  
TGGACTTTTGTTCCTTACTTTGTGACTTTAGATCTGTGCACTTATTAGTTACTCTTCTGTTATTTTAAATATTGATTTTGTGTT  
TTAGTATATACAGCAAAAGATTGGCTAATATTTCAGGTGTTGGTGAAATTGTAGAGAAGTTTACTGTTGGTGAATGGCTGTTA  
TTTATATTGGTTTAGGGTTATTTATTATTATTGAAAAATAATACAATTGCAACAATAATATCAATAATA

## SEQ ID 290

LKKPWCQGGRGFIMRCFMFSTVITAALVLIATAVDLLVILLIFFARANTRKEYRDIYIGQYLGSVILILVSLFLAVLNVPEKW  
VLGLLGLIPIYLGIVAIYDDCEGEKRAKELDEKGLSKLVGIVALVTVASCGADNIGLFVPYFVTLDLVDLLVTLVFLILIFV  
LVYTAQRLANISGVGEIVEKFSRWIMAVIYIGLGLFIIENNTIRTIISII

## SEQ ID 291

ATGACCGCACTTTTAAACCGAAACCCAAAGGAAAAATCAGGATACGCGCCTGATTCCCTTTCCGCCCTGCAACACTACGCTTCT  
GCCCGCGTCAATGTGCTTTGATTCAACGAACAGGCGTGGGCGGAGAACTATTGACCGCGCAAGGCAAGCGTTACATGAGCG  
GGTGGATTCCGACGAGCCGGAACGCTGCAAGGGCGTGCGCTTTGAGTGGACAGTGCATGTTTGGCGGATAAGCTGGGCATCAGC  
GGCATATTGGATTGTTGGTGAAGTGGATACAAAAACAGGCCGTCTGAAACCTGTGGAATACAAACGAGGCAAGCCCAACCTGACC  
CGGGGGATGAAATCCAGCTTTGCGCCCAAGGCTGTGCTTGGGAAGAAATGACGGGGCAACCGTCTCTGAGGGCGCGCTGTGGTA  
TATGCAAAACCCGCCACCGTGTCCCGTCTGTTTTCAGACGGCCTGAGACCTTTGCAA

## SEQ ID 292

MTALLTETQRENQDTRLIPLSALQHYAFCPRQCALIHNEQAWAENYLAQGKALHERVDSDEPETCKGVRFEWTVHVLADKLGIS  
GILDLEVDTKTGRLPVEYKRGKPKPDGDEIQLCAQGLCLEEMTGQTVSEALWYMQTRHRVPVVFSDGLRPLQ

## SEQ ID 293

ATGAGTGATATTGATGATTTCAAAGCTATTTAGAAAGCCACCAAGCGGCATTTTCCGCTTGGGGTAGATTGTGGCTGAAGAAA  
TTCAAATCAATTATCCAATGTCAATTCCTCTGTTCCGGTTGCCAATTTCTAAAAATTGAAGCAAAGCCTGGAGTCAAAGAGAT  
TTCTTCAGCTCTAGCCAAGATTGGCCGAAAAAATTACACTTCACCTCAAACCTCAAATGACTGACTTGGTGGCGGTACGTTTGTG

GCATTGCTTGCAGAACATATTCAAATAGTTTGTGAAATCATTTGAATCCTCATCTCAGTGGAATGCTAAAGTTTCGAAAGATTTTG  
CAGATGAAATTCAGCAAAATCCCAAGCAAT

## SEQ ID 294

MSDIDDFKSYLESHQAAFSAWGRFVAEBIQNQLSNVISPVFVANFLKIEAKPGVKEISSALAKIGRKNYTSPTQMTDLVGVRFV  
ALLAEHIQIVCEIIESSSQWNAKVSDFADEIQONPKAI

## SEQ ID 295

ATGAAACTGTTTCCAACCATCTGACCGGCATCTTTTGGCAACCGCCCTTCCCGCATCCGCACACGGTATGCATAAGAGCAAAC  
CCCTGGCTATGGACGAGCTGCCGCCGATTGTCCAACAATATTTCAAACGCGCCGAAACCTGTTACAACAAAGCCGGAACAAAGC  
AGATTTTCGCACGCAACAACACCAAAATTCCTATTCCAAGCCCTACCTGCCGCCGATTGGGACAGCGTAAGCAAATGTGCCAAATC  
GCTATGGATTCTGTTGCAGAAAAAACCCGCAATCTGAATTGCGAATAAAGCCGCATCAGCAA

## SEQ ID 296

MRTVPTILTGILLATALPASAHGMHRSKPLANDELPPICQYFKRAETCYNKAGNKADFARNNTKFLFOALPAADLGQRKQMCQI  
AMDSFAEKNPQSELRIKPHQ

## SEQ ID 297

TTGCTCAACCCCTCTTCTACCCCTCTCATTTCTATAAATGATTTTACCGCCGCGCGTTTCTGACCGTTCCGGCTTAAAGCCCAAC  
GCCGCATAACGCTTCTCGCGCTCTCCCGCAAATCCACATCCAAAGGCTTGCCCGTCCGCAAATCGACAATCCCTCGCGCTTCG  
CCGTCAAGCCCGTATCCGGGTCGGCAACCTCATACTGACAGCTTTGAACACATTCGGGTCAAAGCCCTTCTCCCTTGGCGCTC  
AAACTTCCCGTTAAGCGCATCAATCTGCGCGCAATCTCCCGCGCTGCCCGTCCGACTTCGCAAAACCATAAGCCCGCGTCAA  
TCGGCGATGCGCTTCTATCTCAAGCTCCAGCGCATCCGCCTCAGCTTCATCTCAAACCCCTGCCGCTTCATCCCCAGCTCGG  
CCTGCTGCACATCAAACGCCCTGTCCGCATTCTCTGCGCATCTCGCGGTTCAACGCACCCCTCGTTCCGCTTAAACGCCGCATC  
AAACCGCCCTTCTGCAACACACCGCTCAGGTTTCGCGCATCTCCGCGCGAGCCGCCGCCAGCCCTTCCCTGCCCAATTCCCTG  
ACCGCCGCTTTTATTATGTTCCGCCACAATCCCGCGCGCGCATTAAGCTGTGCCGCCGTCAACTGACCGTTCAAGGCCCGCG  
CATAAGGCGTAGTCGCCCTCTTATAAGCTCCCGCTCCTCAGGCGACAGCGCATCCGGCCCGGCGAGACCAAAGGACGCTGCCG  
GTCAAATCAGCGACCGGCTTGGCGCCCGGATACATATCCCGTCAAATCCCAAAGGCGCGCGCGTCCGTCCGCCCGCATCCGT  
GGGCGCGTATCGCGCCGCGGAAATCCGCCCGCGCGCGCATCGGGGAAAGCGCTTATCGCCGCCCGGAAACCCCAACCGG  
CATCCGACCCCGTTGAAAGCACCCGCCCGCGCAACCGCGCGCGCCCATCTCTCAATATGTTACGGCTCAAATCCATCACATT  
CCGATAACGCGCCCGCGCCCGCTCATAATTGCGCAACGCTACGCCGCAACCGCATCGGACCGGTGCGCTGTGCCGCCCGCGCTCC  
CGCTCTCCGCCCGCTTCCGGGCTTCTCTTTTCTCTCTTTCTCTCATCTCCCAAAATCCCGCGAGACGGCTCAAACAAAC  
CCATCGCAAACCTCCGAACAAATAAGTCCAAATAAGCAAAACCAAGCCCAATCAAACGCCTAAAGTTAAGAACAACAAACAA  
AATCGCAACCCCGACCAATTACAAACAACAAGTTACAAAAAAACACACCGACGGGCCATTTCCGGGGGCAAATAAAAGC  
CGCCTTGTGCAAGGCGGTTGCATTTCAGAACAGTCTCGGCTGTTTACGGTCCGGTCTT

## SEQ ID 298

LLNPLILTLILINDFTAGRFLTIVRLKAQRITLLALSRKLHIQRLARPQIDNPLALRRQARIRVGNLITDSLEHIRVKALLPLPL  
KL PVKRINLPRNLPAFPVRLRKTISPRQIGDALPILKLQRI RLTLHLKPLPLHPQLGLLHIKRPVRIPLRHLAVQRTIVRLNRRI  
KPPLLQHRILTIVRRILRRSRQPFPAQFPDRRI FIMFRHNPARRIKLCRRQLTVQGPRIIRSRPLIKLPLLRQRIRIPGRHQRTLR  
VKITHRLAAPIHIIPVKSQRRRPSARIRRRARIAPREIRPGPRIGGKRLIAARKPQTGIRTPESTRPAQPPRPILNIVTAQIHII  
PITRRPGLIIRNGTPHRI GTVRLCRRPLPILRPLPGLLFFLLFHLPLKIPGRRLKQTHRPSEQIKSKISKNPSP IKRLKLRTNK  
NRNPGPINQOVTKKHTDGPFPGANKKPLCKAVAFQNSLGLCLRSGL

## SEQ ID 299

TTGGGCATCTATGGAGCATGGTGTTTTATGGGATTAACACAAGAGGTTTAAAGAATTATTAAGATATGATGACAATACGGGAA  
AGTTATATTTGGGCGGAGCGTCCAGAAAGTATTTCAATAGCGGTTTGCAATACAAATCTTGGAAATACCGGATTTTCCGGCAAGGA  
GGTTTTCTTATACAAAGGCAGGTTGGGGTATTTGAAGTTAAAAATATTAAAGAAACATATAATGCACATAGATTAAATTTGGCTT  
TTTGTATTATGGGAAACAGCTTCTTCAATAGGCCATATCAATAGGGATAGAGCAGATAATAGAATATCTAATTTGAGAGATGTTA  
CACATGCTGAAAAATATGAAAAATAGAGGGAGGTTTAAAAATAATACCTAGCGGGCATACTGGGGTTTATTTCCATAAGCCGCTTAA  
GAAATGGCAAGCTAGGATTATGGTTAATAGAAAAATAAATATTAGGTTTATTTGAACATATTGAAGATGCAGCGAAAGCGAGA  
GAGGCAGCATCTAAAGATTTTGGCTTTGTAGTG

## SEQ ID 300

LGIYGAWCFMGLTQEVLEKLLRYDDNTGKLYWAERPRKYFNSGLHYKSWNTGFSGKEVFLYKGRGLGYLKLKIFKKQYNAHRLIWL  
FVYGHASHIGHINRDKTDNRI SNLRDVTHAENMKNRGFKNNNTSGHTGVYFHPKSKKWQARIMVNRKNKILGLFEHIEDAARAR  
EAASKDFGFV

## SEQ ID 301

ATGAACGGGGCGGAATTTACACTGACGCCCCAAACAAAAGCAGGTTATGCGGTCGATTGGGACAGCCCGGACGGGTGGTTTG  
AAAACGGCAACCTTGAAATCACAAATCCGCCCGCGCAAGTCAAACGGAGCGTCGAGCAGAACAGGCGGCTATGGTTTTTGTATCG  
TGAAATTCAGAAAAAGTTTTATCGATGGGAGAAGGTTTAGTCAAGATGTATGGCATGAATTTTAAAAAGAAAATTTATTTGGA  
TGTATTGAAATGCCTAACGGGCAATTAATGGGTATATCAACGACAAAAATTATCAGTTCGGGAAATGTCTGAATATCAAGAAAAGA  
TTATATCTTGGGCATCTATGGAGCATGGTGTPTTATGGGAT

## SEQ ID 302

MNGAEFTLTPOKQVMRSIWSDPDGWFENGLEITIRPKSKRSVEQNRLWFLYREISEKVFIDGRRFSQDVWHEFLKRKF IG  
CIEMPNGQLMGISTTKLSVREMSEYQEKIISWASMEHGLVWD

## SEQ ID 303

ATGCCGTCCCGCGCAAGGAAGGGGGTCTATTATTACAAATCGTGCAAAACCTGCCGCAACAAGGCAGTCCGGCAAAGCGCGCG  
GCGCGCGGAGCCGGCGGATGACGCGCGCAAGGCTGCACGGATACATCCGCGCGCGCACGCGCCCTGCCCGATATTGGGCGCGG  
GCCTGTGGACGCAACCGCGAGGGGAATGCGCGTGACGCGCTTATCTGCCTTACCCCGTATCGGCAAAACCGATATTGGCGGATT  
TGGCGCAACAGGGCGGTTCAGGAGCGCGGAGGCGCGCGGTATAAGGAAACCGTCCGCGGTATCGGCAAGGGGCGGGCGCGATGC  
CGTCCGAAGGCGCGGTTCGCGTATATGTGCGGCTGATACCCAAAGCGAACAAGACGCGCGGCGCAACAAGACCGGTGATCGATTT  
GGACAACGCCCTGAAGGTTACTCTGGACGCGCTTCAAGGCGTTGCCTATCACAACGACAGGCAGGTGCGGCGCATTTGCCGCCGAA  
TATGGCGGCGAACCAGGTAACGGGCGCGGTTTGGCGGTGGAGGTGGGGGAATTGGAGATGGAACAGACGGATGCGGCGAGACGAGG  
GTTGGGATTTTCATCGGACAGGAGGTTGGGATGTC

## SEQ ID 304

MPSRARKGGLLLQIVQNLPPQGGSPAKARGGSSRRDDGGKAARIHPRRARRLPDIGRRPVDATGRGMVRTRLILPYFVSANRYWRI  
WRNRRAVRSAAEAAAYKETVRRRIAQAGAMPSEGAVALVYVRLIPKANKDGGANKTVIDLNLKLVTLDALQGVAYHNDQRVRRIAAE  
YGGEPVTGGGLAVEVGELEMEQTDAADEGWDFIQEGWDV

## SEQ ID 305

ATGCTGAACGCGTACGACGTGGCAGATTTCTTCCTTTCCCTTTTGAAGAAGAGGACGGGGAGCAAATCTCCAATCTCAAACCTTC  
AAAACTCCTGTATTACGCACAAGGCTACGCCCTTGCCATACTTAACCGCCCCCTGTTGCCGAAAATATCGAACACTGGCAGCA  
CGGTCCGGTAGTCCCCTGCATTTACCGCACCTACAAAAATACGGCGGCAGCCCATTCCTGCGGCCCATATCGAACCCGACAAA  
TATCGGACGAAGAGTTGGTTGCTCAACCGTGTCCGTAAAGAGCAGGGCTGCTACACCGCTTGGCGATTGCAATAAACCC  
ATCAGGAAGCGCCGTGGATACAGACCCGGCAGGGCGAAGTCATAGGGATTGCGCTGATGGGGGAATATTTCCGCCATGCGCTGCC  
GCAGACGATTACAATTTCAATCTTGAAAACTCAAACAGCCGTTGAAGACAGCTTTGTCAGCGTCCCGCATTTCAACGGCGCC  
GACGACTTGAAAAATGGTTGGAGCAG

## SEQ ID 306

MLNAYDVADFFLSPFEEEDGEQISNLKLOKLLYYAQGYALAILNRPLFAENIEHWQHGFPVPCIVRYTYKKYGGSPFLPAAHIEPDK  
YADEELVVLNRVRKEQGCTAWALRNKTHQEPWIQTRQGEVIGIALMGEYFRHALPQTDYFNLEKLKTAVEDSFVSVPHFNGA  
DDLEKWLEQ

## SEQ ID 307

TTGTCGGATGAAGGCAGGCATAAACCTACTTCCGCCCAAACCGCGTTTATGATGAAAGGTATGGATAAATTGAGATACCAAC  
GGGATTTTAAATATCCGCCCATTTTACAGCCGGCGAACAAGAATACCTGACCGAATTGTCCGATCGGCTTCCTTTATCTGT  
TTAACCGACTCCGTGCGTAATATTGAAGAAATCGGTATCGATTTGTGTACAGTCTGCCAAATGGAAGGAAACACTTATAAT  
CAATACGATACCGCAGCATTTGCTTAACTCGGGCAAAACCGAGCGGAAGTTATATTCCGATGCGCTTAATGTTAATCAACCTGA  
GGGAAAGTTACCGGCACCTGCTGTCCGGTTTGACAGCCCAAGCCGTTTGACTGGTTGGATTCTTAAAAACCAACCCACAGCCT  
GATTTCCGAAAACCTACTGAAAAAGGCTCCGGCGCGTAGTCCGCCGCGACAGCGTTACTATAAGCGGGACAGACTACACCCCT  
TTATCAACCCGCAAGTTTGGATACGGAATTGAATGGTTGCTTCAAGAAGCCCCCAAAATAGAAAATCCTTTTCGACCGCGCCG  
TTTATCTCCATAATAATTTGGCGTATCTCCGATATTTAAGGACTGCAATAAACGTACTGCCAGAACTGTATGACCTTGTCCGT  
GATGCGCTCCGGTTTTTCTTCCGTATTTCTCCCGACAGTTATCCCGCTATGCCGAGGCTGTCGTAGCCTATTACGAAACC  
GGCGATTACGGTTTTATTCAAGAAATATTTATTTCGGCATAACGAAATACCGTAATAAGTACGGTCCCAGCCTGATGTGGATA  
TTTTCCGAAATTTCTCCATT

## SEQ ID 308

LSDEGRHKPTAPNRVFMKGMKDLRYQRDFLNIRPIFTAGEQEYLTELSDRPLSVLTDSVRNIEBIGIDFVYSPAKLEGNTYN  
QYDTQALLKLGQTAGGKLYSDAVMLINLRESYRHLISGLDSPKPFDWLDFLKTTHSLISENLEKSGGVVRDSVTISGTDYTP  
LSNPQSLDTLKLWLLQEPKIEPNFDRVYLHNNLAYLRYFKDCNKRTARNCMTSLMLRSGFFPCVFPSPDSYPAYAEAVVAYET  
GDYGLFKKYPISAYENTVNKYGPQPDVDFRNFISI

## SEQ ID 309

TTGAACAAAAATGGGAACACTGACATGGCTTTACTGAGCATCCGCAAGCTGCACAAACATACGGCAGCGTAACCGCCATCCAAT  
CCTTAGACTTGGACTTGGAAAAAGGCGAAGTCATCGTACTGCTGGGCCCCGTCGGCTGCGGCAAAATCCACCTCTCGCGTGCCT  
CAACGGTTTGGAGCCGCACCAAGGCGGCAGCATCGTATGACCGGTGTCGGCGAATTCGGCAAGACGTTTCTGGCAAAACCGCC  
CGGCAAAAGTCGGTATGGTCTTTCAAAGCTACGAACTGTTTGGCCCATGACCGTCATCGAAAACATCCTCTTAGGCCCGGTAA  
AGGTACAAAACCGCGACCTGCGCAAGCAGAGGCGCAAGCCGGCAAACTGTTGGAACGCGTCGGACTGCTAGACCGCAAAACGC  
CTATCCGCGCAACTTTCCGGCGGTGAGAAACAGCGCATCGCCATTGTCCGCGCCCTGTGCTGAATCCGGAAGTCATCTGCTG  
GACGAAATCACCGCCGCACTTGACCCCGAAATGGTGCAGCAAGTCTTGGAAGTGGTTTTGGAACCTCGCCCGCAAGGGATGAGTA  
TGCTCATCGTAACCCACGAAATGGGGTTCGCACGCAAGTTGCCGACCGCATCGTCTTTATGGACAAAGGCGGCATCGTCAATC  
GTCCGACCCGCAAACTTTTTCGCCACCAAAAGCGAAGCGCCCGCAATTTCTGGCAGGTATGGACTAC

## SEQ ID 310

MAILLSIRKLHKQYGSVTAIQSLDLLEKGEVIVLLGPSGCGKSTLLRCVNGLEPHQGGSIIVMDGVGEFGKDVSWQTARQKVMVF  
QSYELFAHMTVIENILLGPVKVQNRDRAEAEQAQGLLERVGLLDKRNAYPRELSGGQKQRIATVRALCLNPEVILLDEITAAID  
PEMVREVLEVLELAREGMSMLIVTHEMGFARKVADRIVFMDKGGIVESSDPETFFSAPKSERARQFLAGMDY

## SEQ ID 311

ATGACGAAGTTATACGCGCAAATCGCCAAGACGAGGCGCAGGACGACGGCACGGTCAAAGTTTGGGGCTATGCTCGAGCGAAG  
CGGTGCGATTGCGACGGCGAAGTCGTGCGCGCGAAGCAATGAAGCGCGGCGATTCCCGATTATATGAAGTTCCGCGCGGTGCGTGA  
AATGCACGGCTCAAACGCGCGCGGAACGCGGATTGAATCAACGTGGAAGACGACGGCGCACATTTTCCGGGGCGCATATCGTT  
GACCTGTGCGGTGACGAAAGTCAAGACAGGCGTTTACAAAGGCTTTTCATCGCGCGGCGAGGTTACCGCCCGCAATGATTGA  
ACAAGTCGCAATACGCGGCTTGAAGCTGACGGAATCAGCCTTGTGACCGCCCTGCCAATCCCGACGCGGTGTTTACCTGCTT  
TAAGGCGGACAAACCGAAAGATGAGGCAAGGGCGCGGATAAAGACGGCAAGCCGTCTGACAAACCAACCGAAGGAAGATGAA  
AATCTAAAGACGGCGATAAAGGGCTTAAACCGCAAGATAAAGGCGGATAAGGACGCGCGCAAAAGGACGAAGCCGAAAATCGG  
CAAGCGTGAATTTGTCCGAACTCTGAAATCGCCGCTTTGAAAGCGGTATTGGCTAAAGCCGACAGCCGAAAGCGGGCGCGCGC  
CAAATCAATGTACCAAGTCAAATCACCGGCTGATGTATTGATGTCGCTGAAATGGCTGGTTGAGGACGCATCTACGACAACATC  
GATGAAGCGGTTACCGCGCAAATCAAAGATCGGCGCGCGCTTCCGAATCGCTGAAAGCGTTGGCGGCAAGCGAAGCCGATA  
AGCCGCGCGACGTTTGGCGGCAAAAGCCGCAAAATCAGGCGATCTTGCCAAAGCGGAATCGGCTGACGAATGGCAAAGGCACA  
AGACGCGCTGAAAAAATCGAATGACGCCCTTGCCAAAGCACAGGCGGAAATCGAAAGCCTGAAGAAACAGGCAGTACCGCCGAAA  
GGCAGTACGAAAGCTATCAGTAAGGCAGAGATAACGGCGAAGACCCGTTAAAAGGTTTTACCGCGATTGTAAAGAATGACGGCA  
CGCTGGATGACGTGGCGACACTCATTAAAGCAAAACAAACAGGCCGCTG

## SEQ ID 312

MTKLYAQIAKTEAQDDGTIVKVGYSASSEAVDSDEGVAAEAMKAAIPDYMKFGAVREMHGSNAAGTAIEINVEDDGRTEFFGAHIV  
DPVAVTKVKTGVYKGSIGGSVTARNDLNKSQITGLKLTETSLVDRPANPDVFTCFKADKPKDEAGAADKDGKPSDKPTEEDE  
NPKDGDGKPKTEDKDGDKDAGKDEAGKSASVNLSESEIAALKAVLAKADKPKGGPAKSMYQVKSADVLMSLKLVEDASVDNI  
DEAVTAQIKESAAGLAESLKALAASRADKPADGLAAGKSGDLAKAESADELAKAQDALKKSNDALAKAQABIESLKKQAVPFPK  
GSTKAISKAEDNGEDPLKGFQPIVKNDDGLDDVATLIKAKQTGRL



## SEQ ID 313

TTGACAATCAAAATCGGGGGGATAGCTGATGGCTATCAATGCCGCTCGAAAAATGTGGTTTGGGAAGACGTTGGGGGAGGTTGCCG  
AATATTCAAAAAACCGTATTTGTTCCGATAAACTGAACGAACATAATTACGTTGGCGTGGATAATCTCTTACAAAAATAGAGAAGG  
TAAAAAGTTATCCGGTTATGTTCCAAGCGAAGGAAAAATGACAGAATATATTGTCAATGACATTTTGATTGGAAATATTTCGTCCG  
TATTTGAAAAAATCTGGCAGGCAGACTGCACGGCGGAAACAAACGGTGATGTTTGGTTATCCGGGTAACAGATGAAAAGGTTA  
ATCCAAAATATCTGTATCAGGTATTGGCCGATGATAAATTTTGTCTTTAATATGAAGCACGCCAAAGGTGCAAAAATGCCGCG  
TGGCAGCAAAGCAGCGATTATGCAATATAAAATCCCCATCCCCCGCTCCCCGAACAGGAAAAAATCGTCGCCATCCTAGGCAAA  
TTCGATACCTGACCCACTCCGTCAGCGAAGGCTGCCGCACGAAATCGCCCTGCCCGCAAACAATACGAATATTACCGCGAAC  
AGCTGCTTGCCCTCCCCAAGGCTGCC

## SEQ ID 314

LTIKSGGIADGYQCRLLKNVWVKTLGEVAEYSKNRICSDKLNEHNYVGVNDLLQNRGKFLSGYVPSEBKMTEYIVNDILIGNIRP  
YLKKIWQADCTGGTNGDVLVIRVTDKVNPKYLYQVLADDKFFAFNMKHKAGKMPRGSKAAIMQYKIPPLPEQEKIVAILGK  
FDLTHSVSEGLPHEIALRRKQYFYREQLLAPFKAA

## SEQ ID 315

ATGCTGCCGCCCAACTGCGGAACGGCAACCCCTTATATATTGCGTAACGCCGTAGGATTGGACATATCCAAGTTGACTTTTGACG  
CAACGGCCATTGTCGGCAATGCCGAATATTGCGCAAGTTTGACAACGATTCAAAGGTTTAGATCAGTTTTCGGACCGGTTGAA  
AAGCTTGGGATGTCAGAATCTGCATATCTGCATGGAGGCAACCGGCAATTATATGAAGAAGTTGCCGACTACTTCGCGCAGTAT  
TACAGCGTTTACGTAGTGAATCCGCTGAAAAATAAGCAAGTATGCAAGAACGAGTTCAAGCGAACCAAAACAGACAAACAGGATG  
CAAACTGATAGCGCAGTATTGCCGGTTCGGCGCAGGAAAGCGAGCTTGTAAAGAGGCAAGCCTACGGACGAGCAATACAGGCT  
TTCACGGATGACCGCAGCATACGCGCAATCAAAGCGAATGCGCGGCAATGAAAAACCGTCACTACGCGGCAAAAGATGAAGAA  
CGCGCCAAAGCATATGCGGAAATCATCAAAGCCATGAATGAACAGCTTGAAGTTTAAAGGAGAAGATAAAGAGCAGACGGAGA  
AGCCTAACTGCAAGGAAGGCGTGAAGCGTCTTGAACCATACCGGCAATAGGCAGAATGACCGCAGCGGATTGTTTTCATCATCT  
AACATCTTCGAAATTTGAAACATCAAACAAATTTGCAGCATTCGCGAGGCTTAAGCCCGCAACAAAAAGAAATCCGGGACAAGCGTA  
AGGGGAAAAGGCAAACTGACCAAGTTTGGCAACAGGAATACGCGCGCTTGTGTTATGCCGGCCATGGTCGCATACCGGATAA  
GGGCATTTCGCGACTTCATCAAAGGCTGGAAGAAAAGAAGCCTAAAAAGTCATCATCGCAGCATTTGATGCGTAAACTCGC  
CGTTATTGCGTATCAGTACATAAGAAAGCGGAGATTACGATCCATCGCGTTACAAATCGGCG

## SEQ ID 316

MLPNCGTATPYILRNAVGLDISKLTDFDATAIVGNAEYSAKFDNDSKGLDQFSDRLKSLGCONLHICMEATGNYEYEVADYFAQY  
YSVYVNPPLKISKYAESRFKRTKTDKQDAKLIQAQYCRSAQSESELVKRQKPTDEQYRLSRMTAAYAQIKSECAAMKNRHHAAKDEE  
AAKAYABI IKAMNEQLEVLKEKIKEQTEKPNCKEKGVRLETI PAIGRMTAAVLFHHLTSSKFETSNKFAAFAGLSPOQKESGTSV  
RGKGLKTKFGNKRRLRAVLFPMPAMVAYRIRAFPDFIKRLBEKKPKKVI IAAALMRKLAVIAYHVHKKGGDYDPSRYKSA

## SEQ ID 317

TTGGAGAAGCGTAGCGAAGACATCCCGTTTATATGATTATCAGGGCAAGAAAGACCGATTGGAAGAAGTCATCGGCTTCCGAAGACCCGAGCTTTGGAACGACCCGAAACGTCGCC  
AAGAAATCGGCAAGAGAGCAAAATCCTTGAAGGCATCGTCTGACGCTCGACACATCGCTTCGGGTATCGAAGACAAACCGTATGCTGATTGAATGGCGTCGAGAAACGACGAGAA  
AGGTTTTCGCCCGTGAAGGAAGACGTCGCGGGCTGGAATAACAGATGCGCGATTGGAAGTTCAACCGGATGTTCAACCGACCCCGCGACCCGAACAACTGCTTTATCGACATCACCGC  
GGCGCGGCGGTACCGAAGCGGAAGACTGGCGGGGATGCTGTTCCGTATGTCAGCGCTATGCCGAGCGCAAGGCTTCAAAATCGAAATCCTTGAGGAAGACGACGCGGAAATCGCAG  
GCATCAACCGCGCCACCATCCGAGTGGAAAGCGAATACGCTTATGGTTTGCCTGCGTACGAAACCGCGCTTACCGTCTGGTGGCTACTCGCGCTTTGATTGCAACAAACCGCCATAC  
CTCGTTTGCCTCCGCTGCTGTTTACCTGAAATCGACGATTCATCGAAATCGAAATCAACCCCGCGGATTGCGCATCGACACCTATCGCGCATCGGGTGGCGGGCTCAGCACATCAAC  
AAAACCGACTCCGCGTTCGTTATTACCCAGAGCGGACGGGATTGTTGTCANTGTCAAAACGACCGTTCTCAACCGCAACAAAGCGCGCGATGGAATGTTGAAATCCAACTGT  
ATGAATGGAAATCGCGCAACGCAACGAAGAGAAACAGGCAATTGGAAGAAGTAAATCCGATGTTGGGTTGGGCGACCCAAATCCGTTGATGTTTGGATTCTCAGCATCAAGACTT  
GCTACAGGCTACGAAGTCGCGAACACCAAGCCGATTGGAAGCGGACTTGGACGGCTTATCGAAGCCAGCCTGAAACAGGGTGTT

## SEQ ID 318

LEKRSIEDRVYMDYQKKDRLEEVIGLSEDPENLWPKRAQIEIKESKILEGIVLTLDNIASGIEDNRMLIEMAVEENDEEGFAAVKEDVAGLEKQADLEFKRMFNQPADPNCFIDITA  
GAGGTAEEDWAGMLFRMYSRYAERKGFKTEILEEDGELAGINRATIRVEGEYAYGLLRTEGTGVRHLVRYSPFDSNNKRHTSFASVFPVIDDSIEIEINPADLRIDTYRASGAGQHIN  
KTDSAVRITHEPTGIVVQCQNDRSQHANKAAAMEMLKSKLYLEMRKRNEEKQALEBEGKSDVWGWSQIRSYVLDSSRIKDLRTGYEVGNTKAVLDGLDGPTEASLKQGV

## SEQ ID 319

GTCTCGGATGCACACCGGACAGGCGGTAAAGCGGGTCTGTCTCGGACAGTCAATCTCTTAGGCATACCGTTGCCGTATGCTCAAGCAACCTACCCGAACGCTCGCGGGCAGCGTCATT  
GCGTTCGTGTTGGTCTGCTCGAATGGGGTTTGGCTGCCGATATGTTACCAATGCGCGGTGCGCCCTTACCGCACTTTTACCCCTGCTGCTGCTGCCAAGGACGACATCGCGG  
TTTTGCTTTCTGCTCACTTTCCGTCGCTTACCGCGCCCGCGCT

## SEQ ID 320

VSDAHTGGKPGSVSDSHSRHTVA GMLKQPTRTLGGQRHCVLFLGAPNGVWPAAYCYQMRGAPLPHLFTLACAARAAIGGFAPCSTFRFRVTARGR

## SEQ ID 321

GTGTTTTATATTCCGTTGATGCAGCCCTGATGAGTCGGCAAAAATGCCCTTTTACTCAATAGGACCGGTTTCCGCCCAAGCGGAATAAACGGCTATTTCCTTGCACAAACAGACGAATCA  
GGCGGGTATTTAAA

## SEQ ID 322

VFLYSVDAALMSRTKCLLLNRTGFRPSGNRLFLPLQTDGIRRVFK

## SEQ ID 323

ATGCGCGGATACCGTCTGAACCTTTCAGACGGCATTTTCCGCATAATGAAACCAACCGTTTCCACCGCAGGACAGGCTTTCCCCCCCCAACCGGAAGGCGAGCTGCTGATTGTCAAT  
TAAATACCGCGCTGATTCGCTGTTTTCGCAAGGGAATAGCCGTTTATTTCCGCTTGGCGGGAACCGGTCTTATGAGTAAAGGCAATTTGTCGACTCATCAGGCTGCATCAACGGA  
ATATAAAACACAGCC

## SEQ ID 324

MRRYRLNPSDGIIFHNETHKPPPPDRGTGPPPTGRQPADCHLNLRLIPSVCKGNSRLFLGRKPVLLSKRHFVRLIRAASTEYKNTA

## SEQ ID 325

ATGTCCCGCATCCCGCCCGCACCGGAGAAAAACATTTTTCGGCCACCCCTTCCAGCTTTCCACCTCTTCCATATCGAATTGTGGGAACGTTTTCATTTTACGGAATGCAGGGCATCC  
TGTGATTATTACCTCTACTACACCGCGGACAAAGCGGCTTGGGCATAGACAAAACCTTCGACGGCGGCATTGTGCGGCATACAGCGGCAGCGTGTAACCTGTCCCAATTTTGGCGCGCTG  
GTTTGGCGACCGGATGCGGGTGGCGAAAAACCTCTTCTCTCGGCGCATCGTCTAATGCTCGGCGACATCGTCTTGGCGCGCACCGGCGCTGTAGGGCTTCTAATCGGGCTGATA  
TTCATCGCATTTGGCAGCGCGCGGCTGAAATCTACGGCCAGTTCTATGTTGGCGCATTATACGAACAGGACGAAATGCGCCCGCTCGCGGATGCGGGATTTTCCATTTTCTACATCGCA  
TCAATATCGCGGCTTCTTAGGCCCTTATTGACCGGACTGCTTCAAGAAAACATCGTTTCCATTATGTTTTCGGCGCGCGCGGCTGCGTATGGCAATCGGCTTGTGGCTTATCTCTT

GGGACGTAAAAACCTGCCCCACCCACCGTCCCCCATCCGCTTTCAAAGGACAGGGCAAAACTGCGCGCGCGCTGCGCATCACCTCATCGCCGCACTTGCAACCGCCATCAAAACCGGG  
CTTGTCACCTCGACAATTTCTCGGCATCTCTTATCTACGGTCATCCTTGGCGTCAATGCGCTATTTTGCGCGCGCTGCTGACCAACCCCCGCGTCAGTTCCGACAACAAACCGGCACATCT  
TCGCTTACATCCCGCTTTTCTGACACATCTGTATGTTTGGCGCGTCTGTTTCAGATTATACACCGTGGCAACCGTCTATTTCGACGAAACCGTCAACCGCACCATCGGTTCTGTTACTGT  
ACCCGTCGCCGTGAAAGATTCTATGCAAAGCGCTGTGGGTCTACTCTGTTTTCGGGACTCATGGCGGCATGTGGACAAAAATGGGGCGCAAAACAACCCAAACCCCGCTGAAATTCGCTATG  
GCGGTATTGTTACCGCGCGCTCGTTTTCGGGATTCTGTTCCCTTAATTTCTCTCCGAACCGCGATGCGCTATTGCGGTTTTCGCACATGATCGTCTCCCATCAAGATAGGGGAACATGATGA  
TTTCCCGGATTGGCGCTGTCCATCTCCACCAAAATCGCACCGCGCTTATTCAAACCCAAATGTGTCGCTCTAAATTTCTCTGCGCTTTTCACTTACGCTTCACTTTGGCGGGCGTATTGTTGA  
AAAGGCTATCAGCGCGGCGAGAAATCGGCTTCTACCGGCTGCTGTTCTACATCGGCGCAGGCACAGGCTTCTGCTGCTCTCGTCCCAAAATGAACAAAATGCTCGAAGGCACA  
GAC

**SEQ ID 326**

MSRRPARTGEKTPFGHPQLSTLPHIKLWERPSFYGMQILLILYLYTTADKRGGLGIDKFLAGGIVGAYSGSVYLSTILGAWPADRVWGAKETLPLSGIVMLGHVLAAAPGLYGLLIGLI  
FIALGSGGVKSTASSMVGALYEQDEMPLRDAGFSYFIYAIINIGGFLGPLLITGLLQENIGFHYFGAAAVGMAPGLWRYSLGRKNLPHPTVPHPLSKQQKTAAGVITTLAALATAIKTG  
LVNLNDFSGILLSTVLIVAIYFARLLTNPRVSSDNKRHIIAYIPLFLITCMFVAWVQIYTVATYVFDET VNRTIGSPFVPVANKDSMQSLWVLFSGLMAAMWTKMGRQPKTPLFAH  
AVFVTGASFLGFVFPISSGTPMPIAVFALIVLAIITIGELMISPIALSISTKIAPLPFTQMVALNPLAFSLGFLTGGVLFERQYQAGDEIGFTRLLFYIAGATGFLLLLLVPKINKLEGT  
D

**SEQ ID 327**

GTGCGGGCGGGATGCCGGGACATAAAGGTTCTCTCTAAAGATTTTCTCTCAATACCGTCTGAAACGGATGCGGACGCGCGGCGGTGTTTTTGTATGAAATATCGGTTTTTAACCGCATATT  
TTCATTCTTTTGTCAAACGACGCGCTGCGGTTTTTCGCGGGCGGATGTTTTTATATTGTGTTCAATTCAATGGATGTGTAATTTAGAGGACGTGTCCGATACGGCGCGGGTAAATCCCTTTTC  
TGTCATGGCTTATCCGATAGGCGGPTTTTACT . . .

**SEQ ID 328**

VRAGCRDIKVLKDFLSIPSETDADGGGVFCMKLSVFNRYFHSLSNDALPPFAGGCFYICFNSMDCILEDVFRYGAGKSFSVNGLSDRAWFT

**SEQ ID 329**

TTGAGTGCAGAGAGAAATATGATGAATCCCAAAATCGTGTTTTTCGACATTTCACGATACGCTGTACCGCAAATATACGGATACCTTGCGCCCTTCCTCGTAAAAACGGCGGTGGCGGCTTTCGCGCGAAAGGCTATATTCGACGGGTTCGCCAAGACGGCGCGGCTTTCGCGACGATTCCCGAAAAGGCTACGGGACATGATGCGCGAAAACGGGTATGTGATCGCGTGTATACGATATAACGGACGATATTCGCGCTGTCGACCGTAAAACTGTGCCGAAGTACCGATGGATACCGGTTTGTATGCGACGGGTTTTCGCGCATTTGGATGGCTTGGCGATGCGGTATTACCGTTTTCGCGCGACAGGGGATCGCCGTGTCGCGCTGTGCGAATGCGTGTGCGCGCGCTTTCGACGATATCGCCAGCGATTTTTTTTCGCGATAAGGATTATTTTTCGAAGCAAACCGGTATCAGATGCTGGTGTTCGCGAAGAAAACGAATGCCCTTTTGTGCGATATTTGTGGAACGGGAAGCTTGAAAAACCGTGCCTGGCACGGAAGACCGCTCGATCTGCTGCCCTCGCGGAATGTGCGAAAACAGACGGCATCAGAAGCGTGGTTGAAGCATTTGGGTTTGGAAATGGCAGCATGATGGCTTCGCGCGACGGTTTGAACGATGTGGAATGCTGTGCTGAAGTCGGTTCGCGGTGGCAATGGGTAAACGGGGAACAGGCACTGAAGAAGACGGCGGCAAAATATGTTTTGCCCGCGGTTGATGAAGACGGCGTGTGAGGGGGTTTGCAGGATTTGGGTGTGTT

**SEQ ID 330**

LSARENMMNPKIVFFDIDDTLYRKYTDTLRPSVKTAAVALRGKGILTALATGRSLATIPEKVRDMMAEFGNDVVTTNGQFALLHGKTVREVPMDTGLGRVCAHLDDGLGMDYAFVGGEGI  
AVSALSECVCRALQHIASDFPADKYFSSKPVYQMLVFAEENEMPLWSDIVEREGLKTVRWHEEAVDLLPAGMSKTDGIRSVVEALGLENADVMAFGDGLNDVEMLSVVGFGVAMNGEQA  
AKEAAKYVCPGVDEEDGVLRLGLDGLVI

SEQ ID 331

ATGTCGCGACAAGCAGACGCGGATTTCGGGGCGGCGGGTTTTCAGGTAAGAAAGAAATGTGCCCGCGCAATGAAGTTTCGCGATAACGCGCCATAGGATTTTGTGTTGTGTTGGGGTGTG  
GAGAAGGAATGCTTTGTTGTTTAAAGTTTAACTTTGTGTGGACTGATGTTTCCAACGCACTTGGAGGCGCTGAAAGCACTAGCTTCAACGAAGTTAAAGT

## SEQ ID 332

MSDKOTRFRGGGFDGEKECAAGNEVSAITRHRI FVCGWGVGEGMVCCLRFNFVGPDVSKRHWRPSESTSFNEVKS

**SEQ ID 333**

ATGACCGGATACCCACCGCAGAGATACCGATCCGACGGAAAAACGGCAGCGCGCAAAATGCGGCTCTGAACACCGCCCCCGCCCGCGGCAAAAAAACGCGCCCGCTGCTGAAGCTGTGCGCGG  
CACTGCTGTGCTGCTGCTGATTTTGGCAGTATGTTTCTCCGCGGTGATTCGCCGGTACCGGAAGCAGGTTTGCCGCTTCGGGCTGTATCCAAATCCCGCTCTGGTTCGGCGTAAACATTTCTCTCCCA  
AAACCTTCAAAGGCACATGCTCGACCGGCTTCGACGGGCACAACTGGTCAATGAGAAACCGAGGGGGCAGACCTTAAATTCAGCCGCTTTCGCTTCGCGTGGAACCCGTCGCAATGTATGCGG  
CGACGCTGCGACATCACCGACATCTCCGCGGGGACATTCGCGATTCGACCAACACGCACTCCGCTTGAAGAGAAAGCCGCGCTCAAGGGCTGCCGACAGCATATAGACTGTCCCGCGCGCG  
TCTATCTCGACCGCTTCGAGACGGGCAAAATCAGCATGGGCAAAACCTTTGACAAAACAAACCGTCTATCTCGAAGCCCTTAACCGCGCATACCGTTACGACCGTAAAGGGCACCGCCTCGA  
CCTGAAGGCGCGCGACACCGCTGGAGCAGTTCTGTGCGGGTCAGCCTCGTTCGGCTTGAAAAAACCGGTTTGCCCTCGATACCGCCATTACACCAAAGGGGATTCGAAGGCGAAACCATAT  
CACAGTACCGCGCGCTGACGCGCAGGCTGAGAGATGTGCGCGCCGAATCAGCATTCGAACGGCGGCAATATCCGCTCTCTCGGGAATAATCCGTCATCCACCGCTTTGCGGAATCATTTGGAGTA  
AAACCTTGGAGAAGTCTGCTGCTCAAAGGTTCAACACCATCACTCCGTCGCGCTTCGTGCTCTCCCTGCGCGATCGAGGCTGAAATTTTCGACCTCCGATCCGCTGCTTTTCAGACGCGCAT  
CGCGCTGGAAGAGTCTGCTGATTTGGAAAAACCAAAAGCGCAATTCGTCGACCGCAACGCGCATCCCGCTCGCTCAGGTTTGGCGCGCTTTGTATCCGCGAGGACCGGACGCGTATGCGATATC  
GGCAATACGTCGCGCGCCTGCTCGGACGGGGCGGCATCAGGCTGTCTGGGCAAAATCGACACCGAAAAAGACATCTTGATTTAAATATAGGCATCAACTCCGTCGGCGCGGAAGACGTGTC  
TGCAAAACCGGCTTCAAAGGCAGGTTGGACGGCAGCATCGGCATCGCGCGCAGCACCGCTCGCCAAAAATCTCTTTGGCAATCTGGCACCGGCACCGGCACGGCACGGCAGGCAGCGCCTCGCCAT  
CGAAGCAGACCCCGCAACCGCAGTCGCGGAAATCTGCTGTTCGACACCGTAACTCTCTCGCGCGGGAAGACGCGCTTCGACCGGCACGCGCTATCTCGAGCTGTTTAAAGAGAAATCCCTGCTCAAA  
CTGGAGCATCCGTTCCCGCGCATCGACCTTTCGCGCATTCGATCCGCAATTTCCGCGCAGGCAATACACGGGCTGCAATTCATCTTTGCGGCTGAAGTGGCAAAAGATCTGCGCATAAG  
TGCCTTTTTCGCGCGTACGTGTCACCGCGCTGCGGATTCGCGCGCAGCGCGCATATGTTTACAGATTCGCGCCACTTTTCGCGCGCGCGCTCGATTTCGGGTTGGGGCGGAACATCGTCAAA  
AACAGACGGCGGCTTCGGCAAAAAAGGCGACCGGCTTAACTCAATATCACCGCACCCGATTTATCCGTTTCGGTTTCGGACTCGCGGGGCTCTTAAATGTACGCGGACACCTTTTCGGG  
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CAAGCGCCCGCATGCGCGCGCATATCAAGGGCGGCGCGCTTTCCCTGTTCGGGCGGCGCGCGGTTGTGATATCCCGCGCTGACGCTGGAAGGTACGGGCGCGCAGCACCGCATCCCGCAC  
ACACCGCGCCCATGACGCTGGACGCGCAAAACGCTTCAAGCTCGATTTGGACGCTTCAGGCGGCAATCGGCAAGAACTTACCGCATGGAAAGGCGAGCATTCGCGCATCTCGACATTCGGGCGGCA  
TTCAAACCTCAAGCTGCAAAACCGTAAACCGTTCGAAACCGGCTGCGCAACGATGCGCGCGCAATGCGCAAAATTTGGCAAGTATGGCAAGCAATGGCGAGGCGCATCTCAACTCTCAACATCTTCTTCGGGACA  
GGAAACCTCGCATATTCGGCAAAAGCGCGCGCACGCGGCTGACATTCGCGGAGTTGCAACAATTTCTCAAACCCGCTTCGAAACAATCTCGGTTTAAACGGCGACTGGGATGTGCGCTA  
CGGGCACACGCGCGCGGCTACCTCAATATCAGCGCGCAAGCGCGCATGCGGATTTGCCCGCGCGGCGAGGCTTTGGGTTTGAACGCATTTTCCCTGAAACCGCGCTTTCAAACGACCGG  
ATCGGAATCTGCTTTGACGCGCGCGCGCGTTTCGACGCGATTAACGCGCGATTTCGGGATTCGGCAACGCTTCGCGCGCAATATGGCAAAATCAACCGCTCGGCGGACGAGTACAGCTCTCC  
TTCGCGACTTGGGCGCATTTGAAGCCCTTTCTGCGCGCGCGCGCGCAAAACATTAACCGCGAGCTTGAATGCTTCGCGCAATTCGGCGAGCTGGAGCTCTCGGCTCGCGCGCGGCT  
CAACGCTAGCAGCAACTTCAAGGAAACCTCAACGCGCATATCACGCTCGGCGAAAGCGGCTCTTCGATACCGCACTTTTCGGGCGAGGCTCAACTACGCTTTCGGGATCGCAAGCAATTC  
CGCAACTTCTCATCGGTCGCGAAGAAACGTCAAAGCGCAAGCTGAACTGGCGCGCTTAAACCGCTTCGCGGCGCAGCATCGCGAACCGCACTTGGGCGGCGATATCAACGGCGACAAGCTCTATTACC  
GCAACCAAAACCAAGGCATCATCTTGGAACAACGGCTCGCTCGGTTTCGCATATTTCGAGGAGGAAATGGGTAAATCGACAGCTGAAATTCGGCACGAAGGGACGGCGGAACCTCTCGGCAC  
GCTCAGCATGGAAAAACAGGTGCCGATGTGATATTCGGCGGGTTTCGACAAATACCGCATCTGTCGCCGCCAACCGCGCGCTGACGCTTTCGGGCAACACCGCGCTCGGCTTATTCG  
CGGCAAAAGGCATATCCGTTACCGGATGATTAATAACTGATCAGGGCGTGTTCGGTTCGCAAAATCTCTGATCGCGCTCGCTCGGCGCAGATGTGCTGATTTGGGGAAGTCAAGAAAG  
AGGGCGGGAATCTGCTTCCCGCTCAATATGAACCTGACTTTAGACCTCAATGACGGCATCTCGCTTCTCGGCTCAGCGCGGACGTTTACCATTCGGGGGCAACTGACCTGACCGGCAACG  
GGGGCGGAATGTGCTGGGGTGGGACCGGTCGCGCTTCAAAAGGCGCTTCAAAAGCATACGGCGAGGATTTAGACATTAACCAAGGCAACAGTCTCTTTGTGCGCGCGCTCTCAAGCACCTC

AACTGTAACATCCGCGCGCAACGCCGCCCTTCCGCCGTCGGTGC GGCGGTGGAAAAATTGGGCAGCCTCAACAGCCCGCGCATTAACGTGACGGCAACGAACCGATGAGTGAAAAAGACA  
AGCTCTCTCTGGCTCATCTCTCAACCGTGCCGGCAGCGGACAGCGCGGACAATGCGCCGCTGTCGCGAGCCGAGCGCGCTGCTTGC CGGGCAAAATCAACGACCCGATCGGGCTGGTGG  
TGATTTGGGCTTTACACGACAGCGCAGCGCACAACGGCGAAACCGGCGAACTCAACCCCGCGCAACAGGTGCTGACCGTCGCGCAACAACCTGACCGCGCAAACTCTCATCTGGCTACGAATAC  
GGCATCTCCAGCGCGGAACAGTCCGTCAAACTGATCCGCGGTACACCGCGCATACAGCGCGCTGTCGTTGGCCGGCGGACGACATACACCATACGTTTGC  
AACCGCTCTCTCGGTTCCGACAAAAAGGACTCCGCAGGAAACGGCAAGGGAAA

**SEQ ID 334**

ENDTTDPDTPTENGTRKMPSEHRPAPPAKKRRLPLKLKLSAALLSVLILAVCLFWIAGTEAGLRFLGLYQIPSWFGVNISSNLKGTLLDGFODGNWSIETEGADLKISRFRFAMKPSLWLR  
 RSLHITDISAGDIAIVTKPTPKPEERPPQGLPDSIDLPAAYVLDYRFPETGKISMGKTIDKQTVYLERLNAATYRDKGRRLDLKAADTPWSSSSGSAVGLKPKPALDITAITYTKGFGSEETI  
 RSTARLSGSLKDVRAELITDGGNTRLSGKSVIHFPAESLDKTLDEVLVKGFININPSAFVPSLPDAGLNFDITAIPTSFSDCIALEGSLDEWIKAGPADRNGIPVRQVLGGFVIRQDGTVHI  
 GMTSAALLRGGRIRLSGKIDTFEKDILDLNTIGINSVGAEDVLQTAFGKRLDGSIGIGTTASPKISQLGTGTARTDGSALASDPANEQRKLVDTVNI SAGESLSLTAQGYLELFDKRLIK  
 LDIRSRAPFDSRIDQTPAGNCHINSIHLAGELAKEKFTQKMRFLPTQFPNGVPIAGSADIVYESRHLPRAAVDLRLGRNIVKTQGGPKKKDKRLMLNITAPDLSRFGGLGAGSLNVRGHLSC  
 DLGGIRITFDVLTSGTARNLHIGKAADIRSLDPTLTKGSPSRFMRNADIKGGRLSLSGGAADVDTAGLTLBGTGAQHRIRTHAAMTLDGKPKKLDLDSAGGINRELTRWKGSGITLIDGGA  
 FNLKLNQRMTELEAGAEHVAASAANWQAMGSSNLQHFSWDRKTGISAKGGARGHLIAELHNFFKPPFEHLVLNGDDVAYGNARGYLNISEROSGDVLPQQALGLNAFLSKTRFQNDR  
 IGIILDGCGARFGRINADLIGNAFPGGNMAMTFLGGRTIASLPDLGALKPFLPAAQNTITGSLNASHAQIGGRVGPSPVNAAYNGSSNYGKINGNTITVQGSRSYDTAPLGGRLNLVADAAEAP  
 RNFLPVGQTVKGSNLAAVTLGGSTADPHLGGSSINGDKLYRNRQTQGIILDNGLSLRSHIAGRQWVIDSLKFRHGETAELSGVSPMSVSPVDVICAFVQDKYRLRSRPNRNLTVSGNTRRLYS  
 POKGTSVTGMKTDQGLGSGKSSMPTGDDVVVLVSEVKEAAASLFLVNMNLTLDLNDNGIRGFSQADYVITTEGKLLTAQGVNVRGVTGKVLGRYKRAYQDLDITKGTGVSFVGPLNDP  
 NLNTRAERLSPVGAQGLSGLNLSNPRTITANFPESEKDKLSWLLINRAAGSGSSGNDNALSAAGAAALLAGCINDRIGLVDDLGFTSKRSRNAQGTGLNAPBQVILTVGKQLTGKLYIGTGY  
 GISSABQSVKLYIRLTRAIQAVARIGSRSSGGELTYTTRFDRLPGSDKKDSAGNKGK

**SEQ ID 335**

GTGTGGCGGATTTTCGATTCTAACACTGTTTCGGACGGGGCGGGACGCTTCAGACGGCATACCCCGCGCGGTATTTCGGAGGTTCGCGCCCGCCGAAATGTATCTGCTTGTTPTAAGGCATT  
TTGTTTCCCAATCCGCATATGGAAAAACAGGCTGCGTTTCGGAAATAGTGTGCAAAAAATAGGCAGAAAT

**SEQ ID 336**

VNRISILTLFGRGGTLOAYRRRYFGGCGPPETLLNLRHFVSNPHMENLRFGIVSKNRQD

**SEQ ID 337**

SEQ ID 337  
 TGTGTAGAAATCGAAAATCCGCCACACCGGATGCACGACACCCGTTACCATGATGATCAAAACGACCGCCCTGCTCCTGCCGGCTTTATTTTCTTTCCGCACGATACGGCCCTGCCGCCGACC  
 TTTCCGAAAACAAAGCGCGGGGTTTCGCAATTGTTCAAAGACAAAGCCCCGCACACCGGAATCAGTCAAAATTAACACCCAAATTCGCCGTCCGCATCGACACGAGGACAGTGAATCAAGA  
 TATGGTCGAAGAACACTGCCGCTCATCAGCAGACAGCAGGAAGAGGTTTGTGATAGGAACACAGCGGGATTCCTTCGCCAAGAAGCACCGGACAACGTTTAAACAATGCTCCGCAGCAA  
 GGCATATTTCAGCAGCAAGGTCAGCCTGACCGAAAAAGACGGAGCTTTATACGGTGCATCACACCGGGCCCGCCACAAAATCGCCAACTGCGCGTCGCCCATCTCCGGCGACATCTPTT  
 CAGACGGCAACCTCCCGGAATCTACCGCAACCGCGTCGGAACTTCGCACAGCCGGTAGCCAGCCGATTTCGATCAGGACAGTTGCGGAACACAGCAAAATCTCCGTCCTCGGCGCGGTAAC  
 CGCCAAAGGCTACTCCCGCTGCCCACTCTGCCAACACCTCGGGCGCCGCTCAACCCCGATACCGCCACCGCCGATTTGAAGCTGCTGCTGGACAGCGGGCGGCCCAATTCGCTTCGGCGACTTT  
 GAAATCACCGGCACACAGCGTTACCCCGAACAAACCGTCTCCGGCTTGGCGCGCTTCCAAACGGGCACGCCCTACGACTCTGCACTCTGCACTTCCAAACAGCGGCTCGAACAAAACG  
 GGCATTTATCCGGCGCGCTCGCTACAAGCCGACTTTCGACCGCGCTCCAAGCGACCGCGGTCCCCGTCAAAGTCAGCGTAAACCGAGGTTCAAACGCCACAAACTCGAAACCCGCGATCCGCGTCGA  
 TPCGGAATACGGTTTGGCGCGGCAAAATCGCTACGACTACCACTCTTCAACAAGGGCTATATCAAGCTCCGCTCGCTGCGGATATGGCAAAATACGAGCTTCGCCCGCGGCATC  
 AGCCAGCCCGCGCACTCTGGGGCGCAATCTACGACAGCAAGCTTTCTCAACAAGGCTTCGACACCCCAAGCTCGAAACCGCGCCCTCTCCGCGCGCATCTGGTATGTGCGCGACCGCG  
 CGGGCATCGATCGTACAGCTCGGGGCAATTTCTCGCAGAAGCGCGGAAAAATCCCGGGCTCGGATGTCGATTTGGGCAACAGCCACGCCACGATGCTGACCGCCTCTTGGAACGCGCAGCT  
 GCTCAACAACGTGCTGCACCCCGAAAAACGCCATTACCTCGACCGCAAAATCGGGACGACTTTGGGCAACATTCCTGTCTCTCACC CGCGCTAATTCGCGACCTCTGCGCCCGCGGAGTTATTTC  
 TTCAGCGCCGAAAAACAAAAATCTCGGCACGTTTCATCATACGCGGACACAGCGGGTTACACCGTTGACAGCGCAATGCGGATGTCCTCCCGGGGCTGTTCCGCGAGCGCGCGGCGCTTT  
 CGGTGCGCGGTTACGAACTTGACAGCATCGGGCTTGGCCGTTCCGAACGGATCGGTGTGCCCGAAGCGCCCTCTTGGGTGGCAGCTTGAATACCAATGCGCTTTACGCGGACCGCTGT  
 CGGCGCGGATTTCCAGCATATGGCGATCGCGCGCAATTTCAAAGCTTGAACGTAACAGCGGTTCCGGGATTCGGGTGCGCTGTGTACAGCCCGCTCGCGCGGTTTCTCTCGACATC  
 GCTCACGACACAGCGACAAAAAAATTCGCTGGCAGATCAGCTTGGGAACCGGTTTC

**SEQ ID 338**

VLBSKSMPTMHDRTRTMKPTALLLPALFFPHAYAPAADLSENKAAGFALPKSKSPDTESVKLEPKFPVRIDTQDSEIKDMVEEHLPLITQQQEEVLDBEQGFLAEAPDNVKMTLASK  
GYFSSKVSLETKDGATTVHITPGPRTKIANVGVAILGDILDSGNLAEYTRNALENWQQPVGSDFDQDSWNSKTSVLGAVTRKGYPLAKLGNTRAAVNPDATADINVVVDSGRPTAFGDF  
EITGTRPQPTQVSGLARFPQGPYDILLDLDFQALQNGHYSYGASVQADFDRLQGDPRVPVKVSVTEVRKHLEGTIRLDSEYGLGGKIAIDYNNLCKNGYIGSVVMDKGYETTLAAGI  
SQPNRYRGNWYTSNVSYNRSTTQNLKRAFSGGIWYVRDRAGIDARLGAELAEGRKIPGSDVDLGNSHATMLTASWKRQLNNVLHPENGHLDLFGKGTILGTFLTSALTALRYSARAGY  
FPTPENKLGTFPIIRGQAGYTVARDNADVPFSGMLPRSGGASSVRGYELDSIGLAGPNGSVLPERALNVLGSLEYQLPFTTTLGSAVPHDMGDAANFKRMKLKHGSGLGVRNPSPLAPFSPDI  
AYGSDKKIKRWHISLGTTF

**SEQ ID 339**

SEQ ID 339  
TTGGCGCGAATGATAAAACAAGCCTGTCCCTGCATAGGGCAAATCAACGCACCTCAAACACAGCTTGAAAAATAAAAAACACAGAGAATGAGTTTCTTTTAAAAATACAACATTTTT

SEQ ID 340

1.RRM1KOSLSLHRANORTSKHSLKNKKTORMSFLKYNIF

SEQ ID 341

ATGGCGGTGAGCGAAATCCTTATTTCATGCGATCGGCGCGCTCAGCCTGGTCAGGCAGATTGCCGCCGGTTTGGCGTTGGGCATCGTAATCGGTTCGGTTTCACCGCAACTGGGCTTGGCGG  
CAGGCTTTGTTCCGCAGCCTGTTTGTCCGCGCGCTCAAAGCGGTGCGCGCGGTTTGGTATTATTTTGGTGGCGGCCACAATCGCGCAGCACCAAAAAGGCACAAGCGCGCATATCAGGCC  
GATTATCTGCTCTTACCTCATCGGCACGTTTTCGCGCAGCCGTCAGCCCGGTCATCGCCGGTATGTTTTCGCGAGCCACATTTGTTTGGCGGGCGCGGGCGATGTGTCCGCGCGCGCGCCT  
TCCGGCATTTGGAAGTGTGAAATCGCTGCTGATGAACCTGGTCGCGCAACCCGATTAAACGCGATTGCCAATGCCAACTATATCTGGCATTTTTGGCTTGGGCTTTGGTTTTGGGCGCGCGT  
TCCGGAATCAGCGTTTCGACGTTACCGCGCAGGTCGTGTCCCGATTGGCGCGAAGCGGTTTCCACCGCTCGTAAATGGATTATCCGTTTTCGCCCTTTGGGTATTTCGCGCTGGTGTGTC  
CACAAATCGCGAGACGGGTTTCGGCGCGCTGGCGGGTTATCGGAAGCTGCTTCCGGTGCTGTTGGGCTGTATGGCTTTATCGCGCTGGCGGCTCAATCCCGCATCTGTGTGGTGGAAAAATC  
CGCGCAACCCCTTATCCGCTGGTGTTCACCTGCCGTCGCGGAAAGCGGCGTGATGCTTCTTTACCGCTTCTTCGCGCGCAATATCCCGGTGAATATGCTTTTGGCGAAAAAGCTGGGGC  
TGCACGAAGACACTTATTCGTTTCCATCCCGTTGGGGCGCAGCGCTCAATATGGCGCGCGCGCGCATACGATACCGTTTGGCTTATGGCGCGCGCGCACACCAAGGCATACAGGTGTA  
TTTGTGCCACCGCGCTGCTGTGAGCCTGTGTGGCAGCGTCAGCGCGCTGCGCGCGTGGCGCGGTCGCTGCTGATTCCGCTGGCGTGCAGCCTGTTTCGCGATCAGCAAC  
GATGTGCCATGCAAGTGTGCGCGTCCGCTTCATATCGGCGTGATTACAGGATCGCGGAAACGGCGTTGAATCTTCAACCGACGCTTTGTGTTACCGCTGCCCGCGATTGGGCGGAC  
AGAGAAACCGTCCGGA

SEQ ID 342

MAPGKSLPHAI GRVSLVRQIAGLALGIVIGSSVSPQLGLAAGLFGSLFVGALKAVAPVLVFLVLAATIAQHQKGNKAHRIPIIVLVLGITFSPAALTAVIAGNVFPTHIVILVLAGGVSAAPP  
 SCIVEVLKSLMLNVAMPINAIANANYTIGILAWALVIGLALRNHGSDVTRQVVDLAEAVSTVVKWITIRFAPLIGIFGLVSSSTIAETGFGALAGYAKLLAVLGLCHAFIALAVNPVAVVWKI  
 DVAHQVVAVGVFIIGVIODSAETALNNSSTDVLPFAAADLGRQRRAE

## SEQ ID 343

ATGCCGCTCTGAAGCCCGTTTGGCGTTCAGACGCATATTTTACAATTTTATGGCATATGGCGGAAACAATACCGGCTGCCTTGAATATGTTTCAACACACAGGCGGATACATAAAGCGT  
CGCCCTATGAAGGAGATGATGATGTT

## SEQ ID 344

MPSEARLAFRRHIFTILWAYGNNVPGCLEYVSTHRAHKASPYEGDDV

## SEQ ID 345

ATGAAGGAGATGATGATGTTTAAACGCAGTGTGATTGCAATGGCTTGTATTTTCCCTTTACGCTGTGGGGCGGCGGTGGCGGATCGCCCGATGTCAGTCCGCGGACACGCGTCAA  
AACCGCGCCGCCCCGTGTTGCTGCAAAATGCCGGGAAGGGGTGCTGCCGAAAGAAAAGATGAGGAGCCAGCGGGCGGTGCGCCGCAAGCCGATACGACGACCAACCGCGGAGA  
AGGCAGCCAGATATGCGCGGAGTTTCGGCAGAAAATACAGGCAATGGCGGTGCGGCAACACCGCAACCCCAAAATGAAAGACCGGGGGCGCAAAATGATATGCCGCAAAATGCCGCG  
GAATCCGCAAAATCAACAGGGAACAACCAACCGCGCGGTCTTCAGATTCCGCCCCCGCTCAACCCCTGCCCTGCGAATGGCGGTAGCGATTTTGGAAGGACGAACGTGGCAATTCGTG  
TTGTGATTGACGACCGTTCGCAAAATATAACGTTGACCCACTGTAAAGCGGATCTTGTAAATGGTGATAATTTATTTGATGAAGAAGCACCGTCAAAATCAGAATTTGAAAAATTAAGTGA  
TGAAGAAAAATTAAGCGATATAAAAAGACGACGAGCAACGGGAGAAATTTTGTGCGTTTGGTTGCTGACAGGGTAAAAAAGGATGGAATAACAAATATATCATCTTCTATACGGACAAACCA  
CTACTCTGCTTCGACGCGTTCGAGGAGGTTCGCTTCGGCGGAGATTCCGCTGATTCCCGTCAATCAGGCGGATACGCTGATTGTGATGGGAAGCGGTGACGCTGACGGGGCATTCGCGCA  
ATATCTTTCGCGCCGGAAGGAATTAACGGTATCTGACTTACGGGGCGGAAAAATTCGCGCGGATGCTATGCCCTCGGTGCAAGGCGAACCGCGCAAAAGCGAAATGCTTGTGGCAC  
GGCGGTGTACAACGGCGGAAGTGTGCAATTTCCATATGGAACGCGCGTCCGTACCCGTCGCGAGGAGGATTTCGCGCAAAAGTCGATTTCGCGCAAAATCTGTGGACGGCATTATCGAC  
AGCGCGGATGATTTCATATGGGTACGCAAAATTCAGGCGCCATCGATGGAACGGCTTTAAGGGGACTTGGACGGAATGGCGCGGGGATGTTTCGGAAGGTTTACGCGCCGCG  
CCGCGGAGGAAGTGGCGGGAATAACAGCTATCGCCGACAGATGCTGAAAGGGCGGATTCGCGGTGTTTCGCGCAAAAGATCGGGAT

## SEQ ID 346

MXEMMFKRSVIAMACIFPLSACGGGGGSPDVKSADTPSKPAAPVVAENAGEVLPKEKKDEZAAGGAPQADTQDATAGESSQDMAAVSAENTGNGGAATPDNPKNEAGAQNHPQNA  
ESANQTGNQPGAGSDSAPASNPAPANGSDPGRNVNNSVVIDGPSQNTLTHCKGDSNGWMLLDEAPSKSEFKLSDEKIKRYKDEQRNFVLVADRVRKDGNTKYLIFYTDKP  
PTRSARSRSLPAEILPLIPVQADFLIVDGEAVSLTGHSGNIFAPBGNRYLTLYGAELPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFMENGRFPYSGGRFAAKVDFGSKSVGLID  
SGDDLHMGTPQKFAAIDGNGFKGTWTENGSDVSRFYGPAGEEVAGKYSYRPTDAEKGPFVGFAGKDRD

## SEQ ID 347

TTGATAAATCCCTATAAATTTCCCGCAAAATTGACCGCGAACACGAAAGCGGATAATCCGCCATCTTCAAAACCCCTTCAGACGGCATTTGACGCAATGCCGTC

## SEQ ID 348

LINPYKFPKIDREHEKADNPPIFKHPSDGLCSNAV

## SEQ ID 349

TTGATGTTGATGCCGCCGAAGCGCAGGTATTCATTACGGCGGACGACGCGTTCAATCATCAAAACAGCCCGGAAAAAGGCGGCATCCCAAAATCCGGCACTGAAATTCGCGCGGTA  
TCGCGCGCATTCGCGAGCTGCCGGGAAACCGTCGCGCAGCAGCCGAATGTCGGGTATTTCCGCGCGCTTTTCGCGCTGT

## SEQ ID 350

LMLMPFEAQVFTAGRRVQLIKQAPKEGIPKSGTEIARIGIIPQAGETVGSRRNVGYFRPFFSGC

## SEQ ID 351

TTGCACCGCCCGGATTTCGGAAGGCGATGCCCTTCCCAACACCGGCGGAAACCTCGCGCCCGAAGAGCGGGTTCAAGGCATTATCTCCCTGCTGCTGCCGTTGGAACCGCGGAGTG  
TTGAACACACGCGTTAAAAAACAGGCGCTC

## SEQ ID 352

LHRPDSERRCLSPNRPFCRPEERGSRRHYLPAAGWNRRESVETPLKQAV

## SEQ ID 353

GTGCAACGGGGTCCGCTTATGTGCCGAAAGGTTTTCGCGCAACGATGCGCTGTGAAGCGGGTGCCTTCAGACGGCATTTGTGATGTTTGGGGCGCGGGTCCGCTTCAATCCGCAATCAG  
TTGATAAACCCGTTGTCTTTTCATTTTTCAGAAAAATCTGGCGCATACGACGAGGCGGCGAGGATGATGACAAACAGCCCTGCCATAGTCAGTGTGATTTTGAAGAACAATTCCG  
CTTCGAGAAAAGAAAAACCAAGTTGCACAATCAGCAGCAGCACCCAGCGCGCAACAGTCCGAGACAGGCATAAACCGCGAGCTTAAACACGGTCCCGCTCAAAA

## SEQ ID 354

VQRGAPVYPKGFATVCRLLKRVSDGIVMFGARVRFKSASVDKPVVHFHFLFKILAAAYQGGEDDKQCHSQCDFEOPGFEEKRPKLHNOQHPAGKQSETGINAEHLKHPAPK

## SEQ ID 355

GTGCTGCTGCTGATGTTGCAACTTTGGTTTCTTTTCTCAGAACCGAATGTTTCTTCAAAATCACACTGACTATGGCAGGGCTGTTTGTATCATCTCGCCGCCCTGCTGGTATGCGGCC  
AGTATTTTCTGAAAGAAAAATGAAAGACAACGGGTTTATCAAC

## SEQ ID 356

VLLILVQLWFSFLEAELEFKITLTMAGLFVILALALLVCQYFSEKKMKDNGFIN

## SEQ ID 357

ATGAAGAATACAAAGTCGTCAATTTATCAGGAAAGCGTGTGTCAGCGCTGTTTTCGCGCGGCAAAAGGTCAACCCGTCATTTACAGCGCTTCTCAACAAACAAACCCCGAAGGCT  
GGCGGTCGTGATGATGAAAGAGATTTGCCCGTATGCTGCTGTTTTCAGAACCGAAGCCTACGTCGTCATTTTGGAGCGGACCGTGT

## SEQ ID 358

MKEYKVVYQBSLLSLFPGAANKVNVNFAFLNKQTPGMRVVTMEKDLRRMLFFKREAYVVLERDRV

## SEQ ID 359

TTGTTTGTGAGGAACGCGCTGAAATGACGGGGTGACCTTTGCCGCGCGGAAAAACAGGCTGGACAACAGGCTTCTGATAAATGACGACTTTGTATTTCTTTTCAATCGTATTTCCCTTT  
CGGTGAAACCCCGCCTTTGGGCGGTAGGATCAGACTTTATTTGGGAGGAAACCTTCCAAATCAGGACGATACATAGGCGGTGCTTTATGTATCGCTCTGTGTGT

## SEQ ID 360

LPVEERABIDGVDLCRAERQAGQAFLINDDFVFFHRLSFSVETPPFGAVGSDFIWEGTPSKSGRYIGRCFMYRPVC

## SEQ ID 361

ATCGCGCAAAATTTATGCTTATGCCCCAATGCGGCAATACCGAGCTTCGCCAGCGAGAGCAAAACCGCTTTGCGAATAAATACCCAGTTTGGCGCGGGTGTGCGGTGATGTCAGGTTG  
CGCATCGTGAAGCTGTCCGATCGGTGAGCGGTGTGAACGCGCACTTCGACTTTTCCATACTCAGGCGTTCGCGGTGTTAGTTCAGGTTCGGCGATTCGCTGTTCAAGATCGAGTAGT  
CGTTGCCGCGCGCAGTTCGAGGGTAATTCGCGGTAACGGCTTTGGCGAACCGAGCTTGGGCGGTTTCGCGCAACATCAAGGCTTGGCTGTGCAACAGCGCGCTTGGTAGAGCAAAAG  
TCCGAGGCGCAGGCGCTGATGCGGTATTTGTCGATGCTGTCTGCTTGTGATGCGGTAACCAAGCGTTTCGAGCGATGCGGAACAATCCATGCCCGGGCTTCGTAGATGCCGCGC  
GATTTGGCTTCGATGATGCGGTTCGATTTGCTGCTCATACCAAGCGTGGCGCGCGCGGATGCGGTTCGCTTCGAGGAAGAGTTCGACGGGTGCGGCTATTTTCGCGTTCATAG  
CAACCGGCACGCTTCTTCAAGCGCAGCTGACTTCTTCGGGTTCAATTTGAGGTTTTCGTCAGAGGCAACGCCATGATGGCTTAACGATTTTGTATGCCGAGTTCAAAAATTC  
CAAGTCTTTGGCTTTCGCGGTCGCGCGAGCATATGGAATCGGTGAGTAGGCTTTTCAACCGACATTTTGTAGTTGAAGCGGTTCGCAATCAGAAATTCGCTCATTTTCGTGACGCGCG  
CCGAGTTCGTGATAAATGCTGTCGAGCCAGGCTTTGTAGATTTTCAGCGCGGATTTGGTGAGCAAGCGGTAGCGGTAGAAACGCTCGATGTCGTTGCTTTGTAGGTGCTGCCGTCGC  
CCGAGATATTCATATGCTTCTTTCATGGCGAAACGAGCATGTCGCGGTACGCGCGCGGCCAGAGCGGTGTTGAAATAGCGGATGCCCGCGGTGAAACGTGGAACGCGCGCGCA  
TTGGATGCGCGGATGCTTCTGTGTGCCAGTTGTGCGCGCAGTGCATCAGCGCGCGCTTTTCGCAACCGTATTCATGCTTTTTCGGAATGCGCTGTGAATGCTTTCGTGCGGCTGC



CCAAAGGTTGGCAGTGTAGGCATAAGGCAGCGCCCTTTGAGTTTCATCCACAACACGCGGCAGAGGTATCAAGACCGCCGGAAGGCGATGCCGACTTTCTGAACGACGGGAGGTTT  
G

**SEQ ID 362**

MRRNLLILIAQLRQYRAFAQREQTALRINTQFAGVGDVEVAHRELSDAVERCERRTFDFHTQAFGLVQVGRFVQNRVVAAPQFEGNFAGNGPGDPALGGFAHQHGLAVEPAALVEQT  
SEAQAVDAVLFDGVFVVDAGNQAFVGDVEQCHARGFVDAARPGFDDAVFDLVAHTQAVAAADAVGPEEFDFGVGVFFAVQCNRHAFPAHADFPGFNFVDFVPEGNADGLNDFDARVQRF  
QVFGFVRAEHIGIGGVGFNRHFVVEAVGNQFAHFVTAAEFVDKLLVEPGFVDFQRGIGEQAVAVETLDVVAFVGAAVAPDTHIVFPHGNEHGAGHGAQRGRVETGDAAGGNVERAA  
LDGGDAFVQCQLCAAVDQAGVFRVPHCFPGNGVIVFVGLAKVGSVGRIRQRAFEFHPQQRGRGIRKTAGEGDADFLTDGEVL

**SEQ ID 363**

ATGAACCAAAACCACTACTATTTTACAAAACCTCCCGTCGGTCAGAAAGTCGGCATCGCCTTCTCCGGCGGCTTGTATACCTCTGCCGCGCTGTGTGTGATGAAACTCAAAGGCGCGCTGC  
CTTATGCCCTACACTGCCAACCTTGGCCAGCCGACGAAGACGATTACAAACCCATTCCCAAAAAAGCAATGGAATACGGTGCAGGAAAGCCCGCTGATCGACTGCCGCGCACAACTGGC  
ACACGAAGGCATCGCCGCATCCAAATGCGGCGCTTCCACGTTTCCACCGCGGCATCGCCTATTTCACACACCGCCTTGGGCGCGCCGCTGAGCGGACCATGCTGTCTCCGCCATG  
AAAGAAGCAGATGTGAATATCTGGGCGACGGCAGCACTACAAAGGCAACGACATCGAGCGTTTCTACCGCTACGGCTTGTCTACCAATTCGCCGCTGAAAACTACAAACCCCTGGCTCG  
ACCAGCAATTTATCGACGAACCTGGCGCGCTCACGAAATGAGCGAATTTCTGATTCGCAACCGCTTCAACTACAAAATGTCTGGTTGAAAAAGCCTACTCCACCGATTCCAATATGCTCGG  
CGGACCCACGAAGCCAAAGACTTGGAAATTTTGAATCTGGGCATCAAATCGTTAAGCCATCATGGGCGTTCGCTTCTGGGACGAAAACGTGAAATTTGAAACCGAAGAGTCAGCGT  
CGCTTTGAAGAAGCGCTCGCGTTGCAATGAACGGCAAGAATACCGCGACCCCGTGAATCTTCTCGAAGCCAAACCGCATCGCGCGCCGCAACCGCTTGGGTATGAGCGGACCAAAATCG  
AAAACCGCATCATCGAAGCCAAATCGCGCGCATCTACGAAGCCCGCGCATGGCATTTGTTCCACATCGCCTACGAAACGCTTGGTTACCGGCATCCCAACGAAGACACCATCGAACATA  
CCGATCAACCGGCTCGCGCTCGGACGTTTGTCTACCAAGCCGCTGGTTTCAGACGCAAGCCTTGATGTTGCGGAAACCGCCCAACGCTGGGTGCGCAAGCCGTTACCGCGCAATG  
ACCTCGAACTGCGCGCGGCAACGACTACTGATTTCTGAACCCGAATCGCCCAACCTGACCTACCAACCCGAACGCTGAGTATGAAAAAGTCGAAGGTGCGGCTTACACCGCTCG  
ACCGCATCGGACAGCTCAGATGCGCAACCTCGACATCACCGACACCCCGCCAACTGGGTATTTATTCGCAAGCGGTTTGTCTCGCTGGGCGAAGGCTCGGTATTGCCGCGATTGGG  
CAATAAGCAA

**SEQ ID 364**

MNQNTIILQNLFPVQKVGIAFSGGLDTSAAILLMKLKGALPYATNLIQPDDEDDYNAIPKAMEYGAENARIIDCRAQLAHEGLAIIQCGAFHVSTGGIAYFNTPLGRAVTGTMVLSAM  
KEDDVNIWGDSTYKNDIEFRFYRLITNPALKIKYPLWDQFIDELGGRHEMSEFLIANGFYKMSVEKAYSTDSMILGATHEAKDLFLNSGIKIVKIMGVAFWDENVETPEEVS  
RPEZGVPVALNGKEYADPVELFLANRIGRRHGLMSDIENRIIEAKSRGIYEAQMGALFHIAYERLVTGTHNEDTIEQYRINGLRLGRLLYQGRWFDQALMLRETAQRWVAKAVTGEV  
TLELRGNDYSILNTSPHLYTQPERLSMEKVEGAATPLDRIQGLTMRNLDTITRAKIGIYSQGLLSLGBGSVLPQLGNKQ

**SEQ ID 365**

ATGAAGCACCCGAACCTTATTGCCCGCCGCGGATTTGAAAGAAATGCGCGCCGCTACGATTACGGCGCAGATGCCGTTTACGCGCGCAGCCCGGCTACTCCCTCGCGCGCCGCAACA  
ACGAATTTGCCCAAACCTCGACGCTCTCGAGCAAGGCATTAAAGAACGCGCAGACGCAACAAAAAATCTCTTTTACCGCTCAACACCTGCCGCGCAANTCCAAACTCAAAACCTTCGTTGC  
CGACATGGAGCCGCTGATTGCCATGAAACCCGACGCGCTGATTATGGCGGATCCGGGTTTGAATATGACCGTGCAGGAAATGGCGGAAATGCCGATCCATCTGTCCGTACAGGCGAAC  
ACCACCAACTACTGGGCGTGAAATTTTGGCAGAACATTGTTGTCGAACGATCATCTGTACCGCAATTTGGGATGGAAGAAATTTGCCGAAATCCCGCAAGATGCCCGCATCGAAC  
TCGAATCTTATCATCCAGCGCGATTGTGCATCGCTACTCAGCGCGCTGCTGTGTGCGGCTATTTCACACCCCGCATCCCAACCAAGGCACCTGCACCAACTCTCCGCTTGGGACTA  
CAAAGTCCAACGCCACGGAAGCGAGGCGAGGATGCCAGCTTCTGCAAGGTTTCAACTTTGAAAAAGCCCAAGAAAGCAACCAAACTTTGAAGGCATCAACGGTCAAAAACGC  
CATCCCTACGCGCAAAAGTTTCTGATTGAAGAATCCAAACCGCCGCGAGATGATGCCGATTATGGAAGACGAACACGCGCACTACATCATGAATCCAAAGATCTTCCGCGTATCG  
AAGTCGTGCAAAAACCTCGCCAAATTCGGTGTGGACAGCTCAAAGTCGAAGGCGGTACCAAGTCTCTACTACGTCGCGCGCGTGCAGCTCTACCGCAAGCGATTACAGATGCCGT  
CGCAGGCGCTCGCTTGTATTACAGCTGTTGAGCGAACTCGAAGGCTTTCACACCGAGGCTACACAGCGGCTTCTCGAACGCCACCAACTCAGGATTATCAAACTACCTCAGCGGC  
CATTCACCGCCCAACAAAGCAATACGTGCGACAGTTACCGAAATCGACGAAATGGCTGGGCGGACCATCGAAGTTAAAAACCGCTTCCGCGTGGCGATTCGCTCGAAATCATCCACC  
CGAGCGGCAACCAACCATCAATTTGGAACAAATGACCCGCAAGGCAACCTGTGCGATGTTCCCGGGCAACCGCATTCAGGTCAAAATCCCAATATGACAGGCAAGAAAAAGCCCT  
CATCGCACGCGTGTGAACCCC

**SEQ ID 366**

MKAPELLPAGGLERMRAAYDYGDADAVYAGSPRYSIRARNNEFAKLDVLEBQIKEAHERNNKFFLVNTLPHNSKLKTFVADMEPLIAMKPDALIMADPLIMTVREXWPEMPIHLSVQAN  
TNYWGVKFWQNGIVERIILSRELGMEEIAEIRQCPDIELEVFHIGALCIAYSGRLLSGYFNHRDPNQCTCTNSCRWDYKVENATESEAGDAQLLQGFNFKAQEANQNFEGINGQR  
HPYADKVFLLIESNRPEMPMEDEHGTIYMNKDLRGLIEVVEKLAKI GVDLSLKVGRKTSLYYVARVAQSYRKAIDHDAVAGRPFDYSLLSELEGLANRGYTSGLERHQTDQYQNTLSG  
HSTAKQSQYVGHVTEIDENGWATIEVKNRFAVGDSLRIIHPSGNQTILKELQMTKRGQVVDVAPNGIIVQKI PNMQGEKALIAVLNP

**SEQ ID 367**

TTGTCCGACATATCGGCTTCGCGGGCTGCCTATATGGATGTGCAAAAACAATATCCCTTTGAAACCGTCGCGGTATGCGTCTGCCGAACCATATTACGCCATTGGACGCTGCCGCCG  
ACGATGCGGATTTCTCTACTCCGCGCGCTGATTAAACCAAAATTCCTCCGATATTCCTCTACTAAAACTTAGGGCTGTACTAGATTATCCC

**SEQ ID 368**

LSDISASRAAYMDVQKQYFPFVAVCVLPNHIIHAIWTLPPDDADYSLRLRLIKTKFSAYSPHTKNLGAVLDYP

**SEQ ID 369**

ATGGTTTGTGTTATGAAAAATCCTCGATAGCTTGAATAATCAAGCCATTATCTTATAAATAGAAAAATATTGTAGCCATCATGCGCTCTGAACGGGTATTCGCGCTTTACGGCGGTA  
TT

**SEQ ID 370**

MVLVHEKILDSLKNQSHYLINRRKYQPSRLNGYSVAVSGI

**SEQ ID 371**

ATGAACGCGTTCAACCTCATCATCGGAGACGAAATCTTACACGGCAGCGCCGCAAGACAAAGCATTTGCGCTTTTAAATCCCTGCTCGAATCCAAAGGCTGAAGCTCAATCAGGTG  
AATATCTGCCCGACGAACCGATTGCTGGTCAGGCACTGCGCGCAGCTTTTACAGCGCATACCGACGTTGTTTACCGCGGCACTGCGCGCCACGCGCCGACGCGCCCAAC  
CGCAGCGGCTGCTTTGGATTTCGCGCTCGCTCCGCTTCTGAAGCGCAAGATTATTCAGGAGCAACCGGAAACGCGGCAAGCGCTCGATTGCGCGCAACCGCCACCGCTGAA  
ATGGCGGATTTCCTCGAGGCGCAGAGCTTGTGCCAACCCGTTCAACAACATCGCCGATTTTCATCCGCGACATTATTTCTTCCCGGCTTCTGTGATGGCGACCGCATGCGG  
AATGGGTTTGGAAACTTATTATGCGCGCGCTTCAACCAACCGAACCGGCGAGCGCGAGGTTGATGTTTGGAGCGCCGAATCGCGCATACCGGATTTATAGAGCATATCGAGCA  
AACTTATCCCGCGCTGCGTTCGACAGCTGCCAGCGTGGTGGACGATTTCAGACGCGACGAGTCAAACCGCACATTGAGTTCCGATCAACCGAAGGAGAGCGCTCAACCTT  
TTGGACGCGCGTGGCGGAAGTGTGACAGCTTGGACGAGTGGGAGCAGAGCTGAAAAATCGGTTAAAC

**SEQ ID 372**

MNAFLILIGDETHLSGRQDKHFAFKSLLESKGLKLVQVYLFDEPDLLVRQLRRSFSDGIPPTVTTGGIGATPDRTRQTAALDLPLVVRHPEAAKFIETITRKRKPLDSPEHAQRLK  
MADFPEGAELVNPFPNNIAGFSIREHYFPFGFVMAHPMAEWLETTYAGRFNQTERGSRSVYVFBQFESRITPIEHIETQYTPGVRSYSLPSVGNWTHSDGTQVKPHIEFGIKAEGBAVNL  
LDAANAELHSLDGLGAEKLRVN

**SEQ ID 373**

ATGCATACCGAATCAGAAGAGAAAACGAAGCACCCGAAGCAAAAAATCGCGGGGAAACCTTATGGGAGCGGACATTATGCGCGAAGTGTGCTGTCCGCTATCGGACAGGCGCAGG  
AGCGGATGTGAAAAACATCTGGCGCGCTCAGCACCTTGATTCTGGTTGCCCTGATTGCAAGCATTTCCGAAAAGACGAAGCCGATTCGAGTTGGCGGCAACACGCCCATACCGC

AGTCGTCAACCTGTACGGCAAAATCGGCAACGGCGTAGAAGACCAGGTCAAAAACTCAAAGACGGGATGGAGCGCCTACAAAAACCCGAGGCAAAAGCCATCGTCATCCGCGCCAAC  
AGCCCCGGCGGTTCGCGCGTCTGCTCCAAACACCGCTTTTGAAGAAATACCGCGCTCTGAAGGCGAGCACCCCGGATCCCGTTTATCTGTCGCGAGGATATGTCGCGGTCCGCGTCT  
ACTACATCGCGCGCGCGCGGCAAAATCTATGCGGACCGCGTCCAGCATCTGCGGAGCATCTGCGGTTATTCGCGAGCAGTTCGACCGGACCGCGCTGATGGAIAAAATCGCGCTAAACG  
CAGGGTTAAATTCGCGGAGCAAAAGGATGGCGATCCGTTTTCGCCGAAACGCGGAGCAGTCAAAATCTGGGAAGAAATGTCAGCGGCATACACGGGAATTTATCAAGCC  
GTCAAACCGGACCGCGCGCGCTCAAATTCGACAAATATCCGACGTGTTCAGCGGTGCGGTGACACAGCGCGGACCGCTGAAAGTCGGGTGTTGAGCAGGACTCGGCAATTT  
ACAGCGTGGCGGAGACGTGTTCAAAGCTCCGATGTGGTGGATTACACTCCGAGGACGATTTCGCGAGAATCTTGGGAGACGCTTCGGAGCAGAACTCAAAGCAAGCGTTTCGGAAGC  
TCTGCGCGCGTCCG

## SEQ ID 374

MQYRIRRENEAPEAKNAGETLWERDIMEVLLSAYRDRRREREMKNIWRAVSTLLILVALIAGIFPKDEAALQAGNTPHTAVVNLVYKIGNGVEDQVKKLKDGEAAAYKNPQAKAIVIRAN  
SPGGSFVVSNTAFERIRRLKAQHPGIPVYLVAEDMCASGCTYIAAADKIYADPSSIVSGISVIGSSFDATLMEKIGVKRRVKLAGSNKMGDPFSPETPEQSKIWEMLTGIHGEFIRA  
VKTGRGRLKFRQYDVPFSGRVTGADALKVGLVDGLNITYSVARDVVKAPDVVDYTPKIDFGRILGRFPAGELKASVSEALQAVR

## SEQ ID 375

ATGCACAAAACCTCCCGGGGACAACTGCTTTTGGCGCTTTAAGTGCACGGTAAATAGTAACGCGGCTGACTAGTGGCAGCATACTGGGAGGTGAGTGTTTTGTGTATATTTTAT  
CTGGTATTCCTTAGAAATACTG

## SEQ ID 376

MHKTSGQPAFCGFKCTVNSNAADLVAAYWGGECFCVYFYSIPLLEL

## SEQ ID 377

ATGTTTGTATGGCAAGTAGAAGCAGATGAAAGTTATTTTGGCGGACAAACGCAAGGTAAATGCGGTGCGGTGCTGCCGAAAGTCCAGTATTCAGGCTTCTCAAACGAAATGCCAAG  
TTTCTTTTCCGTCCTGTTATGATCTTCTGTAACATTCGAAGACTTCTTGAACCTTCCCGCGCTTTCGGTTTCTGTATACCCCTCTGTAGATAAGGGGGGGAAGATTGGAAGCGGTGCGC  
GGCTTCTGCGGTCCGTCGGCGCGTCCGTATCACGCGGCAACCTCTTTGTCATCCTTGTCTATCTCCATGTGCGAATCTCTCAAACCGGCAAAAAAGCCCTGTACTGTAGAA  
AG

## SEQ ID 378

MFDEGEADESYFGQKRGKCGRAAGKVAVFRLLKRNKGVSAVRVYRVFTFEDFLNPARRFPGCTPLDKGGEDSKRLPASCRPSARPPSSRRQPLSSLAYLPCANPQKRAKSPVTCR  
K

## SEQ ID 379

GTGAAACCTGACAGCATTTGTTATACGATTTGTTATCGTCGCTATGATGTATTTGGATGCAGGCGAATTTAGCCATTTCCGTATCAATCACAGCACATTTTCCGGAACGACAAAACATA  
TTAATGGAATTCGGAATTTTGGAAACCGGCAAAACCTCATTTACGCAAGTTTTCAGCGCATTTCCAAAGAGCATTTTGAAGCGTATTTAAAGGAGTCCGAACCGCGTTTAAACACAGTGA  
GATAAAGTCTCTGTTCCATTT

## SEQ ID 380

VKPDIVITDCYRRYDVLDAGEFSHPRIHSHTHFAERQNHINGIGNFWNRAKRLKFDGIPKEHFPYLAECERFNNSEIKVLVPF

## SEQ ID 381

ATGATTATTCAAAATGAATTTAATTTATATCTAGTAATATGCTTCTGAAAGGTTTGTATTCTGAAAAGTATGTTCTGATCTCTAACGATACATCTTTAATACCTTATATTCAGCCAC  
ATAATTTTCACTGCTGTTGTTGAGAAATATGGAACAGAGGGGAGAAAGTAGCTTATATATTTAGAAATTCATCTGCTGATTTAAATCTTATCCCATTCGCTAGTAATGGAGAAATGGGA  
AGCTTATTTGATGCTAATGATGTAAACAGGAAATCTAGCGTTATTTGTTATTAATTTAGATAATATAGAAAACCATGAATTTTTTAATAGTTTGAAGAGTGGCTTGAATTAGCAATTAAG  
GATACTTG

## SEQ ID 382

MIQNEFNLYPSNMLPEGFCYPEKYVRI SNTSLIPYIQPHNPHWFWNYGTEGAEVAYIFRNSILPDNLNIPFASNGEWEAYFDGNDVTGNPRVIVINLDNIENHEFFNSFEWLELAIX  
DIW

## SEQ ID 383

ATGTCCACCGCGCGCTGTGGAACGGCGGTTTCCGCGCCAGCCAAATGGGAATCAGGAGGATAAAACAAAATGCTCCGCGGAGGAATATTTCTGTTGATCCGATGATGAAGCCCTGTTGC  
GTAATGATTTGTTGATGATGCTAGATTTGACCGCTGGAAATGCTTGTGGAACAAATGCGCGCGCTTTCGTGCAATGTTGCGGAATAGGCGGTGATGTTGCGCAAAACCGGTGT  
GGTGCACCGCTTCGCGCGTTCCACAGGGTCTGACGACGGATACCGGACACCGCCCATCAGCACGCGCAGGAATTCGACAGGCTGCCGCGCGCGGCAATCTGTCGCCCTTCATGTG  
CGACAGTGTGATGGTGGTCAGCGGAGGAAGAATCGCAACGCCCTACCCCTTGCCAAACTCGCGCCAGATGACGTTGCGGATATCCATGTCGGCATAAATAACAGTGCAGCAATAAAAA  
GTGAAGCCAAAGTTCAGGAAGCTGCGGTTCAGGACAGCGCATATCGATTTTATTTGCCGAACCTCCGATTAACCGAGATAGGAAGACGCGGAGGATGCGGCGCGCGCGCAAGCC  
CTGCCACGCGGAGGTATAGCCCAAGTTGGTCTGCAACACTAACCGGACAGCGGTGACCGTCCCATATACACCATGAAACCCAGAGGTGGCAATTAACCGCGAGGTAAATTCGATC  
TTTAAACAGCGATAAATCGACAATCGGATATTTTCTCCCAATTCCTCAAAACATAAATACGACAAGCACACCGCGGTTATGCCAAGGTAATGATTTCTCCAGAGCGCAACAGTCA  
AGTCTCTTACCCCTGTCAGCATCATCTGTAACGCGCGATACCGACCATCATCAGCTCAGCCGACATAGTCTGCTGCGGTCTGACGCTTTCGCGGTGTTTCAAATGTTTCC  
ATGTAATCATGCGGATATGATCCGATGGGATATTAATGAAGAAATCCAAACCCAAATGCCAGTTTCCGGAATCCAAACCGCGAGTATCGGCGCGGAGCAGGCGGACACGAGCGT  
CATTCGCCAATGCCAGTGCAGATCCGTTTTCGCGCGGATAGGATGCCATTAACAGGCTTTGCGACAGGGAATCAACGCGCGCGGATAGAGCCCTGCAAAATGCGGAAACCAAC  
AGCGATGAGGTTTGGCGCGATGCCGACAGCATGCGATGACGAAACCGCGCGCGCGGTAACAAATTTGACCTCGCGGATACGTTTTCGCAAAAGCCCGTACCGCGCACGG  
AAACGCGGTTTTCGCGGAAAGAAAGTATGACCCAGTCCCTGCGTGGTTGCGCGACCGAGGTTGCGGCAATGACGCGGACGCGGAGTGGCGATGTTGATCTAAACCTCCAT  
AAATACGCAAGCCCAAGACAGCGTAACCCAGCCAAATGCGCGACCTTAAGCGGTGGAATATCCATTTGTTCTCCGTTTCAGACGGCAT

## SEQ ID 384

MSTAAAVERRFRQFANGNQDDKQNAAGEEYFVRSDDREALLRNGIVDDA\*SLTVGNALIGQRRRRFVQCGIGRNVFGRTRVVQRFAPFPQAGDDGYADTAHQHAQRIQAAGGNNLSALHV  
RQCDGGQRQEEHGNAYPLPKLRPDDVADIVHGIKISAPIKSEKQGEAGGYEQAHIDFIAEPAD\*RR\*EDGEDADGRGSKPCPRGGIAQVQLQH\*ROQGORPHIHETQRGNYADGKIPI  
FKQR\*IDNRIFPSQFNNKIRQAHRGYAQGNDFSRGEFVKFLTPVQHHL\*RADTDHQRQPDIVGRRSDGCRFAVFPQMFPCNPCRYPDGDLINEENPTPHVSGNPTAEYRPEDRGDNDG  
HCLQCCQHPFCGRIGCH\*QALRQGNQRPDQKALQNAENNRQLKVRDAAQPRCDETTGCGGGKQFDLADTFQKARQRHNGVCHGKRSDDPRFLRCRTEVAGNDGDGVDGRI\*NLH  
KYGKPRQRNPRQCRILKRWI IHCVLRFRRH

## SEQ ID 385

TTGGCAGGCTCCAGCATCAGGCGCGCGGAGAGTATGAGGATTTTTATGTCGGATGTCCTTGTTCGTGTTGGGAAATCATTECCATTGTACAGTAAGATTCAACAAAATCCGCTCTG  
AAAACGGGGTTCGAGCGGATTTGGCTCAGGGTTTCAACACGCGTGGCA

## SEQ ID 386

LACQHQGGGEYEDFLCRNLSFVAGNHCHCTVRFNKMPSENGVRTALNLRGSTRVR

## SEQ ID 387

ATGAAGATAACACTGCAAAATTAAGAAAGAAAGTACAGAAAGAACCGCTCCGTTCTTTGTACCGGAAGTTACCGCCGCTTCTGCCCGCGATATTTTGGTATTCATCCGATTCGCGG  
CACTGTTTACCGTAAATTCGCAAGGTTACCAACCATCGTTTGGCTTGGCTGCGGATGAGGTTTTCGAGGCGCGCGCGCGGCGGAGCTGTTTTCGCGGAGCGGCTAAAGGAG  
ACGCGTTCGCGCGCGGAGGAAAGCGGTTGCTTTCGCGATTCGGAACGCAACGCGCGGCTTACCTGTTCCGCGGACATGCGGAGCTGAAACGTTTACCCCTGCGCTCAAAAAG  
AAAATCATGCGGAGGATTTGTTTATGCGGATAGCCCGGCGAGCGCGCAAGTTGACGCGCGCGGTTTACCCGTTGCCGATCAACCGTTTCAAGGAATTTGACAGCGCTCGGAAC

ACATTAACGGCATTGGGAACCTTTTGAATCAGGCAAAACGCGCTTGGCAAAATACAACGGAATCGATCGTAAACCTTTCCCGCCGTTGTTGAGGGAATGCGAATTCGACTTAACCTTCGG  
CACACCGTCCCGGACGTAAAAATCTCGCGGATCGGTGTGAATT

**SEQ ID 388**

MKITHCKLKKEVQKEPLRSFVPEVTARSAADILGIHPSAALFYRKIRTVNHRLLAADEVFEPAGPGGSCFGRGRKGRGRGAAGKAVVPGIPKRNGRAYTVAADNAEPETLPPAVIK  
KIMPDGIVYADSPGSRGLDAGGFTRCRINRSKEFADRRNHINGIGNFWNQAKRALRKYNGIDRKPPPLLRCEFRNLNPGTTPSRQLKILRDRCGI

**SEQ ID 389**

ATGAATGAACACAACCTGTTAATTTTCTGTTTAAAGACAATGTTTCAATTAAGTGAATATCTGAAATGGTTGATGGGCTTATGAAAAATTCAATCTGAAACAGTTGTAGAAATACCG  
AAAATCAAATTTATGAATATCAAAATCGTGATTTATGGGGCTTGTCTGAAATTAACGATAATGGTTATTTGGACCAAGTGAGGGGATTCGCTAATAGATAAGGAAAGTATTTTGGC  
TGTAAGAGAAAAATTACAAATTCAGATTTTCTACAGAGCCCTTAGTGAAAAATATTATTATGTAATGCTATAAAAATGAAAAACAGTAATTTTTCATTTT

**SEQ ID 390**

MNEHLLIFCLKDNVSISETTEMVDWAYENIQSETVVEITENQIIIEYQNRGLWGLVSRITDNLWLPFSEGDWLDKESILAVKEKLQNSDPSTEPLVKNIHVLEYAIKNEKTVIFHF

**SEQ ID 391**

GTGGGCATCAATGCCAATCCTAATCTGTCTGATGAAGCAGGAAAACCTGATATGGGAAAACGACCCCGATAAAAAATGGTGGGCTAACCGTATGGATGATATTCGCGGCATCATCCAAGGTG  
CGGTTAATCCTTTTAAACGGGTTTCAAGGAGTAGGGATTGGGGCAATTACAGACAGTCCGGTAAGCCCGGTACAGATACAGCCGCTCAGCAGACTCTACAAGGTATTAATGATTAGG  
AAAATTAAGTCCGGAAGCACAACCTGCTGTGCGGAGCCTATTACAGGACAGTCTTTTGGCGTAAAGACGCGCATTAATTCGCCAGACAATGGGCTGATGCCATCCGAATATAACAGCA  
ACAGCCCAAACTGCCCTTCCCGTAGCAGAGGCCGAGGTACGGTTTGGCCCGGTAAAAAGTAGAACTTAACCCGACCAATGGGATTGGGTTAAAAATACCGGCTATGAAAAACCTGCTG  
CCCGACCTATGAGACTGTTGACGGGGAATGGCAGGTGGGAATAAACCATTAACTCTTACCAACAGCGCCGTGAAAAAGAAAAACAAGTTTAAAGAACTTTAGTAGCAACTGGAG  
TTCAGCAAGTTTGTATTCAGTGCACAAACACTAACTCCCAATGCACCTGGTATTTAACTCTGATAAAGTTAAACTCGATACACTAGTTTAGATGAAAAATTACAAATATAAAGAT  
AACGAAAAACAATTTTGAATCCATGATAATTACGAAAAACAGTATCTTGATTCAAATGGTAATGCTGTGAAAAACCGGTAAATTTACAAGGTAAAGCAAGCAAAAGATTATTACAACAAC  
AACTCATATCAGGAACCTTAGACAAA

**SEQ ID 392**

VGINANPNCADEAGKLIWENDPDKNWANRMDIRGLIQGAVNPFLTFQGVGIGAITDSAVSPVTTAAQQTLOGINDLGLSPEAQALAVASLLQDSAPAVKDGINSARQWADAHFNITA  
TAQTALAVAEAGTVWRGKVELNPTKNDWVKNTGYKPAARPMQTVDEMGAGNPKISLPNSAAEKRKQSPKFPSSNWSSAFDSVHKTLTPNAPGILSPDKVTRYTSLDGKITIILND  
NENNYFRHDSNRKQYLDNNGNAVKTNGLQKQAKDYLLQQTHIRNLK

**SEQ ID 393**

TGACAAGCAAAATAAATTTATTAATATAATCAATTACACAGGTGATGACATTATTATTTCTTAAACAAGAGAAGAGCTTCAATTTATGCGTTCCCTTGTATTGAAATTTATGCAG  
GTGTTTGCATAGATGCGAGAAGAAATTTGAGATTGTGTCAGGAATTCGCAATCTCTCAATTTAGTGCAAGAGCTAGAACAACATTTAATTTGAAGCATATAATCTAATGGATACATCTAAC

**SEQ ID 394**

LTSKNKILMNIINYTGDDIIISLTREKLQLRLSLVIRIYAGVCIDAREFEIVSGIRNPQLVQLEQLIEAYNLMDTSN

**SEQ ID 395**

ATGATTAAATTCGATTAAAAAGCATAAAATTTATATGATATTGATTTTAAAAAATTTACCCCCGAAATTCAGATAAATTTTCATAGATGGATAGATTTCGATATCGGAATCGAAGGAGAAC  
AAGGCTCATCTATTTTTCACCTTTGCATTTGTTCTCTTAAATGGATTCCCATCATTTGTAATAAGAAAGGTTTTTTTGGTCTAATGCATTAAATTTAGAACAGTTTGATCATAAGATTAT  
TAAAGTGAAATTTGATAAAATTTAGAAATTTGCTCAAAAGAACTTTGGGATTTCAGACTTTTCAAACTTATACGATTTTTTTCTTGGGAATTCGAAGATTACAATCCAAACACA

**SEQ ID 396**

MIKLILKSLINLYDIDFEKFTPEIPDNFHRWIDLIGIEBEGSSIFSLCICSPKWI SHCNKEGFFWNAIILEQFDHKIILKSEIDKILEYCSKETWDLTSLNLLRFPSPWEPEDYNPNT

**SEQ ID 397**

GTGCAGATGGCACAAGCGTATATCTCTCCAACACAAAATCAACACCCCTGAATCACTTAACCCCAACGGGAGTGCAGAGCTAATTTGTGTACTAGAGTGTGTGATGAAAAACCT

**SEQ ID 398**

VQMAQGYIVLQLNQTPILNHLTQRECKLILLLVLMKFP

**SEQ ID 399**

TTGTCCGATACAAATAAATATCCGACCTACATTTCTGCGCAGCAAACTTTACAGGGTATTCAGATTAGGAAATTTAAGTCCCGCAGCACAACCTTGGCGGTGCAACCGCATTACAAGACA  
GTGCTTTTCCGGTAAAAGACGCGCATCAATTCGCCAGACAATGGGCTGATGCCCATCCGAACATTACAGCTACTGCCCAAACTGCCCTTGGCGTAGCAGAGGCGCGAGGTACGGTTTGGGG  
CGGTAAAAAGTAGAATTTAACC CGGCCAAATGGGATTGGGTTAAAAATACCGGCTATAAAACACCTGCTGTTGCGACCATGCATCTTTGGATGGGAGATGGCCGTGGGAATAGACCG  
CTTAATCTATAACGTCGAAGGAAAAAGCTAATGCTGCAACCTATCTTAAGTTGGTTAATCAGCTAATAGGCAAACTTAAATAACATTGCGGCTCAAGATTCAAGGTTAGCAAGTGTCTG  
TAAAGAGATTGGAAGAACATACAAACCAATAAAAAGGGGAAATTAATTTGGTATTGGTTCTGCAACTCGTCAAGAGGCTGAACAGTTAGGAAAAATTTGGGTTGGAGACGGGGCTAAGCC  
AGTTAGTAGTCCATCTTGTCAAGGATGTATGTTAAGTGCAGATGGCACAAGGCTATATGCTCTCCAACACAAAATCAAAACCCCTGAATCACTTAACCAACGGGAGTGCAGGTAAT  
TTGTGTACTAGAGTGTGATGAAAAACCTTAACATAATGGACATTTGAATATAAAA

**SEQ ID 400**

LSDTNKYPYIISAQQTLOGIHLGNLSPAAQLAAATALQDSAPAVKDGINSARQWADAHFNITATAQTALAVAEAGTVWGGKVELNPAKWDWVKNTGYKTPAVKTMHTLDGEMAGGNRP  
PKSITSKGRANAATYPKLVNQNLNIAAQDSRLASAVKDWKTIQPNKKGEINFGIGSATRQEAQJLKIWVGDAKPVSPSCQGCMLSDAGTBLRYRPTTKSNTPESLNPITGVQAN  
FVTRSDGKTL/ENGHLNLIK

**SEQ ID 401**

TTGTATCCGACAAAAATATTGACGCGCTATCGTTCCGAGATGCCGCTGTGGAAAAATGTCGGATTTCGAGATCCGATCTACGGCTGC

**SEQ ID 402**

LYPTKIFDAPIVSEMPLENVGFENPIYGC

**SEQ ID 403**

ATGAATATACTATCCATAAATAATCAAACTCAACTATTTCTACTAAGTGAAGTTTGTGTTTACGAGCTATCTTGAATGAGATATATGCGGGCGTATGTTAGATTCAAGAGAAT  
TTGAAATGTATCTGGTGTAGAAAACATGAAGTAGATAATTTACAACAACAGTTTGTGGAATTTATAAAAAATGACAACT

**SEQ ID 404**

MNLSINNQNSTISLTQDEVFLRAILNEIYAGVCDVSREFENVSGVRKHEVDNLQQQFAGIYKMTT

**SEQ ID 405**

GTGGGCATCAATGCCAATCCTAATCTGTGCGGATGAAGCAGGAAAACCTGATATGGGAAGACGACCCCGATAAAAAATGGCGGGCTAACCGTATGGATGATATTCGCGGCATCGTCCAAGGTG  
CGGTTAATCCTTTTAAACGGGTTTCAAGGGGTAGGGATTGGGGCAATTACAGACAGTCCGGTAAGCCCGGTACAGATACAGCCGCTCAGCAGACTCTACAAGGTATTAATGATTAGG  
AAAATTAAGTCCGGAAGACACAACCTTGTGCGCGAGCCTATTACAGGACAGTCCCTTTGGCGTAAAGACGCGCATCAATTCGCCCAACAAATGGGCTGATGCCATCCGAACATTACAGCT  
ACTGCCCAAACTGCCCTTGGCGTAGCAGAGGCTGCAGGTACGGTTTGGGGCGGTAAAAAGTAGAACTTAACCCGCGCAAAATGGGATTGGGTTAAAAATACCGGCTATAAAACACCTGCTG  
TTCGCCACCATGCATCTTTGGATGGGGAAATGGCCGGTGGGAATAGACCGCTAAATCTATAAGTCCCAACAGCAAGCAGATGCTTCCACACAACCGCTCTTACAGAGCGCACTAATGG  
AGAACAAATTAGTAGTGGGATGCTTATAACAAGCATGTCATAAGACAAAGAAATTCAGGATTAAATATCAATTCACCAGCAGATTTGCTCGGCATATTGAAAAATTTGTAGCCAT

CCAACAAATATGAAAGAGTTACCTCGCGGTAGAACTGCGTATTTGGGATGATAAAACAGGACAATAGTTATCCGAGATAAAAAATCTGACGATGGAGGTACAGCATTAGACCAACATCAG  
GTAAAAAATATTATGATGATTTA

## SEQ ID 406

VGINAPNCADEAGKLIWZDDPKNWRANRMDIRGIVQAVNPFLTGFQGVGIGAITDSAVSPVTDAAQQTLOGINDLGLSPEALAAASLLQDSAPAVKDGINSKQWADAHNPNTA  
TAQTALAVAEAGTVWGGKVELNPAKWDVWNTGYKTPAVRTMHTLDGEMAGGNRPKSIITSNKADASTQPSLQAQLIGBQISSGHAYNKHVIRQQEFTDLAINSPADFARHLENIVSH  
PTNMKELPRGRTAYWDDKTGTIVIRDKNSDDGTAFRPTSGKYYDDL

## SEQ ID 407

GTGTTATCTTCATATTTTCGAGGGTAACATATCTGCTAATCTGGTACAGACCCAAATTAATTTGATGGCTTTTATGATCCCGATTTCGGAATAATGCCGTCTGAAAGCTTTTGTGAGGCTTT  
CAGACGGCATTTTGATCATCAAG

## SEQ ID 408

VLSSYFEGNISANLVQTIKLHAFNIPDLKRCRLKVFVRLSDGILLIK

## SEQ ID 409

GGGCGCGGATTGCCCGGAGGATTTTCATCGACCGTCCGATCGACTTCGACACAGTTCGGTACTTTCCATTTCCGGCAATGCCGACCGCGGCTTTTGAACAGCGCGGCTGGGGCGGAAGTA  
TCCACTTTAACCGTCATCGACAAACCGATACGCAACCGATGCTGTCACATCTTCGCGGTTCCAGCAGATACGAGCGGGACCGCTCCACCACTTTAATCCAGTTGCCCGTTGGGTTTT  
GCGCGGAATCAGCGAAACCGCGCTGCCGCTACCTGCGGAAACCTGCCACCTGCGCGGATAAACAAATTTGTTGCGGTACAAATCGGACACCGCTCGGACGGCTGTCGGATTTTCAT  
ATGCCGCAACTGCGCTCTCTTTAAATTTGGCATCCACCCACATCCGACAGCGGACCCACCGCATCAGCGGCGCGCTGCGGCACTGCTGCCGACCTCGACCGAAGCTTCGCCACC  
TGACCGTCCGCGCGCGCGGACTTGGCTCCGCGAAGGTTCCAGCCACGATCTTTCAACCTGCCGATGCGGCTGGAACCTCCGCTGTTGCGCAAAAGAAACATCTCCGCCAAAGCGG  
CGCGTCCGAAGATCTTCCGCCAAAGCGGCTTAACCGCGCGCTGCCCTGAGACACTGCGGTACGCGGCTGTGCGAGCTCTTCGCGGACACCGCACCCGATTCGCCCAAGCGGACCG  
GCGCGGTAAATCATCTGCGCGCGCGCAATCCGACGCGCGCAAGGCAACCTGCCCGCCCGCTGCGAAGTGGCGGCAATTTTGGCGCGGTTTGGCGCACCGCTGAACCAACTCGTTT  
TTTCCCGCTCGTAAGCCAGCACATCATTTATGCTATCCAAACCGCGCAGCGCTGCCCTTTTTCACGGCATCCGATGCTGCTGCAAAACCTTCGCGACCGTCCCGCTTTTGGCGG  
TAACCTGAACCCAGCGCTCGCGCAACATAAGCGCTTCGCTTTCTCTCTGCTGCCACATAAAAAAACCGCGATCCGCGCGCTGCGCGGAAAGCGGAAACAGCGCGCTCAATGCGCT  
CAGCGCGGCTTTGCGTTTGACTTGCCTGTTTGAAGTTTGTCTGCTGTGCGCTTCCATAAGATTGGGTTCCGAATTTCTGATTTTCAT

## SEQ ID 410

GRGLPEDFIDRPFIDRPGVTFPHRQCTRRP\*NRACCGSLHFNHRQTDQRMNPVHFAVQHDTDGDLHFNFPVRCVLRNQRKRAARTCRKPCHPAAINNLFAVQIGHQLGRSLDFH  
MPQLRLFKIGIHPHQRHHRHRRACRHLPLDLHRLHLTVRRADLRPFKVPQPRIFQPADCLNLRFLAQRNLSAQSRACRRFPFRQSRNRLRLRHRCTGVCQLFGGHRTRFRQSGP  
AA\*IILRARQIRTAQGNLRLPRLSGGILPAVLAHRLNLVFCPLVSQHI IIVIQRHQVAFPHGIRIVQNLPHRAALLRRLNLHNSGNISVFRFLVLP\*KKRRSGCGGKREBQRQCR  
QAAPADLRVLKFCFVVRPHKIGFRIS\*PH

## SEQ ID 411

TTGCATGATTCTCCGGCGGTGTCCCGCGGATGCCGTGTGCGGCTTTTAAAGCGCGCGCGGATGGCAGGCTGCCAGCATCAGGCGCGCGGAGATGATGAGGATTTTTATGTCG  
GATGTCCTTGTGTTGCTGTGGAAATCATTGCCATTTTACAG

## SEQ ID 412

LHDSFAGVPADAVCAFLSARPDWQAASIRAAESMRIFYGCPCLLWELIAIVQ

## SEQ ID 413

ATGAAATTAATGATTTTGAAGGAATTAGTTAAATAGTCTCGATAAAGATGAGTTGTATATTTCAAGCAATTGTAGGAGAAATTTATTCAGGCGTATGCGGTGATGTAGAGATT  
TTGAGATAATTCATGGTGTGAAAAAATAAGTCTCTTTTGGATAAAGAACTTAAAAAATATATGATCTTGGGATAAATGT

## SEQ ID 414

MKLIDFEGNLVKISLDKDELYIIQAIVGEIYSGVCVDCRDFEIHGVEKNKVLILLDKELKKIYDTWDC

## SEQ ID 415

ATGAGATTAAATTAATAAATTTATGATTGTTCTGACTTTGATTGGAAGATTTCACAAAGCAAGTTAGAAAAATTTGTATATTTTGACATTATCAATAGGTTTGTGAAAGTAATG  
GTGCTGATTATTTTATGTTTATATATATAGCACCGAATGGTACTTTCAAATATACATAGACCGATGTCATTAAAAAACTCAATTTGTACAAACCGTTTAAATTTGAACACATATTA  
ATTGATAAATGATATATGGAATATGTAATTAACGCTCGAAGATACTATATCAATTTGGCAAAATATTTGACTGGGAATTTGACGATTATAATCTAAATATCCAGAC

## SEQ ID 416

MRLKLKNYDCSDFDLEFPQDKLENFCILLFLSIGFDESNGADYFVYIYSTEWLLSNHRPMSLKNSTVNFNIEHLKLLINDILEICNSTSEDKSISNLAKYFDWFDYDNLNIQD

## SEQ ID 417

ATGGCACTCGACAATATCGGCCCAACAGAAAAAATCACAATTTGCAACTACAGGTATTCAAGCAAAATTTGAAACTTATACATTGATTCAATGAAAAAGAAATAAATTAATAA  
TGGACATT

## SEQ ID 418

MALDNIHQQKKNNHLLQVFKIILKILLIQMKKEIKLEMDI

## SEQ ID 419

TTGCTGCAAAATCCCATTAGTCATGCGAACGGTTTGGATGCCCGTTTGGCGGATGATATCGAGGCAAAACACTACGAACCGGGTGCAAAATACCATCTGTTTGGTAATGCTCGGGCAGTG  
TTAAAAATCGGGTTTGGCGCGTCCAAACATTTGATGCAACTGCGGTCGCGCCATCTACTGCTATTACACACGACGACAGGATTGGAAGGTGTTATCGGCTATGAAACCCATTTTCAGG  
ACACGGACACGAAGTACACAGTCCGTTTCGATAATCATGATTCAAAAAGCACTTCTGATTTCAGCGGCGCGGTAGACGCGCGTTTACCCTTTACCAACTTCATCGGACAGGGTCGGAAATA  
CATCCCGCAGACGGATATGACGGGCTCAAGCGCGCGTTATCCGGAACCAAGGGGCAAGGGATATATACAGCTACCATATCAAGGAACCTCAACCAAAACAAAGATAAACACTGTTTC  
CGCAAGCCCCCTTTTTCAGACCGCTGGCTAAAGAAATGCCGCTGCCGCTTCCGTTTCTCAGCGCTGCGGATGAAGCAGGAAACTGATATGGGAAACGACCCCGATAAAATTTGGCG  
GGCTAACCGTATGGATGATTTTCGCGGATCTGCCAAGTGGCGTTAATCTTTTAAACGGTTTTCAGGGGTAGGGATTGGGCAATTACAGACAGTCCGCTAAGCCCGCTCAGGAT  
ACAGCGCTCAGCAGACTTACAAGTATTAATGATTAGGAATTTAAGTCCGAAGCACAACTTTCGCGCGCGGAGCTATTACAGGACAGTCCCTTTTGGCGTAAAGACCGCATCAAT  
CCGCCAGACAAATGGCGCTGATGCCCATCCGAATATAACAGCAACAGCCCAAACTGCCCTTTCGCGTACGAGAGCGCGGATGAGGTTTGGCGCGTAAAAAGTAGAACTTAAACCGACCAA  
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AATGCTGCAACCTATCTAAGTTGGTTAATCAGCTAAATGAGCAAACTTAAATTAACATTGCGGCTCAAGATCAAGATTGAGTCTAGCTATTCATGAGGTTAAAAAATTTTCCATAG  
GAATGCAACTTATGAAAGAGCAGATAGACTAGTAAATTTGGGTTGGTGGAGGTGCAAGACAACTAGTGGAGGCGGATGTTAAGTAGAGATGGCACTCGACAAATATCGGCCCAAC  
AGAAAAAATCACAATTTGCAACTACAGGTATTCAAGCAAAATTTGAACTTATACATTGATTCAATGAAAAAGAAATAAATTAATAATGAG

## SEQ ID 420

LLQIPISHANGLDARLRDMQAKHYEPGGKYHLFGNARGSVKNRVCVQTFDQATVGPILPITHERTGFEGVIGYETHFSGHGHEVHSPFDNHSKSTSDFSGGVDGGFTVYQLHRTGSEI  
HPADGYDGPQGGYPEPQCARDIYSYHIKGTSTKTKINTVQAPFSDRWLKNAGAAAGFLSRADEAGKLIWZDDPKNWRANRMDIRGIVQAVNPFLTGFQGVGIGAITDSAVSPVTD  
TAAQQTLOGINDLGLSPEALAAASLLQDSAPAVKDGINSKQWADAHNPNTATATQALAVAEAGTVWGGKVELNPTKWDVWNTGYKTPAARHMQTVGEMAGGNRPKSIITSGKA  
NAATYFKLVNQLNEQNLNLAQDPRLSLAHEGKKNPIGTATYEEADRLKIVVGEARQTSGGGWSLSDGTQYRPPTEKRSQFATTGQANFETTTIDSEKRNKIKNHLNIR

## SEQ ID 421

TTGATTCACTGCCATAACCGCTTCTGCCAAGGAAAAAATGAATTTGCCATTCAAAATTCATGATGCTGTTGCGAGCGCAATATCGTTGCTGCAATCCCAT



## SEQ ID 422

LHFAITACCQKQNEPAYSKIHDAVCSGNIVAANPH

## SEQ ID 423

ATGCGGGCACGGTCTGATACCTATTCTTTTTCAGTTTATTTTATCCGCTCGGGACACTGACAGGTATTCATCGCATGGCGGAGGCAACGCTTCGCGGTGCAACAAGAACTTG  
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CTACTCCATTGATGACATGATTCGCGCGGAATACATAAACAGCCCTGCGGTCCGACCGGATTACCTTATCCGCTTACGAAACCACCGCTGAAACAACATCAGGCGGTTTGACGGGTTTA  
ACCATTCTTTATCTACACTTAATGCCCTTGCACCTCTCGCGCACCCAAATCAGACGGTAGCGGAAGTAGGAGCAGTCTGGGCTTAAATATTGGCGGGATGGGGGATTATCGAAATGAACCT  
TGACGACCAACCCCGCGGACACTGCTTTCTTCCCACTGGTGACAGCGGATTTTCTCGCGCGCATAGACGTTGTTCTCTGCGCAATGCGGATACAGATGTGTTTATTAACATCGA  
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CCAAAAACCAATGCGTTTGAAGTGCCTATAAAGAAATACGCAATTGTGGATGGGCGGTATAAAGTAAGCAAGGAATCAAACCGACGGAAGGATTGATGTCGATTTCGCGATATCC  
AACCATACGCAATCATACGGTAACTCCGCCCATCCGTAGAGGCTGATAACAGTCTAGGGGTATGATACAGCATGAAGCAGTCCGACACATAGACAAGGCAACCT

## SEQ ID 424

HRARLLIPILFSVFLSACOTLIGIPSHGGKRFAVEQELVAASARAANKMDLQALHGRKVALYIATMGDQSGSLTGGYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTGL  
TTSLSLWAPALSRQSDSGSSSLGLNIGMGDYRNETLTTPRDTAFSLHLVQTVFPLRGIDVVSANADTVFINDVPGTIRNRTEMHLYNAELFKAQTKLEYFAVDRINKLLIK  
PKTNAFEAAIKENYALMNGPYKVSGLKPTGELMVFSDIQPYGNHTGNSAPSVEADNSHBTGYSEDAVRHQQQP

## SEQ ID 425

TTGATGATTGACATAGGGTCCGAGATATAGTCGATATGGGCTTCAGACAGCCATTATTATATGAGATTATAGTGGATTAAATTTACAATT

## SEQ ID 426

LMIDHRVGRYSRINASDShLLYGDYSGNLQF

## SEQ ID 427

TTGGAATCAGGGATTCCCGTCAGCTTCGCGCGCGCGTACCGGTGCAACCGCAGGAATCTAGTTACACGGCAAGCGGCAACCGCATTGGCAATCCGATCCGAGGCTCGCAACAG  
CCCTAATCAATGCCGCCGCAATTCAGCAGACCGCGGCAACTCGCGCGCGCAGTGTACCGGCTTCACAGCTACTTTGGCAAGCAATCGTCGCAAGCGGCAATACGACTGTCA  
GGCAGGTTCGTTCCACGTCCGCGCGGTATGCGCGCAATGCTGCGT

## SEQ ID 428

LESIGIPVSPGGVPVANGRLNLTQQAANGIGKSDSEACEHALINAARKFQQTAGKLGGRSVTGFHSYFGKQSLQGGYDCQAGSFHVRAVMRANVVR

## SEQ ID 429

ATGGTCAATCATCAATCAGCAGTGGACAGTGTGCTTCTGCTTCGCCGTAATGACCGGTTTGGCGGATGCCGAAGACGAGCATTTAGAGCTTGGCTTCGCGGCGAG  
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CAATATTTGAATGGCTTTAGGACGGCGTAAGTTTCAGCGATTGTGCTGATAGACAGTCCGAGTTGTAGCGCGCTTTGATGCCCAAGGTTTCAATGCGTCTTTGAGTCCCAAGCGGTT  
ATCAGGTCGCCATCATGCCCATGTAGTCGCGCAGTGGCGCGGTCCATGCTGCTGCTTGTGCGAGATACGCCCGGAAATGTTACCGCGCGGCAACGATACCGACTTGCACACCCATT  
TCAGATTTCGGCAATTTCCGCCGACAGTTTGAACAATGGTATCGTGATTGATGCCGAACGGATCGGAACCCATCAGGGATTTCGCCGAGAGTTTCAG

## SEQ ID 430

MVHQSAVDQCAFPVAGNDAPERALPGDAEDDIELFAABGKGRVHDFEVPFIQGFVKSNGFVACGGRVFFVCGVHAVDVGGFEHVAHVHFAAQCAGSVGREERTTGTGGENHDFAPF  
QILNGFRITGVFSDDLHRQCGLYARFDAQGFKCVFECQGVHGRHHAHVVGSAVHAACLCRYAAENVTAADNDTDLHTEHDFGNFADSLNNGIVDAERIGTHQGFAGFQ

## SEQ ID 431

ATGACACAGCAATCAATAACAACCGCTATTACTGAACTCTCCGGCGAATCCCTGATGGGTTCGATCCGTTCGCGCATCAATCAGGATACCATTTGTTCAAACTGTGCGCGAAATTCGCG  
AAATCGTGAATAATGGGTGTGCAAGTCGATATCTGTCGCGCGCGTAACATTTTCCGCGCGGTATCTGCACAAGCAGGACGATGGACCGCGCACTGCCGACTACATGGGCAATGATGGC  
GACCGTGATGAACCGCTTGGCACTCAAGACGCAATTTGAAACCTTGGGCATCAAGCGCGGTACAATCCGCACTGTCTATGACGCAAAATCGCTGAACTTACGCGCGCTCTAAAGCCATT  
CAATATTTGAAGAAGGCAAGTCGTGATTTTCGCGCGCGGTACCGGTAATCCGTCTTCACGACCGACACTGCGCGCGCATTCGCGCGCGGAAATGAAGTCGACGTGATGCTCAAAG  
CCACCAAGCTTCGACCGCGGTGACACCGCAGACCCGAAAAAGACCCGTCGCCACACGCTACGAAACCATTAATTTTGACGAAGCCTTGAAATAAAACCTCAAGATCATGGACCGGACCGC  
CTTTGCCCTTCGCGGACGCAAGCTCAATATCGTCGTCTTCGGCATCGCAACAAAGGCTCGCTCAACCGCTCATACCGCGCAAGACGAGGCACTGTGCCACTGCT

## SEQ ID 432

MTQQLKYRVLKLSGESLMSDPPGINHDTIVQTVGEIAETVKGVQVGVIVGGNIFRGVSAQAGSMDRATADYMGMMATVMNALALKDAFETLGKARVQSALSMQQAETIYARFKAI  
QYLEEGKVVIPAAGTGNFFTTDTAAALGAEMNCVMLKATNVDGVYADPKKPSATRYETITFDEALNKNLKVMDATAPALCRERKINIVVFGIAKQSGSLKRVITGEDBOTLVHC

## SEQ ID 433

TTGCTGTGTCATGGGATACCTTGCTTTCTGAAATGTCGTGCGTGGAGTGGGACGTCTGAATTTCAATGTCGGATTACAATGATATGGTGTGCTTCTATTATGTTTGTGTTTCAG  
ACGGGCTTTATATTCGTCGCT

## SEQ ID 434

LICHGIPCFLECRRELGRINPKNSDYNMVCRSIIVLFSGLYIRSS

## SEQ ID 435

GTGGAAATCCTTTCCGTATTTCCTCAAAATCTAGGAGATTCAAAATGGCAGAAATTAATGCAAAAATGGTTGCCGACCTGCGCGCCCTACCGGCTGGGTATGATGGAATGCAAAAAG  
CCTTGGTTGAAGCTGAAGCAACTTCGACAAAGCCGAAGAAATCTGCGTATTAAATCCGGTGGCAAGCGGCAAACTGGCTGGCGCTACTGCTGCCGAAGCGCTATTGGCTTATGCAAT  
CAACGGTAATGTCGCGCATGCTGCAAGTAACTGCGAAACCGACTTCGTGCTAAAGACCGCGCTCTGTAAGATTTGCCAACTTCGTTGCGCAAACTGCTGCCGAGAAAAACCGGCT  
TCTGTTGAAGAAGTGAAGCACTGAGCGAAGTGAATCAGAACGCAAGCCATCATCGCTAAATTTGGGCGGAGAACATGTCTGTCGCGCGCTTCCAAGTATGACACTGCCAACCAACTGGTTCCT  
ACATCCACGCGCATTTGGCAGCCGAGCGCTTTTGTGAGTACAAAGCGCTCAAGATGTAGCAGCGCAAAATCGGTATGCACATCGTTGCCGCCAAACCGCAATGCGTAAGCGAAGCGG  
AGTAGAGTCTGAACCGTTGAAAGAAGACGCCACATCTACACCGAGCAAGCCATCGCTTCCGCAAACTGCCGACATCGCGCTAAATGGTTGAAGCGGTATCCGCAAAATCTTGGCT  
GAAATCACTCTGAACCGCAAGCATTCGTGATGAACCTGACCAACTGTGCGCAATTCGCTAAAGAAACGACACTGAAGTGGTTAGCTTCACTCCGCTACAAAGTAGCGGACGGTATCG  
AGAAGCCGTTGTGACATGCGACCGCAAGTAGCCGACCGCCAAAGTG

## SEQ ID 436

VENPFRISQSRFPKAEITAKMVADLRAATGLMMECKKALVEAGNFDKAEILIRIKSGAKAGLGRTAABGVLAIVAINGNVGALEVNCEPDFVAKDAGFVEFANFVAKTAAEKKPA  
SVEELSELVESERKAILAKLGENMSVRRFQVIDTANQLVAYIHGALATEGVLVEYKGSSEVDARKIGHIIVAAKPCVSEAVDAETVEKERHIYEQALASGKPADIAAKMVEGRIRKFLA  
BITLNGQAFVMPNDQTVAQPAKENDTEVVSPFIRYKVGDIKAVVDYAAEVAANAAY

## SEQ ID 437

ATGCTCTAAATTAATCTGCGTCAGATGATGAAGCCGGTGTTCACCTTCGGTCAACAAACCGGTTCTTGGAAACCGGAAATGGCTCAATACATTTTCGCGCGCGCAACAAATCCATATCG  
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CGAAGAAGCAGCCCGCGCGGTATGCTTTCGTCGACCAACCGCTGGTGGGCGGTATGCTGACCAACTACAAACCGGTTAAGCAATCCATCAACCGCTGGAAGAAAAACCGCAGCCTTG  
GAAATGCTGCGCAAGCGGTTTCAGCAAAAAGAAATTCGGAATGCAACCGCAGCTTGAAACCTGCAACCGCTCTTTGGGCGGTATCAAAACATGAAGCGCTCCCGCAGCGCAATT

TCGTTATCGATACCGGCTACCAAAAGGTACTTTGGTTGAGGCTGAAAACTGGGCATCCCGGTTATCGCCGTAGTCGATACCAACACAGCCAGAGCGGCTGAAATACGTCATCCCGG  
CAACGACGACTCCGCGCAAGCCATCCGCTGACTGCGAGGCATCGCGAGCGAGTTTGGAGGGCAAAACCAAGCGCTGCAAGAAACCGTAGCCGTCGCCAAGAAACCGCTGCGAG

## SEQ ID 438

MSQITWRQMEAGVHGHQTRFWNPKMAQYIFGARNKIHVLEKTLPMFQEAQZAVRRLVANKGTFLVGTGRQARDIIREBATRAGMPFVDRNLGGNL/TNYKTVKQSTIKRLEKTAAL  
ENAAESGFSKRELEMQRDVEKLESLGGIKNMKLPDAIFVIDTGYQKGLTVEAKLGPVLAUVVDTNNSPDGVKYVIFGNDDSAKAIRLYCRGIADAVLEGNQALQETVAAAQETAEE

## SEQ ID 439

TTGGGACGGGCTACGGTTTCTTCGAGCGCTTGGTTTTGCCCTTCCAAAACTGCGTCGGCGATGCCCTCGCAGTACAGCGGATGGCTTTGGCGAGTCTGCTTCCCGGGATGACGTAT  
TTCACGCGCTCTGGGCTGTGTGGTATCGACTACGGCGATAACGGGGATGCCAGTTTTCAGGCTCAACCAAGTACCTTTTGGTAGCCGATCGATAACGAAAAATCCGCTCGGGCA  
GGCCTTTCATGTTTTCGATACCGCCCAAGAGCGTTCAGTTTTTCAACGTGCGGTGCAATTTCCAGAAATTTCTTTTGTCTGAAACCGCTTTTCGCGAGCATTTTCCAGGCTCGGGTTT  
TCTTCCAGCGGTTTGTAGGATTGCTTAAACGGTTTTGTAGTTGGTCAGCATACCGCCCAACAGCGGTGGTGGACGAAAGCATACCGCGCGGGTCTCTTCGCGGATGATGTCGGT  
GCTGGGCTTTGGTACCTACGAACAATACCGTACCTTTTGTGGCAACGACGAGTACGGCTTCTTGGCCCTCTTGGAAACATCGCGCAGGGTTTTTCCAAAGTTACGATATGGATTTTGT  
TGGCGCCGCCAAAAATGATTTAGACCAATTTTCGGGTTCAGAAACGGGTTTGGTGACCGAAGTGAACACCGGCTTCAATCATCTGACGCGATAGTAATTTGAGACATGTTATTTCTTGAAA  
GGGTAAAGAGCACACATTCATTCGCA

## SEQ ID 440

LGSGYGLQRLVFPQNCVGDAVAQADGPGVVVAGDDVFAVNAVVGIDYDNGDAQFFSLNQSTFLVAGIDNENRVQAAPHVFDTAQRAFQFFNVALHFQNFPPAETAPGSIPOGCGF  
FPQAFDGLINGFVVGQHTAQPAVVERHTGAGRFPADDAVACLAFTYEQYRTFVGNQTYTGYLRLLEHRQGFQVYDNDFFVAAENVLSHFVPETGLVTEVNTGFNHLTHSNLRHVLSLR  
GLKSTHSA

## SEQ ID 441

ATGTGGCAGCATCTGCCCATCGGCTATCTTTTGTGTCCGTTATGTATTCGCCCGCGCAGCCGAGTATTGCGCGCGCTTTGATTATTTGGTTTTTGGGTGGTTCTGCCACCGTGTTCA  
CGGTCTTCCCGTAACGCTCCGCCCGCAACCGCTGATGGGCGACGAGAACAGGAGAAATCCGAACAGCAGCGCCCAACGCGCAAAAGACAGCGGCACAAACCC

## SEQ ID 442

MHHIVAIGYLFVAVMYSAAQPSIARALTYLVFVVVLPVTFVAVTVRRNRRLMGQQEQAESBQRAQRQDSGTRP

## SEQ ID 443

TTGTAAACATCAAAACAGGACGACACAATGTGCACATCGTCCCATCGGCTATCTTTTGTGTCCGTTATGTATTCGCGCGCAGCGGAGTATTGCGCGCGCTTTGATTATTTGGTT  
TTTTGGGTGGTTCTGCCACCGTGTTACGGTCTTCCGCCTAACCGTCCGCCCGCGCAACCGCTGATGGGCGACGAGAACAGGAGAAATCCGAACAGCAGCGGCACAAACCGCAAAAG  
ACAGCGGCACAAACCTGAATCCCTTTTCAGACGGCATCTTATCCGCTATAATCCGTCAGTTTTCATTTTCGAAACACACTATTTT

## SEQ ID 444

LLTFKQDAHVHRRHLSFCCRYVFRRAEYCARFDLPGFLGSAHRVHGLRNRNPPQPDPGAAGTGRIRTAARTTAKRQRHKTLPNPSDGLSALTQPSISETHYF

## SEQ ID 445

TTGTGTGCGTCTGTTTGAATGTTAACAATACTGTTATAATCGCAACATCTTACCGCAATCTGAAAGCGGCTGAAATGAGGAACGAGGAAAAACGCGCCCTCGCCGCCGAATTCGCGG  
GGCGGCTTCGCAAAATGGGCGGACGTGCGGGCGCGCGCGGTAATAATCAACCGCTGCTCAACGTTATATCAAGCGCGCTCGGAAAAACGCGGTGATTGCGCGATGGGCAAGGA  
ATTGCGTTTGGCGCGCTTTGTCCGCGCGCGCAAAACGCGCGCAAACTCTATCTGCTTATATCGAACCGCACACGCGCGGATGTGGTTTACCGCGTATCTGAACCGGAAATGGAA  
CGGGAACGCAAGCGCGGTAGGCGGAAGCTGCATGTCCCTCAGTTTTCAGGCGCGCAAAATCCGCGTGACAGGTTTTCGCTATGCTCTGCTCCGCTGTGTCGCGCATAGACCGGAGGCTTACC  
GTTTGGGCGAGCAGCGCGCTATTACGATGCGACGCTTTCCGCGATGAATAACCGTTTCAGCGCGAAAAACCGTGGCGTGGGCTTTGCTGCCAGTTGGTGGACAGGCTCCACGCGAGGC  
GCACGACCTGCGCGCTGACGCTTTGTATCGGAAGCGGGGATATTGTGTTTT

## SEQ ID 446

LCASCLNVNKIVIATFYRNPERSMRNEEKRALRRELRRRSQMRDVRAAAIVKINRLKRYIKRGRKIGVYWPFGKELRLGGFVRAAQKRAKLYLPYIEPHTRRMFTFVPERGME  
RERKRGRAKLVHPQFAGRKIRVHGLSVLLVPLVGLDREGYRLQAGGYDATALSANKYRLQAKTVGVGFACQLVDRLPREAHDLPDGFVSEAGILCF

## SEQ ID 447

AGTCAGTATTTAGATGCAATATTCAAAAAACAACGCTTCAGTGCCAAAACGAAAAATATATTTCGTTTATATATGACATGGCAACACCGCGCGCCGACCAT

## SEQ ID 448

SQYFRNIQKTHQVAKIKIYFYI\*HGKHRRPH

## SEQ ID 449

ATGCCGCTCGAACCGCTAAAAACACAATATCCCGCTTCCGATACAAAAACCGTCCAGCGGAGGTGCTGCGCTCCGCTGGGAGGCTGTCCACCAACTGGCAGGCAAGGCCACGCCCAAG  
GTTTTCGCTCGAACCGGATTTTCATCGCGAAAGCGTCCGATCGTAATAGCGCGCTGCTGCCCCAAACGGTAGCTTCGCGGTCTATGCGGACAAAGCGGAGCAGCAATACCGACAAC  
CGTCACGCGGATTTTCCGCTCGAACTGAGGGACATCGAGCTTCCGCTTACCGCGCTTCCGTTCCATTCGCGGTTACAGGATACGGGTAACCAATCCGCGCGGTGTGCGG  
TTCGATATAAGCGAGATPACAGTTTTCGCGCGCGGTTTTCGCGCGCGGACAAAGCGGCAAAACGCAATTCCTTTCGCGCATCGGCAATACACGCGGATTTTCGACCGCGCTTGATATAA  
CGTTTACGAGCGGTTGATTTTACCGCGCGCGCGCGCGCGCACGTCGCCGCCCATTTTGGCAACGCGCGCGCAATTCGCGCGCAGGCGGCTTTTCTCGTTCTCATTTTCAGACG  
GCTTTTCAGGATTCGCGTAGAATGTGCGATTATAACGATTTTGTAAACATTCAACAGGACGACACATAATGCGCATCTGCGCCATCGGCTATCTTTTGTGCGGTTATGATTTCCG  
CGCGCAGCGGATTTGCGCGCGCTT

## SEQ ID 450

MPSERLKHTQYPRFYKTVQRQVRLAWEPVHQLAGKAHAGFRLQTVFRRKRRIVLAACLPTVFAFVADXRDEQYRQTVHADFPCKLRDMQLRPTALAPPFHSAFRIIRKPHPRVR  
FDIRQIEFCAFLRRADKAQQTPLAHRPIHADFTALDITFEQAVDPYRRRRPHVPHLRTPAQFAAQGAFFLVPHFRFPRIAVECCDYNDFVNIQTGRTQCGTSSPSAIFLLPLCIP  
PRSRVLRAI

## SEQ ID 451

GTGTTTTAGCGTTTCAGACGGCATTTCCGGCGGAAATGCCGCTGAAGCGGGAATATGGGAGAAAAGGATGTCGGAAAGGATAATCTGCCGTTTTCCTCAFTGGGCGCGGTACGGTTC  
GAACCGTTGATGTGATCA

## SEQ ID 452

VFLAVQTAFAEMPSEGGILGEKDVGLWTAGFVIGRETFTVFGCAS

## SEQ ID 453

ATGATTTTGAACAGGTGTTTATCCGTTTCCGCCGTGCCGATGCCCATACCATGTGAATCCGATATCCAAACCGGAAATCTCGGTTTCAAAA

## SEQ ID 454

MLQQVPIRPRADAAYHVNPISKRGICGSK

## SEQ ID 455

TTGATGTGATCATGAACCGGTTTTCGCGAGGCGGTTTCGATGGGAGGTTTGAAGCTGGGGTAACGTCGCGGCCCATCCGATAGGCTGGCAGACTATATCGGGACAGCATTTGG  
CAACGCGTTTGGCGTTTTCGCTTGTGATGAAGAGCGGACAGGTTGTCGGGACAAACCGGCTATTATCATTTTGAACCGCAGATTCCGCTTGGATATCGGATTCACATGTTATGGG  
ATCGGACCGCGGAAACGATAAACACCTGTTGCAAAATCATGCTGTGGATTACGATTTGATGTTTGGTTTGTCTGTGCGCGGATGGCGCAGGATATTCGAACTTGCCTCGCAA

CGTGCCATCGAACGGCTGGGCGCGGAAAAAGACGGCGTGTGGTATGCATATGCTCCGTAAAGACGGCAGTGTGGCGATACGGTTGTGTACAGTATGCTGAGGGAAGATTGGTGCAAAA  
ACAGGGAATCTGACGGCGAGGTTGGCAGGGTATGGCGTGCAGGTG

**SEQ ID 456**

LDVHETGLREAVDCGEVWKLGVTSAPHPDRVADYIGTALATRLAFVDEADRVVGTAYYHFEPQIPRLDIGFTWYAASARRKRINTCKIMLLDYAFDVLVCCAGWRTDILNLSQ  
RAIERLGAEKDGLVRMHLRKDGSRDFTVYSMLREDWCKNRELLTGLRAGYGVQV

**SEQ ID 457**

TTGTGACATATCGCGTTAAAGTTTAAATTTGAGAFACTGCCTCACACCTGCACGCATACCTGCGAACCTGCCGGTCAGGATTTCCCTGTTTTGCACCAATCTTCCCTCAGCATA  
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TGGCCATCCCGCGCAACAGCAAAACCAAAACATCAATCGGTAATCCAACAGCATGATTTGCAACAGGTGTTATCGGTTTCCGGCGTCCGATCGCGCATACCATGTGAATCCGATATC  
CAACCGCGGAATCTCGCGTTCAAAATGATAATACGCCGTTGTCCCGACCACTGTCGCCCTCTTCAATGCACAACCGCAACGCAACGCAACGCGTTGCCAATGCTGTCCCGATATAGTCTGCC  
ACCTATCCGGATGGGGCGCGGAGTTACCCAGCTTCCAACTCCCATCGCAACCGCGTCCGCGCAACCGGTTTCATGATGCACATCCAAAGGTTGCAACCGTACGCCGCCAA

**SEQ ID 458**

LSAYRVKFPKFWYASHLHAIPQAPAGQDFVPFAPIFPQHTVHNRIATVFTZHMHTQHAVFPFRAQPFDTGLRGKVQNIAPSRATANQNIKCVIQHDFATGVYPPFPCRCRIPCESDI  
QTRNLRFKMLIRRCPDHVRFLIDNRKRTQCCPDIVCHPIRMGRGRYPQLPNLPIANRLAQTRFMHIIQRFEPYAAQ

**SEQ ID 459**

GTGAATGTAGTGGATTTTACTGGGAAATGCAAGTTTTCTGTGCCGCCCAAGCCGGGAAGTGGCAACAAAAATAAAATAGTTATTATCTATATATCAAAATTTTAATAGACA  
AAAAATCAAAATGTTTATATAT

**SEQ ID 460**

VNVDFTGKCKVFLSPAKPGNCEKKNKNSYLSIYIKFLIDKSKLFIY

**SEQ ID 461**

GTGCTCGGACACACACATTGCCGGTTTCCCTGCTTTTGGCATTGAGCGTTGTAGTACGGCAATAACCATAGGGCAGAAGATGCTGTTTTTAGGAGTAAACCATGCG

**SEQ ID 462**

VLGHTFLPVSPAFAIQAFVVRQITIRAEADACFLGVNHG

**SEQ ID 463**

ATGGCTGAAGCGACAGAGTGTCTTGGTGGGCGCGGCATTATGAGCGGACCTTTGGGCTTTTGTCTAAAGAACTCGAACCGTCTTGGGAAATCACCTGATTGAACGCTTGGAGATG  
TGGCGTTGGAATCGTCAAAACCGCTGGAACAACCGCGGACGCGGCATTTCGCGCTGTGCGAATTGAACTATGCGCGCTGGGTGGGACGCGGTCATCAATCCGGCGCGCGCTGAATAT  
TGGCAACAGTTCATGTGACGCGCAGTTTGGGCGGACGCTGGTTCGCGGAAGGCAAGTTGGAAGACAATTCCTTCATCAATGCCGTGCCGATATGCTTTGGTGTGAACGAAGACAC  
TGGCGTTACCTGCAAAACCGCTATGATGTGTTTAAACGCGAGAACTTTTGAATAATGGAATTTCCACCGATCGGAACAAAATTTCCGATTTGGGCTCCGCTGATTATGCGCGCGCGG  
ACGAAAGCAACCGCTGCGCGCAACTATTCGCGGAGCGACGATGTCGATTTGCGACGCTGACGCCAGATGTTGAAATATTTGCAAGGCAAGGCGTAAAAACCGAGTTCAACCG  
CCAGTTCGAAGACATCAAAACCGAATCCGACGCGCGTGGTGTCTAAACCGCGGTACCCGCAACCCAGACTGGCAGCTCACCTCCGCAACCGCTTCTCTCTCGCGCGCGCGCGC  
GGCGCACTGACCTGTCTGCAAAATCCGCGCATCCCGAAGGCAAGGCTACGCGCGCTTACCGGTGTCGCGCTGTTCTTCCGCAACAGCAACCCGAAACCGCGCAACACCAACGCCA  
AAGTGTACGGGACGCTTCCGTGCGCGCGCGCGGATGTCGCTCCCGCACTCGACACAGCAACGCTAGACGGCAACGACACCTTATGTTTGGTCTTACGAGGTTTCCGTTCCAACTT  
CCTCAAGCAAGGCTCGTTTATGGAATTTGCCGCTGTCCATCCTATGAGCAACCTCTATCTATGCTGCGCGCGCGCTGGGCAATATGCCCTGACCAAAATACCTGCGCGCAATTTGGT  
AAAACCAAGAGAACGCTTTGCCCTCCCTGCTGGAATACTACCCGAGGCAACCCGAGCACTGGGAATCATCACCGCAGGCAACCGCTTCAAAATCATTAAGAGATCCGAAAG  
CGCGCTGTGTCAGTTTGGTACGGAGATTGTGCGCCACGCGGACGCTGCTGCGCGCATGCTGGGAGCGTGGGAGCGTGGCGCGCATCGACCGCTGTGCGCTGATGATCGCGCTGATGACCA  
ATGCTTCCCGAGCGCGCGCTCTTGGGAGGTGCTGAAAGAGCTGTTACCGGTTACGCGCATCAAGTTGAACGAAACCTCGAAAGGCGGATGAATATATCGCTATACCGCGAA  
GTGTTGGATAT

**SEQ ID 464**

MAEATDVVLVGGGINSATLGVLLKELEPSWEITLIERLEDALESSNAWNAGTGHSALELNYAFLGADGVINPARALNIAEQFHVSQFQWATLVAEGKLEDNSFINAVPHMSLVNNEH  
CRYLQKRYDVFTQKLFENMEFSTDRNKISDWAPLIMRGRDENQPVAAANYSAEGTDVDFRLTRQMVKYLQSGVKTEFNRHVEDIKRESGAWVLKATDENPDWQLTLRLTRFLPLGAGG  
GALTLQKSGIPBGKYGGLPVSGLFFRNSNPETAQHNKAVYQASVGAAPMSVPHLDRNVDKRRHLMFPGPYAGFRSNFLKQGSFMDLPLSHMDNLYPHLRAGWANNPLTKYLLGELR  
RTKEERFASLLLEYTPANPDWELITAGQRVQIIRKDSKGVLPFGTEIWAHAGDSLALLGASPGASTAVPLMTRIAHQCFPERAPSWEGRLKELVPGYGIKLNENPERADEIAYTAK  
VLDT

**SEQ ID 465**

ATGGCAACACCGCGCGCCGACCATGCGCGTCTGAAGAAAATACACAAATACCGCGCTTATATACAAATCGCGCGCGCGTTCGAAACCTCCACAC

**SEQ ID 466**

MAHTAARTMPSENYNTAAAYITIAAPWFENLPH

**SEQ ID 467**

ATGACCAATTCATTTTCGTAACCGCGCGGCTGTGCTCTCTACTGGGTAAAGGTATCGCGCGCTTCTATTTGCCGCTCTCGAATCGCGCGCTTGAAGTTACCATGCTCAAGCTTG  
ATCCCTATATCAACGTCGATCCCGCACGATGAGCCGTTCCAAACCGCGGAGGTGTTCTGTAACCGACGCGCGGAAACCGACCTCGACTGGGACACTACGAACGTTTCAATCGATT  
CAGCATGACCCCGCGCAACAGCTTCAGCACGGGTGAGGTGACGAAACGTTATCGCCAAAGAACCGCGCGGCTATCTCGCGGTACGGTTCAAGTCATCCGACATACCGACGAA  
ATCAACGACGCTACCAAGGCGCGCGGTTACGATGTGGGATTTGTCGAAATCGCGGTACGCTCGCGACATCGAATCGCTGCGCTTTTGAAGCCATCCCGAGATCGGAAGCC  
AGTTGGGACGCAACACCTGTTGCCCACTTGAGCTACGTTCCCTACATCGCGCGCGGAGGAAATCAAAACCAAGCGACCCAGCACACCGTGAAAGAAATGTTGAGCATCGGCTT  
GCAACCGGACATCTGATTTGCCGTATGGACAGGAAATGCCGCGAGACGACGCGCAAAATCGCTTGTTCGCAACGTGGAAGAGCGCGGATTTGTCGCGAGCTACGATGTGGACAG  
ATCTACGAATGCCCGAAATGCTGCACGACCAAGGATCGCAACATCATACGAGCAGTTGACGCTTAAAGTGCAGCAGGCGGATTTGACCGCGTGAAAAAATCGTCCACGCGTCA  
AAAACCGGAAACACCGCTCAAAATCGCGATGCTGCGCAATACGTTGATTGACGAACTCTACAAATCATTTGATTGAAGCTTTGAAACACGCGGCGATCCATACCGAAACCGATGTCGA  
GATTACCTTCGTTGACAGCGGAAAGCATCGAAGAAACAGGGCGAGCTTCCGCTACTCAAGATATGGATGCCATCTCTGTTCCGCGCGCTTCGGTTCCGCGCGCTGGAAGGCAAAATC  
GCCGCGTGCCTACGCGCGTGAAGCAACGTCCTACTTGGGCTCTGCTCGGTATGCGATTTGCGCTGATTGAATACGCGCGGACGTTGGCAGGTTTGAAGGTGCGAATTCCTCTG  
AGTTGACTTGAATGCGCTGCCCGCTGCTGCCCTGATTGACGAATGGCAACCGCGGACGCGTTCGAAACCGGTGACGAATCCCGCGATTTGGCGCGCATCGCTTTGGCGCG  
GCAAGAGTCGAATTTGAAGAGGCGAGCTCGCGCTCAAAATCTACGCGAGCGGACATTCGCGAACCCACCGCCACCGCTACGAAGTCAACAACTATGTTTCCGCGTGAACAG  
GCAGGTTTGGTCATCGCGCGCTATCCCGGACGCGAAGCTTGGTGAAGACATCGAATGCGGAACCATCTTGGTTCTTCCGCTGCGAGTTCCATCCGAGTTACGTTCAACCGC  
GCAAGGCGCATCTTGTGTTACCGCGTTTGTCAAGCGCGTGAACAAATAAAAGCG

**SEQ ID 468**

MTKFIPTVGGVSSLGKGLAAASIAAILESRLNVTHLKLDPIYINVDPGTMSPPQHGVEFVTDGAEITDLGLHYERFIDSTMTRNSFSTQVYENVLAKERRGDLGGTVQVPHITDE  
IKRRIHEGAAGYDVAIVEIGGTGDISSLPLFLAIRQMSQLGRNWTLPALHSVVPYIAAAGEIKTKPYQHTVKEMLSIGLQPDILICRMDRMPADERRKIALPCNVEERATVGSYVDS  
IYECPEMLHDQIDNITTEQLQLNVQADLTAWKLIHVAKNPKHTVKLIAMVGKYVDLPESYKSLIEALKHAGIHTETDVQITFVDESIEKNKGDSVLKIMDAILVPGFGSGRVBEKI  
AAVRYARENNVPTLIGICLMQIALIYARDVAGLKGANSTFPLKCAAPVVALIDENQTDAGSVETREDSEADLGGTMRLLGAQFVELKAGSLAVKIYSGSHIRERHRYEVNNYVSALEQ  
AGLVIGGVSAGRERLVETIELPNHPWFACQPHPEFTSNPRKGHPLFTAFVKAALNNKA

## SEQ ID 469

ATGCGCTCTGAAACACCGGACAGCGCGCGTATCCCGCTGCCGCCCTGCCCTCAAACCGCGGACCGCGCGGAAACCGCGCTTTTACAACTTTATCCAAATTTCTGTTTATTCAGGATA  
CGCGACATPAGAAATGTCAAACCGTCCGAAACGGGCAAACTCCCATCTCCAAAGGAATAAAATGAACTTCTGACCAACCGCAATCTGTCTTCGCAATCGCGTCAGCAGTATGGC  
TGCTGCTGCCGCGCAGCAACACCCACCGTTGCCAAAAAACCGTCAGCTACGCTGCCAGCAAGGTAAAAAGTCAAAAGTAACTACGCGTTTAAACAAACAGGCGCTGACCCACATCGCC  
TCCGCGCTCATCAACGCGCAACGCTGCAAAATGCCCATCAATTTGGATAAATCCGACAAATATGGACACGTTCTACGGCAAGAAGCGGPTATGTCTGAGCACCAGCGCAATGGACAGCA  
AATCTTACCAGCAACGCGCTATTATGATTACCGCACCTGACAAACAACTGCTCTCAAAGACTGTTCCCCACGT

## SEQ ID 470

MPSETPDRPYPACRPLKPPNRPNPPFYKLYPISCLPQDTPTLEQTVRNQTPHPHSGIKHKLITAILSSAIALSSHAAAGTNNPFAKKTIVSYVQGGKVKVTVYGFNKQGLTTYA  
SAVINGKRVRQHPINLNDKSDNMDTFYKGGYVLSFGAMDSKSYRKQPIHITAPDNQIVFKDCSPR

## SEQ ID 471

ATGAAATATTGTGAAATATAGAAGATGTTAAAGCCATCCGTAAGAACCGGGATGAACAGATAGACTTCTGGGGCAAGGTGCGCTTACTAATCCGAGGTTACGCTACGAAACCG  
GCCGTAAAGATGCCCAACCCGTACCGCAATGCTCCGCTCGTCCATATCGAATGCTCGATTGGCAAAAGTCAACAAAAAGATATGGAATTCGCCGCTGTTGAAAAACACCATCC  
CGACTGTATGCCGAGTTGTCACAAACAGACCAAGTCCGAAAGAAAAACAAAGT

## SEQ ID 472

MKIPENIEDVKAIRKKTGMQIDFWKVGVTQSGGSRYETGRKMPKPVRELLRLVHIECLDLAKVNNKIMETAILLKKHHPDLAELSKQTKSERKQS

## SEQ ID 473

ATGCAATATAAAACAGCGCTTGACCCGCGACATACGAAAAACAAAGCAAAATCGGAATTTGCCCGCAACAGAAAACTTAAAGGAAGTTTTA

## SEQ ID 474

MQYKRLDPHYENKANRNLPRNQKRLKEVL

## SEQ ID 475

TTGTTTACGACTACCACTCAACGTCCAAAGCGGCTATCCCGCCCCCTCCACTACGGCAACCGCGCTACCCCAATCTGCTGCACCTCCGTCACCAACGTCATCTGCCACGGCATT  
CCGACGACAAGCGCTCAAGAGGTCATATCAACATCGACTCCACATCAAAAAAGAGCGTTTCACGGCGACTCCAGCGTATGTTTACCGTCGGCAAGTCTCCCCCATCGCCCA  
ACGCTGATCGAGTCAACCCACGCTTATGATGGCGGCATAGAAGCGCTCAAACTGGCGCGGCGTACGCTGCGCGCTAGGTTACGCTGCCAGAGGTTCGCGAAAATGCAAGTTATTCG  
GTTGTACAAGAAATCTCGCGACACGGCATCGGCGCGGTTTCCACGAAGCCCGCAAGTGTGCACTACGAAAAAAGGGCAGGTCCTCTTAAACCGGGTATGATTTTACCGTTCG  
AACCATGATCAACCAAGGCAACGGCACCTGCGTATCTCAACGACGCTGGACGTTGTTACCAAGACCGCTCCCTCTCCGCCAATGGGAACACGAAGTCTTGGTAACCGAAACCGG  
CTACGAATCTCACCCTCAGCCCGCCACCGGCAACCC

## SEQ ID 476

LPFTTSTSAAIIPPLHYGNPPYKSCOTSVNHIYCHGIPDDKPLKEGDIINIDLTKKDFHDSRRMFTVGKVSPIAQLRIDVTHASMMAGIEAVKPGATLGGVGYACQVVAENAGYS  
VVEFGCGHIGRFGHEAPQVLHYKKGQGPVLKPGMIFTVEPHINQKRLRLIADGWTVTVDRLSLAQWEHEVLVTFETGYEILTVSPATGPK

## SEQ ID 477

GATGCAATATTCAAAAAACACGCTTCAGGTGGCAAACTGAAATATATTTTCGTTTATATATGACATGGCAAAACACCGCGCGCCGACCATGCGCTCTGAAGAAAACACTACAAATACCG  
CCGCTTATATTACAATCGCCGCCCGTGGTTCGAAAACCTCCACAC

## SEQ ID 478

DAIFKQRFHQN\* KYISFIYIMANTAAATMPSEENYNTTAAVITIAAPHENLPH

## SEQ ID 479

GTGTTCTCCCGCTGACTTATCTGGGTGCGAAAAAGGCCAAAGACGCGCAATACACCGTTTATGAAAAACAGGGCGGGTACGCTTTGCGAAAAAGGTAAAAGATTACCGTGGCTGA  
ACAAGTCGGCTTATGTGTTGATATGTACGGCTTCTACAAACCGGCTAAAAACCTGACTTTGCGTGCAGGCGTATATAATGTGTTCAACCGCAAAATACCACTTGGGATTCCTTGGCGG  
TTTGATAGCTACAGCACCAACCGGCTCGACCGAGATGGCAAGGCTTAGACCGCTACGCGCGCTCAGGCGGTAATTACCGCGTATCGCTGGAATGGAAGTTT

## SEQ ID 480

VPSRLTYLAKKAKDAQITVYENKRGRTPLQKVKDYFWLWNSAYVFDHYGFYKPAKXN/FLRAGVYNVFNRYKTTWDSLRGLYSYSTNAVDRDGRGLDRYRASGRNVAVSLWKPF

## SEQ ID 481

ATGCGCTCTGAAACCGCTTCAGACGGCATTTGCCGACACCCCAAGCAACATCAAAATGGCAAAAAACCGAACAACCCCTCAGCGTGACCCCAAACTCTGATACCGCGCTATTGCT  
TCATCTGTATCACCGCCATTCGGCGCATTTGGCAGTAGGCATCTGTCAGCATTTCACCCGACCGCGCAAAACCCCTCCAAACCGAACCGCAACACCGACAGCCCCCGGAAACCGAATT  
CTGGCTGCCAAACGGCGCGCTCGGACAAGATGCCGCCAACCCGAACACACCGCGCGCTTCATCGAACCAGCGACAGCGGACAGGACAGAAAGCGGACAGGCTCGCGTCCCT  
CGCGACCCCAAGAAAAACCGGCTCAAAACCGCGCTTCGGATGCGCGCGCGCGAGCGATTGTTAACCGGACCGGAACACAACTGAAACACACTCAAGAAACCCCGTACTGCCCA  
CAACCGCCCCCATCCCGAAACCCGAAAGAAACACCCGAAAAACAGCGCCAAAGAAACACCAAGAAAGAAAGAACCCCAAGAAACCATACCAACCGGACACCCCGAAAAA  
CACCGCGCCCAACCCCAAGAGATTCTCGACAACTCTT

## SEQ ID 482

MPSEPPSDGIARHPKSTIKMAKPNKPFRLTPKLLIRAVLLICITAI GALAVGIVSTFNPNGDRTLQTEPQHTDSPRETFWLFNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSLPSP  
AAPKKNRVKPRPSDARAADSLTGTGTQAEVTLKETFPVLPTNAPHEPRKETPEKQAPKETPEKETPKENHTKPDTPKNTPAKPHKEILLNLFP

## SEQ ID 483

ATGAAACCCAAACACACACCGTCCGACCCCTGATGCGCGCGTCTCAGCCTTGCCCTCGCGCGCTGCTTCAGCGCAGTCTGCGCGGGGCGCGCTCGCGCAAAATCCGTCATCGAAC  
GCCGAACACCGCGCGCAACCGATGACAACGTTTATGGGTTTGGTATCGAAACACCGCGCTTCTACCTGCGCCAAACAAACAAAGGCTACACGCCCCAAATCTCCGTCGT  
CGCTACACCGCCACCTGCTGCTGCTCGGACAAGTCCGACCGGAGGCGAAAAACAGTTGCTGCGTCAGATTGCAAGTTCCGAACAGGCGCGGAGCGGTATACACTACATTAACGTC  
GCTCCCTGCGCGCAGTTCGCGGACATTCGCGCGGACACTTGGAAACAGTCCAAAGTCCGCGCCAGCTGCTGGGATCAGCCCCGCTACACAGCGCGCGTCAAAATCATTAACCTACG  
GCAATGTAACCTACGTTATGGGATCTCCACCCCGAAGAACAGGCGCAGATTACCAAAAAAGTCAGACACCGCTCGGCTACAAAAAGTCATTACCTTACAAAACTACGTCACAG  
C

## SEQ ID 484

MKPKPHVTRLIAAVLSLALGGCFSAVVGGAAVGAHSVDRRTTGAQTDINDVMALRIETARSYLQNNQTKGYTPQISVVGYNRHLLILGQVATEGEKQFVGQIARSEQAABGVNYITV  
ASLPTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTVYVSGILTPERQAQITQKVSFTVGVQKVIITLYQNYVQR

## SEQ ID 485

TTGCCAGCTCGCGCATTTTTCGATTCTTCGGGGGTTTGTATGATGATGCGGTTCAATAAGCTTCTTGGATTGCGGGTGTGCTGCGGTGCGGGTCAAAAGAGGTTGTGAGAAATCT  
CTTTATGGGTTTGGCGCGCGTGTTCCTCGGGTGTCCGTTTGGTATGGTTTCTTTTGGCGTTTCTTTTCTTTGGGTGTTTCTTTTGGGTGCGGCTGTTTTCGGGTGTTTCTTTTTCG  
GGTTTCGGATGCGGGGCTTTTGTGGGCACTACGGGGTTCTTTGAGTGTGTTTTCAGCTTGTGTTCCGCTGCGGTTAAACGAATCGGCTGCCCGGGCGCATCCGAAGGGCGCGTTTG  
ACCGGTTTCTTTGGGTGCGGAGGGAAGGAGTCCGCTGCGGCTTTCTTCTGTCGCGTCCGCTGTCGGGTTCGGATGAGGCGCGTGTGTGTTTGGGTGCGGCGCATCTTTGTC  
CGACGGCGCGTTTGGCAGCGAGAATTGCTTTCGGGGGCTGTGGTGTGTTGCGGTTTCGGTTTGGAGGGTTTGTGCGCGTTCGGGTGGAATGTCTGACGATGCTTACTGCCAATGC  
GCGATGCGGTTGATACAGATGAGCAATACGGCGGCTATCAGAGTTTGGGGTTCAGCTGAAGGTTTGTGCGTTTTCGCAATTTTGAATGTCTTTTGGGTGTCGCGCAATGCGG  
TCTGAGGCGGTTTCAGACGGCATTCGCGAGTACGCTTGAGCGTAGTTTGTGAGAGGTAATGACTTTTGTACCGCGAGGTGTGCTGACTTTTGGGTAATTCGCGCTGTCTTCG



GGGGTGAGGATGCCCATAACTAGGTTACATTGCCGTAGGTAATGATTTTGACGCGCGCTGTGTAGCGGGCTGATGCCAGCAGCGTGGCGCGGACTTTGGACGTGTTCAGTGTGCGC  
CGGCGATGTGCGCGCAGTGTGCGCGCAGGAGCGGACGGTAATGTAGTTGTATACGCTTTCGCGCGGCTGTTCGGAACGTGCAATCTGACCGACGAACTGTTTTGCGCTTCGGTGGCGAC  
TTGTCCGAGCAGCAGCAGGTGGCGGTTGTAGCCGACGACGAGATTTGGGCGGTGTAGCCTTTGGTTGGTTGTTTTGGCGCAGGTAGGAACGGCGCGGTGTTTCGATACGCAACGCCATA  
ACGTTGTATCGTTTTCGCGCGCGGTGTTTCGCGGTGATGACGATTTTTCGCGCGCAGCGCGCGCGCGACGATCGCTGAAGCAGCGCGCGGAGGCGAAGGCTGAGGACGCGCGCAA  
TCAGGTCGCGCAGGTGTGTGTTGGGTTTCATCGGGACTTCCTTTCTTGGCGGTTTCAGACGCGATTGCTTTGCGCGATGCGCT

## SEQ ID 486

LPSSRIFSISSGVLMMPFIMLPNIAGVPAVPGQKRLSRISLWGLAGVFPVSGLVWVSLGVSPSLGVLGACFSGVSPRSGWGAFFVSGTSLVSVFACVFPVFNESAARAASBGRGL  
TRPFLAAGDGSPLFLSSVPSGCAGSDEAANWCSGWAASCPAPFPGSONSVSRGLSVCCGSVMRVLSPFGLNVLTMPTANAFMAVIMQNTARIRSLVSLKGLFGFFAILIVLLGCRAMP  
SEGGSDGLAESALDVVLVEGNDPLYADGGADFLGNLRLFFGGEDAHNVGYIAVGNDFDARLCSGADAQQRGADPGRVPSVAGDVARSARQGGDGNVVVYAFGLFGTCNLTDLELFPAPGSD  
LSEQQQVAVVADDGLGRVAFGLVVLAVGTGGGFTQQRHNVVIGLRAGGSAVDDGFCADGGPADDCAEAAABGKAEDGNGGADGVWFGPHRGLPFLVSDGIALRHAV

## SEQ ID 487

ATGCTGCAATGCTGATGAACGACGCAAAATCTGGCCTGCGGCAACGGCGGTTCCGCTGCCGACGCGCAACTTCGCCGCCGAAATGACCGGCGGTTTTGAGAAAGAACCGATCGGAAC  
TCGCCGCCGCTGCCCTGACCCAGACACCTCCGCGCTGACCGCCATCGGCAACGACTACGGTTTCGACCAACGATTCAGCAACAGTGTGCGCGCGCTCGGACGTGACGGCGACGCTCTCGT  
CGGCAATTCACCTCCGCAATTCGCCAACGTCATCGAAGCGCTCAAAGCGCACACGACGCGATATGCACGTATCGCCTGACCGCGCGCGCAAAATCGCGCCATGCTC  
AAGACACCGACGTTCTGCTCAACGTCCCCATCCGCGCACCGCCGCTTCAGGAAACACATCTGCTGATACGCGCATGTGCGACTGTATGACTCGCTACTGCTGGAAGGAATG

## SEQ ID 488

MLQCLMNDGKILACNGGSAADAQHFAEMTGRPEKERMELAAVALTDTSTALTAIGNDYGFHVPFSKQVRALGRAGDVLVGLISTSGNSANVIEAVKAAHERDMHVIALTGRDGGKIAANL  
KDTDLVNLVPHFPAIRIQENHILLIHAMCDICDSVLLBGM

## SEQ ID 489

ATGCGCTTAAACCAACAGGGTACGCGAGGGGAAGATCGCGCACTTGCCCTTCCTCAATCCCAAGGCTGCACGCTGCTTGGCCGCAACTGCGCTACGGCGAAATCGACCTGA  
TTGTCAAAAACCGCGCATGATTTCTGTTGTAAGTAAATAACGCAAAAACCAACGGTTCGCGCGCGCGGCATACAGCAATTTCTCGCTCAAAATTTATGAAACTGCAACGAAGGTGAGA  
GTATTATCTGCAACAGAACAGGCTGACAAACGTACCGTCCGCGCTCGATCGGTACTTTATCGAAGAAACCGCGCGCGCGAGTGATGAAAGATATTTACAGGT

## SEQ ID 490

MRJNHQGTAGEDAALFLQSGCTLLARNWHCAYPEIDILVKNMGMLFVEVKYRKNQRFGGAAYSISPKLLKLQRSVEYTLQONRLTNVPCRLDAVLIENRPPENIKNITG

## SEQ ID 491

TGTGGTTTAAAGCCATAATCGGTTTAACTTTATAATGCTGCTGTTTTTCAGACGCAATTTTTATGTTTCAGAAACACTTCAGAAAGCCTCCGACAGCGCTCGTGGAGGGACATTTATAG  
TGGTTGCCACGCGCATCGGCAATTTGCGCAGACATTAACCTGCGCGCTTTGGCGGTTATGCAAAAGCGGACATCATTTGTCGGAAGACACGCGCTTACTGCGCAGCTTTTGAAGCGGTA  
CGGCATTCAGGCGAGGTGCTGCTGCGGCAACACAGAGCGGAGATGCGGACAGGTAATCGGTTTCCTTCAGACGCGCTGTTGTGGCGCAGGTTTCGATGCGGGTACGCG  
GCCGTGTCGACCGCGCGCGAACTTCGCCCGCGCGTGCAGGAGGCTCAAAGTTCGTTCCCGCTGTCGGCGCAAGCGCGGTAATGCGCGCGGTTGAGTGTGGCGGTTGCGCGAAT  
CGGATTTTATTTCAACGGTTTGTACCGCGAAATCGCGCGAAGTGAAGAAATGTTGTTGCCAAATGGGTGCGCGCGGCAATTCCTGCTGCTCATGTTTGAACCGCGCGCAATCGGGC  
AAGCGTTGCCGATATGCGCGAATGTTCCCGGAACGCGCTGATGCTGCGCGCGCAAACTCAGCAAAACGTTTGAACGTTCTTAAGCGCGCAGGTTGGGGAATTCAGACGCGATTCGGG  
CGGACGCGCAACCAATCGCGCGGAGATGCTGTTGCTGCTTATCCGCGCAGGATGAAACACGAAAGGCTTGTCCGAGTCTCGCGCAAAATCGATGAAATCTTTCGCGCGGAGCTGC  
CGAACAGCGCGCGCGGAGCTTTCGCCCAAGATTACAGGTGAGGCGCAAAAGGCTTTGTACGATTTGCGCACTGCTGCGGAAACAA

## SEQ ID 492

LWFKRIIGLFTINSVFQTAFFMQHLQKASDSVVGGLYVYVATPIGNLADITLRLALVLRADIIICABDTRVTAQLLSAYGIQRLVSVREHNERQADKVIQFLSDGLVVAQVSDAGTP  
AVCDPGRKLARRVREAGFKVFPVVGASAVMAALSVAAGVASEDFYFNGFVPPKSGERRKLFARWRAAPVVMFETPHRIGATLADMAELFPERRLMAREITKTFETFLSGTVGRIQTALA  
ADGNQSRGEMVLVLYPAQDERHEGLSESAQAMKILAEPLTKQAELAAKITGEGKALYDLALSWMKX

## SEQ ID 493

ATGTCGCCAACAACAGAGCTGCAAGGCATCTCTCTTTTGGGTAATCAAAAACCAATATCCGACCGGCTACGCGCTGAAATTCGGAAGCATTCGACAACAACATCCGACAAAG  
ACTATTTCTGCAAAATCTGCTGCGCCGAATTCACAGGCTCTGCGCGATGACCGCGGCGAGCTTCGCCACCATCGTCATCCGCTATATCCGCAATCAAAATGTTGGAAGCAAAATC  
CTGAAACTCTACCTCTTCAGCTTCGCAACACAGCGGATTTTCATGAAGACTGCGTCAACATCATGAAAGACCTCATGCGCTGATGATCCGAATACATCGAATGTTTCGCGGAG  
TTCACACGCGCGCGCGCATCGCGTTTCATCCGTTTGCCAACTACGCGCAAGCAGGACAGATTTGAAGCATTTGGCAGCAACCGCTGTTTCGAGCAGCAGCGCACAA

## SEQ ID 494

MSRNEELQGISLLGNQRTQYPTGYAPEILBAPDNKHPDNDYFVKVPCPEFTSLCPMTGQPDFATITVIRYIPIHKMVEKSLKLYLFSFRNHGDFHEDCVNIIMKDLIALMDPKYIEVFGH  
FTRPGGIAPHFANYGKAGTEFEALARKRLFEDAQ

## SEQ ID 495

TGTGCTTTAAACTTTCCGCGAGTCGCGTGAATTTGAAAACCTTAAACCGCGAGCATTTACTTTCAGCGGACAGATATCCGCTACTACGCTGATTCACACCGCTGTGAAACCACTA  
ATTATGTTTCTCACTGTCTGATCAATCCAATGGAACGAGCTGTTACGACGCGGTGACAGATATCCGTTACGATATACCAAAATGACCGCTCAGGAATGGAATGCGAGTGTGCTG  
TGACAAAACACCGCTGCGACCAATCTATAAAGGCTGGAGCGGATTTGTCGTTTGGCGCGCACTGAATCAGGCTTGGCATGTGCGTTACGACATTAATTCGCGCTACCGGTGTCGCC  
AATGCGTCCGAATGTATTTCACTTACAACCAAGGTTCCGGTAATTTGGCTGCCAATTCACCTGAAAGCGGAGCGCAGCACCACCACTGCTCTGCAAGGCGCGCAGGAAAG  
GTACTTTGGATGCCAACCCTGATCAAAACAAATACCGCAACTTCTGCTGTAAGAGCAGAAAGCTGACCAACGCGCGGATGTCGCGTGTACTCAGATGAATTAATACTACGCTATGTGTAG  
CAATCTTATTCGAAAAACCGGAATGCGAGATGCAAAATATCGATAAGGCCGGAATCCGTTGCTGAGCTGACAGGCGCTGCAATGTGGAACAAATAGCGTCTTTTGTCTGAGGGC  
TGAATTTGTTGGCTCGCTGGGTTATGCGAAAAGCAAACTGTCGCGCGACAAACGCTGCTGTCACACAGCGCGGAAAGTATTGCGGTTGCGACTCAAGACCGCGAGCGAAAAATG  
GGGTGTGTTCTCCGCGC

## SEQ ID 496

LSFKTFASRREFENLRDDYYFSQGISRTSSIQHPVKTTNYGFSLSLQIQNDVFSRRADIRYDHTMTQELNABEHCADKTPPAANTYKWSGFVGLAAQLNQAMHVGYDITSGYRVP  
NASEVYFTYNHGSGNWLPSNLKAERSTHTLSLQGRSEKQTLNANLYQNNYRNLSEBQKLTITSDVGCTQMNYYYGMCNPNYSEKPEWQMNIDKARIRGLELGRNLVNDKIASFPVEG  
WKLPGSLGYAKSKLSGDNLSLSTQPKVIAGVDYERAKNGVCSFA

## SEQ ID 497

ATGGAATAAATCTGGTTAGAAAGCTACGAGAAGGCGTCACTGCCGAAATCGACATCACGCAATACAATTCGCTCAGCGACGATTTCCGCCAAAGCGTGGAAAAATTTGCCGCTGCGCG  
CTTTTCAAAATATGGGCAAAACGCTACCTATGCGGAAACCGGCAACTGGCGACGATTTCCGCTCTTATTCGCAAAACGCTCTCAAGCTGCGCGCGCGGAGCGTGTGCCATTTATGAT  
GCCGACGATTTGCAATATTCGATTCGCTTTTTCGGTATTTTGACAGGCGGTTTGGTGGCGGTGAACACCAATCCGCTCTATACGCGCGCGGAGTTGGAGCATCAGCTGAAAGACAGCGGT  
GCGACCGCATCATCTGTTTGGAAAAATTCGCCAACACGCTGAGCTGTGCTGCGCGCACGCGATCAACACGCTCATGCTGCGCTCCGTCGCGGAAAGTTCGCGGCTGCTTAAAGGTT  
CGCTGATCAATTTATCATCCGAAAAATCAAGAAAATGGTTCCCGAATACCGTATTCGCGGAAACCGTTTCTTTCAGACGCGATTGAAAGAGGGGCGAGACGCTTTTCAACCTGTGCG  
ATTAACCGCGAAGATACCGCATTTGTTGCAATACAGGGCGGCGACGACGCGGTTGCCAGAGGCGCGGTGCTGAGCCACGCGCAACATTCGCGCAATATGCTTCAGGCAAAAGAAATGGATT  
AAAAACCAATTCGCGGAGGGAAGAAACCGTTATCGCGCGCTTCCGCTGTACACATCTTTCGCGCTGACAGTGAATCTGATGATTTTGGCAATGCGCGCTGCAAAATGCTCTGATTG  
CCAACCGCGGATATGAAGGCTTTATCGCGCAACTGAAAGCAGCGGTTTAAAGTATTTATTCGCGGTGAACACGCTGTTTAAACGCGATGTTCAACCGCGGATTTCCGCGAAGTGA  
TTTTTCAGGATTCGCGCTGACTTTGGGCGCGGTATGCGGACCCAAAAAGCGGTTGCCGAAAAATGGAAGAAAAATCACCGCACGCCCATCTGCGAAGCTACGTTTTCAGCGAAGCCAGC

CCGCGGCTGTGCTGCAACCCCTTAAACATCGAATCATACAGCGGAGCATCGGTTTCCCGTCCCGTCCACGGAAGTCGAATGCGCGGACGCAACGGCAAGTCCCGCTGGGCGAGC  
CGGCGGAATFGTGGGTAAAGGCCCGCAAGTGATGCAAGGCTACTGGAACCGCCCGAAGAAACCGCAAGCCATAGACGCGTGGCGCTTTTGGAAACCGCGGATATTGCCGTGATGGA  
CGAAAAAGGCGCTGTAAGCTGGTGCATCGCAAAAAAGACCTCGTCTGCTTCCGGATTCAATGTTTATCCGAACGAAATCGAGGAATTCATCGCGCACCACGAAAAAGTTATGGAAGTT  
GCGTGTATCGCGCTTCCGACGAAAAACCGCGGAGGCACTCAAGTGTGCTGCTCAAAAAAGACCGCTTTGACCAAGAAAGAACTCACCGCTTTCTCGGTACCGGTCTGACCGCAT  
ACAAAGTCCGCAAGACATCGAATTCGCGGAGGTTGCCAAGTCCAATGTCGCAAAATCCTGCGCGGAGTTGCGCAAGTGCAGGAAAGTCCGCGGAA

## SEQ ID 498

MEKIWLESYKGVSAEIDITQYNSVSDVFRQSVKPARLPAPQNMGRITLYAETGKLATDFASYLQNVLELPRGERVALMPPNVLYQYPIALFGILQAGLVAVNTNPLYTPREHLQKDSG  
ATALLVLENFANTLELVLFRTQIKHVIVASVGEMFGLLKGSLINFIIRIKKMVPEYRIRETVSFQALKEGAKHVFPVALNREDTALLQYTGTTGVARGAVLSHGNICANHLQAKEHI  
KNQLREGKETVIAALPLYHIFALTIVNLMIFANAGSKIVLIANPRDMRGFIGELKKQVRNVFVIGVNTLFNAMVNRDPFAEVDPSGLRLTLGGMATQKVAEKWKKITGTPIVEAYGLTEAS  
PGVCCNPLNIESYSGSIGLVPFSTEVELRDANGKEVPVGPQGLWVKGPQVMQGYWNRPESTAKAIDACGFLGTGDIAMDEKGRLLKLVDRKDLVVVSGFVNPNEIEFIAHHEKVMVEV  
ACIGVPEKGTGEALKVPVVKRDPSTLTKRELTAFCRTGLTAYKVPKDI EPRDELKPSNVGKILRRELRSAGK

## SEQ ID 499

ATGCGCTCGTAAACATCTTCAGACGGCATTATAAAATCTGTTACCTTTTCAGATGAGTAATGTACACCCCTATACAATTTTGTCTACCATGCACCATAAATCCACGGCTAAAGATAATT  
GGGTATTATCTTTATTCAGAAACATCCAGATACGGATCAGGGCTATACTATAGGCTTATATATTACACGATTCTCATTCATCAAGGCGGAAACCGCAAAATCTGAAACACATATC  
GATCGAATTG

## SEQ ID 500

HPSENIFRRHYKICSPFQMSNVHPYITPATMEHKSTAKDNWVYSFIQKQSRVSVITIGLILHDSHSHIKAENRTNTEYLSIDL

## SEQ ID 501

ATAAAATTCACAAAATTAACCGTTGCCGAATATATTGTGTAAACCGTCATTGTCATATCGTAAATAACGTAATAAAAAATACAA

## SEQ ID 502

IKFNKIKRLREYICVTVHLHIVNKRK\*K\*Q

## SEQ ID 503

ATGAACACAAACCACTGCGGTTTACGACCGCTTGACACGCGCGCTGCACTGGCTGACCGTTCGCGGCTTCATCGGCATTCTGAACACCATTTGCTCTGTGGACAATTTACGAAGAGCGG  
AATGGCGGGCAGCTGTTCGCGCTGCACAAATCTTTCGCTTCCTCATGCTGACGCTGATTCGATTGCGCATCGCTGTGGCGGCTTCCCAACCGCGCCCAAGCGTCCGCAAGCGACAGCA  
GGCGGCGAGCGGACGACGCGATTCTGTATCTGCTCATGCTTTCGCTTCCGCTTATCGGCATGATCCGCAATACGCTGGCGGAGCGCGCGCTTGAAGATGTTCCGCGCTTGAAGTAATG  
CAGGGTTCGCGGAAAAATCGAGTGGATGCAAACTTGGGCAACAGCTTCCACGCGCAATTTGGCTGGCTGCTGTTTCCGCGCTGCTGCGGACAGCTGCCATGCTGCTGCTCCACCGTG  
TTCAAGGCAAGACGCTGCTGATCGCATGACGGGCGCTGCTCGT

## SEQ ID 504

MNTNQPAYVDPLTRALHMLTAVAGFIGILITIVLWITYEEAEWAGSLFGLRKSFGFLMLTVIALRIVMAVANRAKRPQSDSKAAAGHGILYLLMLAVPVIMIRQYGGGRGPKVFGVEVH  
QGSPEKLEWMANLGNTPHGNLWLLFAAVVGHVAVVVRVQGDVLYRHTGRV

## SEQ ID 505

TTGCGCCAGATTACAGTTCAGGTGAGGCAAAAGGCTTTGTACGATTGGCACTGTCTGTGAAAAACAAATGATGCCGATGGACCGGACCATAGTGGCAACGGAATCAACGGACACGCCCC  
GTCTATCGGTACAGCAGCTTTCCTTGAACAGGTGGACGACGACCATGGCGAGCTGCCGACGACGCGGCAACAGCAGCGACGCCAAATTCGCGTGGAACTGTTGCCAAGTTTG  
CCATCCACTCGATTTTTCGCGGAAACCTGCATTACTTCAACCGCGAACACTTTCACGGGCGCGCTCCGCCACCGTATTGGCGGATCATGCCGATAACGGGAACGGCAAGCATGAGCAG  
ATACAGATTCGCGTCTGCTGCGCTGCGCGCTGCTGCTGCTGCGGACGCTGGCGCGCTTGGCAACCGGCCACACGATGCGCAATGCAATCACCGTCAGCATGAGGAAACCGAAAGAT  
TTGTGCGAGCGCAACAGGCTGCCCGCCATTCGCGCTCTTCGTAATTTGCCACAGGACAATGGTGTGAGATGCCGATGAAGCGCGCAACGGTCAGCGAGTGCAGCGCGCTGTCACCG  
GGTCTGTAACGGCGGATTTGTTGTGTTTCAAAAAATCTTTATCATATGTAAACGTTTGAACGGACATTCGCTCGGCTCGGAATGTCAAAAAGCGCGATTGTACAAAGAAAGTTGGAC  
ATATTGTTGTTGCGAGCTGAGATTTGCTTAAAAATTCATTAAGATGGGCAAGCAAAATAGTTTCTCGCGGTATATTGAAATACCGCTTATACCTTATAATGTCGCGCAAAATCTGTTT  
AGACGCGCATCAAAATATGGAATCCGCGTGAACCCCTATTAAAAACCAACAAACAGAGCAT

## SEQ ID 506

LPRLQVBAKRLCTIWHCRGKTNDAGWTGTIVRTESTDTPRHAVQHVFALNTVDDHDGSDVDDGGKQPAQIAVERVAQVCHPLDFFRRITLHYFNAEHFQRAASATVLADHADNGNGKHEQ  
IQNAVSCRCLVALRLTLAGVGNRPDAQCNHROHEETERFVQAEQAARFRLFVNCQDNGGQNADEAGNQPVQARQCRVINGRLVCHVKKILICNLGNHSHVSGSEQKGAIVPKKLD  
IFCLQAEOLLKSLRWAEQIVSPRYIEIPLIFVYVGRKSVQTAASKHAIKRLPKYLPKNTKSI

## SEQ ID 507

ATGAATTCATCGACGAAGCAAAATCGAAGTCCGCGAGGCAAGGCGGTAAATGGCGCAACCAAGTTTCCGCGCGGAAAAATTCGTATCCCGCGCGCGCGCGGACGGTGGCGACGCGCGCA  
AAGCGCGAGCGTCTGGCGAGAACCGAGCAAAACACCAACCCCTGTCGAATACCGCTTCGCTCAACCGTACCAAGCAAAACCGGCGAAAAAGGCCACGGTTCGACCGCTACGCGC  
AGTGGCGGACGACATTCCTCAAAATGCGCGTCCGCGACCCCTATCCGCGACCTCGACACCGCAAGAAATCGTTCGCGACCTCACTACCGACGACGCGCTGCTGCGCAAGGCGCG  
AAAGCGCGCTTGGGCAACATCCACTTCAAACTCCGCTCAACCGCGCGCCCAAAACATCCACGCGCGGCAAGAGCGGAAACCGCTTCCTGCAACTCGAACTCAAAGTCTCGCGGATG  
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CATCGACGAAACCAACAGCTTTCGTATGGCGGACATCCCGCGCTGATTGAAGCGCGGCGAGAGCGCGAGGCTCGGCGCACCGCTTCTCAAAACCTATCACGCAACCGCTGCTGTTA  
CAGCTGTGCTGATTGGCACCCCTTCGACGAAACCGTCAATCCCGCGCAAGAGCACTCGCCATCATCAACGAATTACGCAATACGACGAAGAACTTTACGGCAACCGCGCTGGCTGGTGC  
TGAACAACTCGATATGCTCGACGAAGAAAGCCCGGCGGCAACAGCGCGCTTCTCGAAGCGCTCGCTGGGACTACCCGCAACCTGATGACCGTTTCCAAATTCGACATGAAACCCC  
GCGCTCTTCCAAATCAGCGCGCTGACACATCAAGGACGCGAGGATGTTACACAAATCAACCAATACCTGCGCGAGAAAAACGATTCGAGGCTGAAAGAGCGGAGCGGAGAAAGCA  
CGGCAAAATGTGAATTTATCGAACAGCAGCTAAACGGGATCTGGCGGTGTTAAGCGGAG

## SEQ ID 508

MKPIDAEKIEVAAGKGGNGATSFRRREKVPFRGGPDGGDGKGGSVWAEADENTNLVEYRFVKRYQAKNGEKHGSDRYGAGADDIVLKMFPVGTILRLDLDTEIVADLTTHGQRVCLAKGG  
KGLGNIHFSSVNRAPKQSTPGEEGSTRSLQLEKVLADVGLLGMNAGKSTLITAVSAARPKIANYPFTLHPNLGVVRIDENHSFVMDIPGLIEGAABGAGLGHRLKHLSTRTGLLL  
HVDLAPDFETVNPAAELAIINELRYDEELYGKPRWLVLNKLMLDDEEARARTAPLEAVGWDPEDDRFQFDMETPRLPQISALTHQSTQELVHQINQYLAEKRIEAEKAEKA  
AANVEIIBQQPKTDTGVFKPE

## SEQ ID 509

ATGTACAAAACATAGATTATTTTCAGGCATTGGCGGAATACGCTAGGCTTTGAAAAATACGGGTGCACCAATGTATTCTCATCGGAATGGGACAAATATCCCGGACAAAGTGTATGAG  
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GGGATTGAAGATACGCGCGGAACATGTTTTCATATTCGCGGAATCTGAAACCAACAGCGCGAAGGCTTTTCTTCTGGAACCGTTAAGCGGCTGACTACGACGATTTCGGGACG  
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CAGACAACTCCCTTTTACTTTCGGAACCCATAAACCAATATCGGCCATTTGGCGAATCTGCTGGAACAGATTCGAGATGTCGAACCAAGCTATTTTATCAGATACCTTGAACAAAA  
ACGTTTGGCAGCTTAAAAAAGCTCCGCGCCACCCATCAATTTGGCATGAAAAATTTGGCGGGAATGTTTCCGCACTTCCATATTCCTGTGCTTAAGGCGCGGGGAGTTTACAAATTAT  
TTGGTGTAAACGGAGTAAGAAGGCTAACAGGAAGGAAATGTAAGATTACAAGGTTTTCGCGATGATTGTAATCAATATCCCTTACTCGCAAGTCAGGAAGTCCGCGGAAATCTG  
TATCCGTCCGTGTAAGAGCCATCCGGAATAATGCTCGCTCTCTTTCGCGCAAGGTGCAACAAAAAGGCAATTTGGAATTTATTTGAGGACGGA

## SEQ ID 510

MYKTIDLFSGIGIRLGFKEYGCTNVFSSSEWDKYARQVYEANPGEKPPGDIINGIDPSIDPDHILLAGFPQPPSIAGKGLGPEZTRGTLFFNIARILKTKQKAPLLENVKRI/THDSGR  
TFRIIILETLKQLGYTVYFKVLVFLDFLGPQRRIYIVGFSNIPFYFPEPINQYRPLGELLENDRIWPSYFLSDTLKQKRLAALXKAPPTPSIWHENIGGNVSALFYSCLRAGGSYNY  
LVVNGVRRLTGREMLRQGFDDFEINIPYSQVRKVAGNSVSVFVIEIAENMLASLSGKVEQRGQLDLEAG

## SEQ ID 511

ATGACCGCTTGAAGAACAACAGCCAAGAAGCATTTGACGGCATTTACAAAAATCCCGTGTCCACCTTTATAAACCACTTCAAAATTCAGAGAAATTTATATCATGACCGTGTATATAAAC  
AGTTGGATTTTTTAAATTTAGATACCTTACCGCAACCAATTAACACGCTGGAGGATGAATCTGCCGTCGGTTTTTAGGGCGGATTTCTACTTCATCTGCAAAATTTCAAGATAATCTGTT  
TGAAAAAATGCAATACCGCTGAAAAATAGCGGTATTTGGGAACATTAACAGACAGTCGGACGGCGGGTGAATCGTACATTTATAAACAGTPTTTCATTCGTTTTCCCAATGAGC  
GAAGCATTTGCTTATGTCGCAATACAGACAGATACTCTTCAACTGTCTGAATTTCTAAATTTATTTTGGCTCGAGCCGGGATTTGAAAAGAAGTATAGACAAGATATATGAATCGTTG  
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GCCGAAAAATAGCATTTAAAACTTCTGCAAAATCCATCGTGTAGGCGTAACCAATGCTGCCGATAGAGGTTGGATATGTGGTCTAACTTCGGATTCGCATACAGGTCAACATCTC  
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AAGCCCAATTTCAAAACATCGTAACCTGAGGATGATTTGATAAGTTGGTACGAAAAAGCATTTGAGAGGCCAATATCCGATTGCGAGAGCGTTGTTGGAAAAATATTAACACTGAAATTTATGCG  
TGAATTTCTCGCGTTAATGAAGCAATGAATTTTATGATTTCCGCCAAAAATCCCGGATATGACATTACTGTTACTCATTTTC

## SEQ ID 512

MTLEEQAQKALDGLIKSRVHLKYPIQIAEILYHDCIKQLDFLNLDTYRQSKRWDEICRRFLGRISTSSAKFQDNLFEKNAIPPEKLAVLGLNRSQDGGVESTYKQFFNFRSQMS  
EALAYVGNTRYSFQLSEFLNLFWLEPLKRSIDKIYEVVYALFDALVSELGITVSIDFPKENLFWEEYQDFAEKIITMPKNEHLKPAKIHVRVGTNAADRGLDMNSHPLAIQVKHL  
SLDEBLAEDIVSSISADRIYVCKKAEQSVIVSLTQIGWKSRIQNTVTEDDLISWYKALRGQYPIAEALLENIKTEIMREPPAVNEANEPLDFAQNRGYDITVYHF

## SEQ ID 513

TTGACGGGTAAAGSGTGTGTAGATGGCGGTCAATTCATCAAGTAAGTTTAGAAATGAGTAACAGTAATGTCATATCCGCGATTTTGGGCGAATTC

## SEQ ID 514

LTGKGVVDGGHIIHQVLSMNSNVISAILGEI

## SEQ ID 515

GTGCGTATGTACGTCTGCGGCATGACCGGTTTACGACTATTGCCACTTAGGCCATGCCCGTGTGATGGTGGTGTTCGACATGATTGCCCGTGTGTCGCGAGTGGCGTTATCCGCTCACTT  
ATGTGCGCAACATCACGACATCGACGCAAAATCATCGCCCGTGCGGCTGAAACCGGCGAAACCATCGGGCAACTGAACGCGCGTTTCATTAGCGGATGCAAGATGCCGATGCTTT  
GGCGGTGTTGCGTCCGACATCGAGCGGAAGGCGACGGAACCATCCGCAATGATTTGCCATGATTGAGACCTTGATTTCAAACCGCAAGGCATATCTCGCCGCAACGGCGACGTTTAC  
TACGCGGTGCGCGAGTTTGGCGCTTACGGACAATATTCGCGCAATCGTTGAGCAGCTCGCTGCGGGCGAACCGGTGGAAGTGGACGCTTTCAAACCGCATCCGCTTGATTTGTATGT  
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CGGCGCGGGCGCGGATTTGCACTTCCCGCACCATGAAATGAAATCGCCCAAGCGTGGTGCCAGCGGTACACCTGCGGTGATGACACCGCGCAACCCACCACGCTCAAGTATTGCC  
AGCCACGTCAAAATACGTGCTGCAACAACCGCTTATCCGCTGAGGCGGCAAAATGTCAAATCGTGGGCACTTCTTTACTATCCGCGAAGTATTGAAACAATACGACCCCGAAGTGT  
TGGCTTTCTTCATCTCGCGCCCACTACCGCAGCCCGTTGAATCTACTCCGACCGCATTTGAGCAGCGCGAAAGCGCGGTGACCCGCTGTCACACCACTTGAAACACACCGCGCGC  
TGAGTTTGTATTGTCTGAAACGCCAACGGCTACACCCCGCGTTTCTAGCCCGCATGAACGACGATTTTCGTTACGCTCGAAGCGGTTCGCGGTGTTGTTGAGCTGGCAGGCGAAGTGAAC  
AAAACAATGACGCAACCTCGCGCGCTGCTGAAAGCTTTGGGCGGCATCATCGGCTGCTGCAACGCAACCGCATGAGTTTCTTCAAGCGCGCGAGTTTCAGACGGCTCTCCAAAG  
AAGAAATCGAAGACTTGATTTGACCGCGCGGCGCATCGCGTTTATCCGTTTGCCTTACGCAACTACGCGCAAGCAGGACAGAGTTTGAAGCATTTGGCACGCAACCGCTGTTGAGCAGCGAG  
CGGCACGACTTGGCGCGCGGT

## SEQ ID 516

VRMYVCGMTYVYDCHLGHARVMVVFDMIAWLRRCGYPLTYVRNITDIDDKIARAENGETIGELNARFIQAMHEDADALGVLRPDIEPRAPENIPQMIAMETLIQNGKAYPAANGDVY  
YAVREFAAYQQLSGKSLDRLRAGERVEVDGPKRDPDLDFVLWKAAGKAGAPAWESPWNGRPFWHIECSAMSENLPDITFDIHGGADLQFPHHENEIAQSVGASGHTCGHDAQTHHQSLA  
SHVKYTWLENGFIRVDGEMKSLGNFFTIREVLYQYDPEVVRFFILRAHYRSPLYNSDAHLDDAKGALITLTYTLKNTPAAEFDLSENANGYTRRFYAMNDDFGFVEAVLVELAGEVN  
KTNDLAHLAGCLKALGGIIGLLQRNPIEFLOQGAUSDGLSNEETEDLIARRKQARADKNMAESDRIDLLNEHKIILEDASAGGTTWRRG

## SEQ ID 517

AAAACTAAGGAAACCTATGTCCCGCAACAGAGAGCTGCAAGGCATCTCTTTTGGGTAAATCAAAAAACCAATATCCGACCGGCTACGCGCTGAAATTTCTCGAAGCATTCGACA  
ACAAACATCCCGCAACAGACTATTTCGTCAAAATTCGTCTGCCCGAATTCACAGCCTCTGCCGATGACCGGGCAGCCGACTTCGCGACCATCGTCATCCGCTATATCCCGCACAACAA  
ANTGGTGAAGCAAAATCCCTGAAATCTTACCTCTTCAGCTTCGCAACACCGCGATTTTCATGAAGACTCGCTCAACATCATCATGAAGACCTTCATCCCGCTGATGGATCCGAAATAC  
ATCGAAGTGTTCGCGGAGTTTCACACCGCGCGGCGCATCGCGTTTATCCGTTTGCCTTACGCAACTACGCGCAAGCAGGACAGAGTTTGAAGCATTTGGCACGCAACCGCTGTTGAGCAGCGAG  
CAAA

## SEQ ID 518

KN\*GNPMSRNNELQGISLLGNQKTYPTGYAPEILEAFDNKHPDNDYFVKFVCEFTSLCPMTGQDPFATVIRYIPIHKMVESKSLKLYLFSFRNHGDFHEDCVNIMKDLIALMDPKY  
IEVFGEFTPRGGIAVHPFANYGKAGTEFEALARKRLFEHDAQ

## SEQ ID 519

TTGTGCTCTTGAAGCGGACTTCGATTATCAGAAAAACCAAGTGGCGCGGTAAACAAAGGCTCGTTCCCGATGGATTATTCACCTGGACGCGCAACTATAAATCAGAAGGATTGG  
GACGAAATATACAAACCGCAGCATGGACACCGATTCAACAGTTTTACTTTGCGTATGGACAGCAACCGTTGCAACTGGGCGGCAACATCGTTTGTGCTT

## SEQ ID 520

LSLLKADFQKTKVAAVNNKGSFPMYSTWTRNYKSEGFGRNIQPHGHPIQTFYFAYGQPTVATGRPTSLVV

## SEQ ID 521

ATGCCAATAGCGGTGATCCGTCGCGGATTTTCATATCGGCAGACAAATCAGCCTCTCGCGCTTTGAGTTCCTGCAACGACAGACAAATGTCTGCGCCGATGCGCGATGTATTGCTAAAAA  
CTTTTTTTGAGCGCGGAGCGGATCGCGTTGACGTTGGCGGAAATGATTTTAAGCATATAAAAAATAGATTCTCACAATGTTCCCATACAAAGCGGCAACCGGTGCGCGCGCGGTATTT  
CCCATTCGCTCTGCTGCTC

## SEQ ID 522

MPIAVHPVRIPIHIGRQISLLRPEFLHADNVARCVDVFKTFFVGGADAVDVGNDPKHNKNKFSQCSHTQSGTRCAARYFPFGPAC

## SEQ ID 523

ATGCACGGCTATTGGCATTGCGCGGAGAAGCGCGTTACAGCGGTGTGGCGGTGTACAGCAAAACGCAAAACCGACAAATGTGCAAAATCGGCATTGGGCATTGAGGAATTCGACCGGAGAGGGC  
GTTTGTGCGTTGCGATTTCGGCAGGTTCGGCGTCAATTTTCCTTTATTTGCCCGAGCGGACGAGCGCGGAGAACGCGCAGCAGGTGAAATACCGTTTCCTGATGCGTTTACCCCTATGCT  
CGAAGCGATGAAAAACGAAGGCGCGACATCGTCTGCGCGGACGTCGCAACATCGCCCAACAAACATCGACCTGAAAAATTTGAAAGGCAATCAGAAAAATTCGGGCTCTCGCGCGAA  
GAGCGGAGTGGATAGGCAAGTATCCATACGCTGGGCTGGAGCGACATGTGGCGCACGCTTATCCCGATGTGCGCGGTATACATGTTGGAGCAACCGCGGCGAGCGGTATGCGAAG  
ATGTCGGTGGCGCATGCAATTATCAGATGGTACGCGCAACTTGCAGCAAGCGGTGTCGCAACAGCTTTATAAGATGAAAAATTTCTGGATCACGCCCTTTAGTTGTGAGATATGA  
CTATGCTCCGAA

## SEQ ID 524

MHYWHCAEKRYGSSVAVYSKRKPDNVQIGMIEBFDREGRFVRCDPGRIGVISLVLPSGSSAEERQVYRFLDAFYPHLEAMKNBGRDIVVCGDNIAHQNIDLNWKNQKNSGFLPE-  
EREHIGKVILHIGWIDMWRILYDVPVGYTWSNRQAYAKDVGRIDYQVMTPELAAKAVSAHVYKDEKPSDHAPLVVEIDYAAE

## SEQ ID 525

TTGTGGAGTATGACTATGCTGCCGAATAAGGTTTGGGTAATATGATTTGGAATGTGGACGGAACAGGAAATAGGCGCGCATGGGTTGTGCTGCTTTATCTGCCCATATTTGGTGT  
GGGCGGTGTTTATGTTGTGCGCGATGCAAGGCTGGCTTGGCGGACCAAGGCAACCCGATATGGGCGTGGTGTGGCTGCTGATTTGTCTGCCCTGCCCTGCTGATTCGGGCAAAATGTTT  
GGTGTGAAAGGCTGGCGGGGGTGGTGAATATTTTGTCTGCTGACCGCTGCGCCATATTGAGCGTACCGGCTTGGCTGCTCATCGCTTTACCTCCGGGACCTGCTCAAA

## SEQ ID 526

LWSMTLPLNKVLGKYDWNVDGKTGIGAAWVAAFILPLVNAVFMLSRMQGLAPTKANPIHALVLLICLPCILLIAARCLGKGRWRRVNVIFVCLTVCAILSVPASLLIAFTLRDLK

## SEQ ID 527

TTGAGCAGGTTCGGAGGGTAAAGGCGATGAGCAGCGAAGCGGTACGCTCAATATGGCGCAGACGGTCAGGCAGACAAAATATTACACCCGCGCCGACGCTTTCCAAACCAAAATTT  
TGGCCGCAATCAGCAGGCGAGGCGAGCAAAATCAGCAGCACCAACGCCCATATCGGGTTGGCTTGGTGGCGCAAGCCAGCTTGCATCCGCGACAACTAAACACCGCCACACCA  
TATGGGCGAGGATAACCGAGCGACAAACCATGCGCGCTTATCTGTTTTCGCTCCACATTCGAATCATATTTACCAAAACCTTATTCGGCGACATAGTCATCTCCACAA

## SEQ ID 528

LSRSRRVKAMSSEAGTLNMAQTVRQTKIPTTRRQPPQPKHLAAISROGRQISSHTNAHIGFALVGASQPCIRDNINTAHTNMGRINAATHTAAPIFVFPSTFQSTLPKTLFGSIVILHN

## SEQ ID 529

ATGGAAGGTTTCGAGCTTGAGGATTTGACGCTGTGGCTGATACCGGATGCGGATGAAGCGGAAATGTGGATAGACCGTGGGCGGTGATTTACCGGTGTGCGAGATGTCGGAAGGTGCG  
CAAACCGCAGCACGGAAGCGTGGCAAAGCGGCTTCAGACGGCATTCGAACGGATACAGGGCAGGCATATCGCGTGTGCGCACACGGCGGGCGCGGCGCATCTCTGGCGGTGGCTGTA  
CGCGCCGACATCTGACGCGAGAGAAATCGCGGATATCTCTGATATCGCGGTCCGATATTTTCCCGACGATGCGGAACACACTTTCACCGCGTCCGCTGCTTCCGCGTCC  
GCAITGGTGTGTCGAACCGCGCGCTGCGCACGGTTGGGCGCAAAACAGCGGATTTGTGGAACCGCGCTGTGGTTTCCCGCATTCGGCAGTTTGAACGATGCTCGCGG  
GCTGGCAGTGGGATGAGCTGATGACGGAATGTGCTGGG

## SEQ ID 530

MESFELEDITLWLRDADEAEMWIDRWAVSYFVQMSSEASANGSTEAWQSALQTAPEIRIQGRHIAVVAHGAGAAFLAWLYRADILTKKLAGIILVSPRPDIIPDDAETHFQVRVPCRA  
ALVVEHGVPHQWQKQADLMNARILLVSPHSSSLNMLGGWQWGMKLMQEHLLA

## SEQ ID 531

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ACGCTTCCGTTCCGTTGCGGATTCGCGGACGCTTCGACATCTGCACAAACGGGATAACTGACCGCCCAACGGTCTATCCACATTTCCGTTTCCGATCGCGTATCAGCCACAGCGTCAAAATC  
CTCAAGCTCGAACTTTCCATTGTCGCGGACTATTTGAGCAGGTCCCGAGGTAAGGCGATGAGCAGCGAAGCGGTACGCTCAATATGGCGAGCGGTGAGCAGACAAAATATTC  
ACCACCGCGCGCGCTTTCACACCAAAATTTGGCGCAATCAGCAGGCGAGGCGAGCAAAATCAGCAGCCACCAACCGCCATATCGGGTTTGGCTTGGTTCGGCGCAGCGACGCTT  
GCATCCGCGACAACTAAACACCGCCACACCAATATGGGCGAGGATAACGCGAGCGAACCCATCGCGGCTTATCTGTTTTCGCTCCACATTCGAATCATATTTACCAAAACCTT  
ATTCGGCAGCATAGTCATCTCCAACTAAAGGGCGTATCCGAGAATTTTCATCTTTATAACGTGTGCGGACACGGCTTGGCGGCAAGTTTCGGGG

## SEQ ID 532

VFGHHQGTARTADALESVFRIVGKNIOTRRYENDTGEFLLRQDVGAVDPRQECGRARAVCDNGDMPALYPFBCLRLKRALPRPRAAVCGRFGHLNGITDRPTVYPHFRFIRIAYQPQRQI  
LKLETPHCPRLPEQVPEKGDEQRSGYAGDQADKNIHPPAPFTQTTGRNQAGQTNQPHQPRVRLGRRKPALHPRQHKRPHQYQDKRSDNFCRAYSCFVHPIIPTQNL  
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## SEQ ID 533

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CTTCCAGCCTTGGCGCAGCGGCTGGAACGCTACTGGATTGAACGCGCGCTCTCACTGCGCATGAAAGACGACGCGATTATCGCCCTCGACCCCTCAACCGCAACGCTACGACAC  
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CAAAGTGTCCGATTCTCTCGCAGCGAAGACTATCCGAAAGCAACTTCGCGTACCGCTCGCGGCGAGCTGATTTCGCTGATTGACGTGATTGGGCAACCGCGAGTCCAAAGAGAA  
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CGGACGCTGTCCGCTGCTGCGGACGATCCGCAACTGGGCGATGGCGGCGAATATCATCAGCGCTTACCGTGGCGACCACTTTTGTGGGTGACGCGCAACGATCGCGCGGCTG  
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## SEQ ID 534

MKVGFVGRMNVGSVLMQRMKEENDFAHIPBAFFPTSSNVGGAAPDFGQAARTLLDANDVAELAKMDIIVTCQGGDYTKSVFQALRDSGNGYVWIDAASSLRMKDDAIIALDLPVNRNVIDN  
GLKNGVKNTYGGNCTVSLMLMGLLFQNDLVEWATSMYQAAAGAGAKNMRILISGMATHAQVADELADPSSAILDIDRKVSDFLRSEYPRANFVPLAGSLIPWIDVLDLNGQSKSE  
WKGGVETNKLILGRSGNPVIDGLCVRIGAMRCHSQAITLKKDLFVSEIEAILAGANDVWKVPNEKAGIRELTPAKVTGTLSPVVGRIKLNGGSEYISAFVVGQQLLWGAAPHRV  
LRVLGSL

## SEQ ID 535

ATGAAACCAATACATGCTTCCATTGCGCGCTGCTGGCAGTATTTTCGGCAATCCGGTCTTGGCAGCGGATGAAGCTGCAACCGGAAACACCCCTTAAAGCAGAGATAAAGAAG  
TGGCGGTAAAGACAGCTTAATGCGCTGCAACCGTGAACGCTGCAACCTCGACGCAATCAACGAAATGATACGCGACAAACAGACTTGGTGGCTTACTCCACGAGCTCGGCTT  
GAGCGATAGCGGCGGCATCAAAAGGCTTTGCTGTGCGCGCGTGGAAACCGTGTGCGGTGACGATTCAGCGGCGTGAAGCTGCTGCTGATTCGCGAAGAAACTCCTGTATGACAGT  
TATGGCAACTTCAACAGCTTCGCGCTCTATCGACCCCGAACTCGTGGCAACATCGAAATCGGAAAGGCGCTGACTCTTTCAATACCGGTAGCGGCGCATTTGGTGGCGGCGTGAATT  
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CGACCGGTGATGCGCTTTGCTGATTTCGCAACGCTCGGCTCATGAGACCGAAAGCGCGGCGAGCGTGGCTATCCGCTAGAGGGTGTGCGAGCGAGGAAATATCCGTTGCTGCGCA  
CGCGGTATCCCTGATCCGTCCAAACACAAATACCAACATCTCTGGGTAAGATTGCTTATCAATCAACGACAGCAGCGCATGCGGCGATGTTTAAAGCGCAGCAGGCGCAATATCA  
CGATT

## SEQ ID 536

KRPLHMLPIALVGSIFGNPVLADEAATETTPVKAIEKEVRVKDQLNAPATFVERVNLDRIQQEMIRDNKLDLVRYSTDVGLSDSGRHQKGFVAVRGVEGNRVGVSIDVSLPDEENSLYAR  
YGNFNSRLSIDPELVNRIELAKGADSPNTGSGALGGGVNYQTLQGHDLILLDDRQFGVMKNGYSSRNREWTNLGFGVSNDRVDAALLYSQRRGHETESAGERGYVPEGAGSGANIRGSA  
RGIIPDSKHYHNLGKIAYQINDKRIIGASFNQGGHNYTI

## SEQ ID 537

TTGTTCTTAAACAGATGGAATTCATCCGCGCTACTGCTGCAACCGCAATCCCAAAAGAAATTCGATAAAGAACTTTACATTTTCCCAATACCGCGT



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ATGAAAGATAACACACTGTCAAATTAAGAAAGAGTACAGAAAGAACCGTCCGTTCTTTTGTCACCGAAGTTACCGCCCTCTGCCGCCGATATTTTGGGTATCCATCCGATTCCGGGG  
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ACGCGGTTCGGCGCGCGGCAGGAAAACGGGTGTCTTCGGCATTCGGAACCAACGGGGCGGGCTATACCGTTGCGCGGGAACAATGCCGAGCTGAAACGTTGCCCGCTCGCGTCAAAAAG

AAATCATGCCGGACGGTATGTTTATGCCGATAGCCCGGGCAGCCGGCAAGTCGGACGGGGCGGTTTACCCTGTCGCGATCAACCGTTCGGAGGAATTCAGACCGTCGGAAC  
ACATTAACGCGATTGGGAACCTTTTGAATCAGGCAAAACGGCCCTTGGGAAATACACCGAATCGATCGTAACCTTTCCCGCGGTGTTGAGGGAATGCGAATTCGACTTAACCTCGG  
CACACCGTCCCGCAGCTAAAAATCCTGCGGATCGGTGTGAATT

## SEQ ID 552

MKITHCKLKKEVQKEPLRSFVPEVTARSADILGIHPDSALFYRKIRTVANHLALAADGVFEGPAGPGSGCPGRRKRRRGRGAAGKAVVFGIPKRNGRAYTVAADNAEPETLPPAVKH  
KIMPDGIVYADSPGSRGKSDAGGFTFRINRSEFPADRNHNGI GFWNQKRALRKYNGIDRKPPPLLRECEPRLNFGTFSRQLKILDRCGI

## SEQ ID 553

GTGTTAAATCCCGCTTTAAAAACCCCGCTTCCAGCCATCTCGGTATGAATACGACATCAAACTTCCAATATCATCGTCGGGCTTTCCGGCGGTGCGATTCTTCGTAACCGCGG  
CCCTGCTCAAGCAGCAGGTTTATCAAGTCGCGGTGTGTTTCATCAGAACTGGGAAACGACGACGACGAATATTCAGCATCAAAAGGATTCGTCGATGOCATCGCGGTTCGCGA  
TATTGTCGGCATCGACATCGACATCGTTAATTCGCGCGCAATATAAGACAAAGTTTTCGTTTATTTCTTCAGGAATACAGTCGGGGCCGACGCGGAATCCGGATGTGTTGTCAT  
GCCGAAATCAAAATTCAAATGCTTTTGGACTACGCGGTAGGCGAGGCGCGGATACCATTCGACCGGACACTATGCGCGCAAGAGCCGCAACGCGGTGTCATTACCTGCTCAAGGTT  
TGGATCGAAACAAAGACCAAGCTATTCTCTACCGCTCAAGCTTTCCAATCGAACGCGGATTTTCCGTGCGCGGTTTGGAAACCCGAGTGGCGGCTTCCGCGCGAAT  
TAAFTTCCGACTCGCGCTAAAAAGACAGTACCGCATCTGTTTCATCGCGAGCGTCCGTTCGCGAGTTTCTGCGAATACTTTCGCGACGCAACGCGCAAAATGTCAGCCCGAA  
GGGAAACCATTCGCGCAACAGTCGGGCTGATGTTTACACATTTGGTCAGCGCAAGGATTTGGCATCGCGCGCGCGCGGCAACCGTGTGTTGTCGCGCTAAAGATTGACGAAAAACG  
AACTCATCGTGTCAAGGACAGGACATCCGCTGCTCTATACCGCAGCTTGTGATGAACGATTGAGTTTCACGCTGCGCGAACGTCGGAAGCGAGGACGCTATACCTGCAAAACCGG  
TTACCGTATGCGCGACCGCGCTTCCGAATTTGCTATTGATGATGAAACCGCGAGCTGTTGATGTCGCAACCGCAATGGCGGTTCACGCGGTCAGTCCGCGTGTCTAGCAGCTC  
GACATCTGTTTGGCGCGCGCATCATCCAAACGACGCAAAACCGCTCATCATCAGCGA

## SEQ ID 554

VLKSAFNRRPQAILRNMNTSNTSWIIVLSGGVDSVTPAALLKQGYQVRGVFMQNWENDNDDEYCSIKQDSFDAIAVADIVGIDIDIVNFAAQYKDKVPAYFLQESAGRTFNPDLN  
AEIKFKCLDYAVGQADTIATGHYARKEARNGVHYLLKGLDRNKDSYFLYRLKPFQLERAIFPLGLEKPEVRRLAAEFNLPTAAKDDSTGICPIGERPREFLQKYLPTDNGKHVTP  
GKTIGEHVGLMFYTLQGRGLGIGAGEPFWAADLTKNELIVVQGHDPHLLYTRSLVMDLSFTLPERPKAGRYTCKTRYRHADAPCELCYLDDETAELVDFEPQWAVTPGQSAVLYDV  
DICLGGIIQTTRKPVITR

## SEQ ID 555

TGCGCGCGAAGCGCGGGAATCGGAACAGCTTAAAAATATGCCCTTTTTCACACGGGGCGGCATCCGTCCGAATCTGTCCGATTTGCGCGCGGACAGACTGCGCGCGCGCGCGG  
GGTTTCAACATTCAGGGAATTCATTAATGAAATGGCTTTCACCTTTTGGCGTACTCAATATTCGCGTATTCGCGCGCACGTTGGCTTATAAATGGCGGTAAAGCGCGCGCGCGCT  
GCCGGAACACCGCGCGTTCGAAACACGCGCCCGCAACGCGCGCGCGCGCAATGCGCGGCATCCGTGGAGGATACGCGCGCACTGCTCAAAACCGCGCGACATCTGAGCGAAGAACAG  
GCGGAGCAGTTGCGCTTGAAGAAAGAACGCGGAACAGAAAAAAGCTGAGGAGAAAAACAGCGTGAAGAAAAAGCCGCGCGGAAAACTCGCGCGCGGAAAGGCGCAGGCGGAACGTGAAA  
ACGCGCGCGCGGATGCTTATGCGCGCGCGCAGGCAAGCTTCAGATGGACGAGACGACTACCAACCGCATCAAGAGGCTTTTGGGCAATGTCGCACTGCCAGCAGGAGCGTCGAAAA  
ACGCAACCGCAAGGCAAACTGCGCAAAACCTACCGCGTCTGCTGCGCGTTTCCGCGATGCCGAAATCAGGCGCGGAGCTGCTGCCAAAGGTTTCAACCCCATACCGTTTTCGAC  
GGCGCATTTAGTTTGGGTGTCGCGAACGCGCGGAAAAACGCGCGCTGCAAAACCGACTTCCGCGATCGCGGATTCGCGCGCGCGCATATTTGTCGAACACTTTCGCGAAGCGGACAGCG  
AGGACGATTCCTTTCGCGGTGTCGCGTATGACGCTTTGTTTACGCGCGGTGAATGCGCGGATCGGACGAAATCCGTAAATACGCTCCCTATACGCGAACTGAACCTCAAGCTTTCGAA  
A

## SEQ ID 556

LPPKAGNRNFTLKYAFPHGAASVRIPOSAAQTAARAGGVSNIEILMKWLTLLAVLNIAVFGTVGYKLAVKAAGGVENRAVENTPPATPAAGNAAASVEDTAALLKPGDILSEBQ  
AEQLRLKKEABQKLRKREKREKREKLAEEKAQERENGADALCAQASLTDEDDYHRIKGLLKGKSHVASRSVEKETAKAKPADKTYRVVLPVSADAENQAELSAKGFNPFPD  
GALSIVGNSRENAQALQNLADAGPGGAHIVEFAEDRQDLSVSRMTVLFTGVNADADEIRKITSLYGLKLNKSK

## SEQ ID 557

ATGTATGTCCTGTATATGCGGACTCCAAGTGTGAAAGTGAATTTGTGAGGGAATACAGTGTTAATGTTTCGGAACGACGCGCTCCGAGTGGTTTGTATTATACGCTAATAATAATTA  
TCAATAAAAAATTAATAATAATTCGGATTTTTTG

## SEQ ID 558

HYVSYPPTSVKNCEGIQCLMVRNRLPSGFDYTLIIIIINKLNKLNADFL

## SEQ ID 559

TTGTTCAACACGCGAGGCTTCTTTCCGACAGGACGGAAGCCCGCTCATGCTGCCGACCCCGATTGTCGCGCGCAATGAAAGTTTGGCGACCCAAATCACAACATCGCGGACAGG  
TTAATTTGTTTATTTTTCATCGCATTAACAAAATCCGATTTATTTTAAATTTTAT

## SEQ ID 560

LPKGRLLSDRHEAPFHACRPRFVRNRESLPTQITNIGQVNLFIHRIKTNPHLFLNFI

## SEQ ID 561

TTGAACACCGTCCGATTTGTCGCGACAGGTTGCCATTGCGGGGTGTTGAGCGCGGATTCGGGATGCAAAAGCGGTAAACCGTTGCGGATGAAGGCTTACGGATGCCCGAGGTAT  
TTTTAATGTATTCAACGCAAAACTCCCTTCTATTGCGCTACTTAGGCTTGCAGCAGCAGCTGCGCGCGGGAGTCCGGGTGTTTGTGTTGCGGTGTCGGGCGCGCGCAAGG  
TTTTCCGCGCGGTTCCCTGTTCTCAGCAAAAGCGGTGATGCGGGGAATGCGGTTTCCCGTTTGGGCGCGGATGCCGTC

## SEQ ID 562

LNNRPIWCGGCGSGVFERGFGDAKAVKPLRMKAYCPEVLNVFKRNSLLLPYLGLAQPARRGVVRVRLRCRGRGQFPAGFPVPHDKAVMPGNGLPVNDRDAV

## SEQ ID 563

TTGGCATTCGCGGAATATTGAAAGGCGGCAAAATGCCGTCTGAAGGCTTCAGACGGCATCGCGGCCCAACCGGCAACCGCCATTCCCGGATCAGGCTTTGTCGTGAGGAAC  
AGGGAACCGCGCGGAAACCTTGCAGCGCGCGCGGACACCGCAACAGCAACACCGGACTCCCGGCGCGCAGGCTGCTGCGCAAGCCCTAAGTACGGCAATAGAAGGAGTTTGT  
CGTT

## SEQ ID 564

LAFGLLKKAAKMPSEGFRRHRGPKRANRHPASRLCREEQNRPENLAARPDATNETPGLPGAQAAQALSTAEBSFV

## SEQ ID 565

ATGCTCACCTGTACGCGGAACTTTCCCTTCGCGCTGCTGCTCGGACGCGCGCTACCGACCCCTGAAATCCTCAACAAATCCGTCCGAACCGCGCGCGCGGATGATTACCGTCT  
CGCTGCGCGCGCAGGATTCGCGCGCGGAGGCGCAGGTCAGGGTTTGGTTCGCTGCTTCAAGAAACCGCGCTTCCGTCTTCCGCAACGCGCAGGCTGCAAGCGGTGACGGAAGCGGT  
AAGCAGCGCGCAATTCGCGCGGAGTGTGTTGAACCGATTTGGATAAAATGGAACTCATCGCGCAGCAGCAGCTTGCAGCGGAGCTGTTCCAACTCGTGAAGCGCGGAAATCCGT  
ATTAAAGACGGCTTCAAGTGTGCTTATTGCAACGAGAGCTGATTGCTGCGCGCGCTGCTGATGCGCGCTGTCAGGCGTGTGATGCGCGTGGCGCGCTCCCATCGGACGCGGTTTGG  
GGCGGTTACGCGCTATGCGCTCAAAATCCTGCGGACGCGCTGCCGACGCGCGCTGATTATCGACGCGGCTTGGGTTTCCCTTCCCAAGCGGCAAGTGTGATGGAATGGGTTTGA  
CGCGGATTTGTTAAACACCGCGCTTCCCGCAGCGCGGACCCGTCACATGCGCGCGCTTTCGACTCGCGCTCGAATCCGCGAGGCTGGCATTTGAAGCGCGCGCGTGAAGCGCGA  
ACCAAGCCCAAGCGCAGCGGACGTCGGAACCGTTTGGCATTCGCGGAAATAT

**SEQ ID 566**

MKTLYGETPTPSRLLLTAAAYPTPEILKQSVRTARPAmitVSLRRTCGCGEAGHGGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREVFEETDWTKLLELIGDDDTLQPDVFPOLVEAEKL  
 LKDGFPVLPTCYTEDLIACRRLLDAGCCQALMPWAAPIGTGLGAVHAYALKILRERLPDPTPLIIDAGLGLPSQAAQVMEWGFDGVLNNTAVSRSGDPVNMARAFALAVESGRLAFEGAPVEAR  
 TEACASTPTVGQFPWHSAEY

**SEQ ID 567**

ATGTAGTCGATCTGACCGCCGACAGCAACAGGAAGGCACCTCTTCGGCTGGTGCTTTTCCATATCCCTCATCACTCGCCGCCAGCAACTATCTGGTGCACTTCCCTCTCCGGGATTTTCGGCATCC  
ACACCACCTTTGGGGCGGTTCCTTTCCCTTCATCTTCTCGGCACCGACCTGACCGTCCGCAATTTTCGGTTCCGACTTGGCGCGGGCGGATATCTTTTGGGTGATGTTCCCGGCCCTTTT  
GCTTTCATACGCTTTTCGGTTTGTGTCACAAACGGCAGTTGGACGGGCTTGGGCGCGCTGTCCCAATTCAACACCTTTGTGCGGACGATCGCGTGGCAAGTTTGTGGCGCCTACGGCGCT  
GGACAAATCCTTGATATTTTCGTATTTCGAAATATACCGCTGTGAAGCGCTGGTGGAATGCCCCGGCGCATCAACCGTTCATCGGCACGTGACCTGGAATAGTATTTTTCGGCTGTG  
CCTTTTACGCAAGCAGCGATGAAATTTATGGCGGCAAACTGGCAGCATCGCTTTTTCGATATACCTGTTCACAACTACCGCTTCGCAACCTCTTCTCTCGCCCGCCTACGGCGTGATACT  
GAATCTGTCGCGAAGAAAATCATCGGGCCCTGCACAAACCAACAGGCGCAAGACCGCCCGGTGCCCTCGCTGCACAAATCCG

**SEQ ID 568**

MYIA/TAACQQQKALFRLVLPHILIIAASNYLVQFPFRIFGIHTTWGAFSPFFIFLATDLTVRIFGSHLARRIIFWVMFPALLSYVFSVLPHNGSSWTGLGALSQFWTFVGRIALASTAAYAL  
GOILDIFVFDKLRRLKAWMTAPAASTVIGNALDVLVFFAVAFYASSDEFAANWQGIADVLYLPLTVCTLPFFLPATGVILMLTKKLLFALQTKQAQDRFVPSLQNP

**SEQ ID 569**

AFGATCTCTTATTATTTTGTATGTCGGGCAAGTCCGGATTTTGCCCGCACCGCATCTCTTATCCCTTACCGCAAAAGGAGAACTTATGAGCGAAACCGAAAACCAAGCCCTGACGTTTGCCA  
 AACGCTCGAAGCGGATACCAACGGCGGTTACGACAGCGTGGATAACCTCGTATGTCTGTCAACCGTTTGTGACGAAAGAAATCATACATAAATTTTGTAAACTCGCAATCCGTTCCGCA  
 CAAAGCGGTTGATCATATCTATAAAGACCCCGAGTGTGAACAAAGCCATTTCCGAGCTGGAATACTAGGCGCGATACGATGCCGTAAACGCAAGACTTTGAAAGACTTGGGCGAAGAGCCTTAC  
 AAAATTCGACAAAGAAATGCCACACGAAACCGGCAACAAAGCGCTCGGCTGGCTTAACTTTGCGCCGAAGGATCCAATTTGGGCGCGGCATTTTGGTTCACAAACGCGCAACCTGCGATTATCA  
 CCGGCGGAACACGCGCGCGCCACCTCGCTCCGATACCGGACCGTGGCGGCAATCTGGCGGCCCTTCGTGAGCACCCTGAATGGCCCTGAACTTAACTTCGGGAAGCAGAAGCAGAGCCAT  
 TCAACGCGCGCGAGGAGGATTTGCTTTCTATATAAGTGATTCTGCGTGAAACCTTCGGTTTTCGCGGAAGGAACAGAAGCCCGGAAGGCATGATGCCGCACAGACAT

**SEQ ID 570**

MLILYVFCMRASPDFARTASLSLFDKGELMSSTENQALTFAKRLKADTTAVHDSVDNLVMSVQPFVSKENYIKFLKLQSVFHKAVDHIYKDPFLNKAISELEYMARYDAVTDQLKDLGREFY  
KFDKELPHETGCKNAVGWLYCAEGSNLGAALFKHAKLDYTTGEGGARHLAPHEDGRGKHWRAFVEHLNALNLTPEARBAEAIQGAQZAFAPYKVLIRETFPLPGCTEAPEGHMPRRH

**SEQ ID 571**

SEQ ID 371  
ATGAAAAAATTTATTTGGCAGCCGTGATGATGGCAGGTTTGGCAGGCGCGGTTTCGCGCGCGGAGTCCATGTGAGGACGCGCTGGGCGCGCACCACTGTGCAAGGTATGAAAAATGGGCGGG  
CTGTCATGAAATATCCCAACGACGAAGCGAAACAAGACTTTTTCGCTCGCGGAAGCAGGCCGCTGCGCGACGCGCTCGAAGTCATACCCACATCAACGACACAGGCGTGATGCGTATGCG  
CGAAGTCAAAGGCGGCGTGCCCTTTGGAGGCGAAATCCGTTACCGAACTCAAACCCGGCAGCTATCAGCTGATGTTTATGCGTTTGAAAAAACAACCTGAAAGAGGGCGCAAGATTCCCGTT  
ACCGTGAAATTTAAAAACGCCAAAGCGCAAAACCGTCCAACCTGGAAGTCAAACCCGCGCGCATGTGCGCAATGAACACGCTCATCACGCGGCGAAGGCCATCAGCAC

**SEQ ID 572**

MKKLLAAVMMAGLAGAVSAAGVHVHEDGWARITVEGMFMGGAFMKIINDEAKQDFLLVGSSPVADREVEVHTHINDNGVMRMREVKGGVPLEAKSVTELKPGSYHVMFMGLKTKQLKEGDKIPV  
 TLKFNKAQAQTVOLEVKTAPMSAMNRGHHHGEAKQH

SEQ ID 573

TTGTGCGGACGCGATGCCCTCTGAAAGCCGGCGCGTGCCTTTGGGGTTTCAGACGGCATTCAGCCGCCGACGACGGGGCCGACGATGTGCATTTTGTCGTTTTCGTGTAAACACGGTTTCCG  
TATACCGCCCTTTGGGGATGAAAAACGGTGTGTGACCGCCACCGCAAGAGGTTTTTTCGGCCGCGGTTTGGGCGATGAGGTCGGCAACCGCTTGTGCCG

**SEQ ID 574**

SEQ ID 974  
LSDAMPSESRERRAFGVSDGIOPPTTGRMTSILSFSCCKTVSVYAPLQMKTVLTATAKGFCGAVWAMRSATLVP

**SEQ ID 575**

SEQ ID 575  
ATGAACATCATCTTAAACGGCGGACCGCGCGAATTCACGGGCACAAGCGTTGCGGACCTCATCGCCCAACCGCGCGCGCAAAAACCTTTGCGGTGGCGGTCAACACCGTTTTCATCCCCA  
AAGCGCGGTATACGGAAACCGCTTTTACACGAAACGACAAAATCGACATCGTCCGCCCGCTCGTGGCGGC

SEQ ID 576

SEQ ID 970  
 MNIILNGGPAELGTSVADLIAQTAPQKPFVAVAVNTVFTIPKGAYTETVLHENDKIDIVRPVVG

SEQ ID 577

SEQ ID 577

ATGTGGCATATCATCAAAATTCGTCATTCCCGCTCAGGGCGGGAATCCGCGGAAAACTTGAGAAACCATCATTGAAAAACAGTTTCGGAATTTCAAAAATGGATTCCCGCTCGCCGGGA  
ATGACGCCAACCGGCGGTTGCGTATCAAAAAATAAAG

**SEQ ID 578**

MMHTIKFRHSRSGGNPPENLRNHHLKNSPRI SKMDSRLRGNDGNRPVAYQKIK

SEQ ID 579

SEQ ID 579

ATGACCTCTCCCGCCCTAAAATCCCTACTTTAAATCTACGCGCTGTTCCACCGCCGATTTGGGTGGGGCGCATGGTCAAAGCAGGTGCCGACACGGTGCAACTGCGCTGTAAAACCTTGC  
ACGGCAACGAANTTGAAACGCGAAATCGCCCGCTGCGTTCGCCCTGTCAAGCGACGCGCACACAGCTTTTCATCAACGACCACTGGCGCGAGGCAATCGAAGCGGGCGCATACGGCGTACA  
TCTCGGGCAGGAAGACATGGACACCGCCGCACTTGCGCCCATCGCGCGCGCGCGTTTTCGCTTTGGGTTTGAGTAGCAGCACTCGTTCGCGGAACTCGACCGCGCCCTGTTTCGTACACCCCGCG  
TACATCGCCAGCGCGCGGATTTTCCAGACCACGACCAAAACAATGCCACCGCCCGCGAAGGCTTGGACAAAATTCGCGGAATATGTGGAACAGGCTCGCGGCAACGCTTCGCGCCTATCG  
GCGGCATCGAATTGAACAACCGCCGAGCGGTGCTGGCCACCGCGGTTTCTCTCACTCGCGCGCGTCCGCGCGCTAACCGGAAGCGGCAAAATCCCGAAGCGGTGGTTAAAGCGTTTCAGGCTTT  
TGCGGATGGA

SEQ ID 580

MTFPPKLSLLKPYAVVPTADWVGMRVKGADITVQLRCKTLHGNELKREIARCVAAACQGSRTQLFINDHWREAEAGAYGVHLGQEMDTADLAAIAAAGLRLGLSTHSVAELDRALFVHPG

SEQ ID 581

ATGACCCGCTATCGCGCTCTCGGAGGCGCCCTTTCCGGAAGGCTGACCGCATGTCAGCTTGCAGAACAGGTTATCAGATTGAACCTTTTCGACAAAGGGCACCGCGCAAGGCGCAACACGCG  
 CGCCCTATGTTGCGCGCGCGATGCTCGCGCTGCGGCGGAAGCGGTGAGGCGCAACGCCGAAGTCATCAGGCTGGGAGGAGAGCATTCGCGCTTTGGCGGGCATCCGATGCGGCTCTGAA  
 CACGCTCAGATGATGCAGGAAAACGGCAGCCTGATTGTGTGGCACGGGAGGACAAGCCATTATCCAGCGAGTTCTGTCGCCCATCTCAAACCGCGGCGCGGTAGCGGATGACGAAATCGTC  
 CGTTGGCGCGCGATGAAATCGCGGAACGCGAACCGCACTCGGGGAGCGTTTTCAGAGCGGCATCTACTCGCGGACCGAAGGCGCAGCTCGAGGGCGGGCAATATTGTCTGCACTTGCG  
 ACGCTTTGAGAGCACTGAACGTCCTTGGCAATTGGGAACACGAATGCGGCCCCCAAGACCTGCAAGCCCAATACGACTGGGTAATCGACTGCGGGGGCTACGGGCGGAAAAACCGGTGGAA  
 CCAATCCCCCGAGCACACCAGCACCTTGCGCGGCATACGCGGCGAAGTGGCGCGGGTTTACAGCGCCGAAATCAGCTCAACCGCCCGCTGCGCTGCTGCAACCGCGCTATCCGCTCTAC  
 ATCGCCCCGAAAGAAAAACACGCTCTTCGTCATCGCGCGACCAATCGAATCGAAAGCGAAGCGAACGCCGCCAGCGTCCGCGGCTGGAACCTCTATCCGCGCTCTATGCGGCTGCAC  
 CGCGCTTGGCGGAAGCGGACATCTCGAATATCGCGCGCGCTCGGCGCCACGCTCTGATCAACCAACCAACCGCGAATTCGCGTACAGCGCGGAACCGCGCTCATCGAATCAACGGGCTTTT  
 CGGCGACGGCTTTATGATTTCCCCCGCGGTAAACGCGCGCGCTCAGATTGGCAGTGGCACTGTTTTCAGGAAAAGACGCGCGCGGACGCTGATGAAGAAGCGGTTTGGCGTATATCGGA  
 AGACAAGAT

## SEQ ID 582

MTRIAVLGGGLSGRLTALQLABQGYQIELPDKGTQGEHAAAYVAAAMLAPAAEAVEATPEVIRLGRQSIPLWRGIRCLNTLTHQDENGSLIVHGDQKPLSSEFVRHLKRGGVADDEV  
RNRDELAEREPQLGGRPSDGIYLPTEGQLDGRQILSALADALDELNVPCHEHECAPDLQAYDVIDCRGYGAKTANNQSPHSTLRGIRGEVARVYTPETILNRPVRLHLHPRIPLY  
IAPKENEVPIGATQIESRSQAFASVRSGLLELSALYAVHPAFGEADILEIAAGLRPTLNHNPEIRYSRERRLIENGLFRHGFMI SPAVTAARLAVLALFDGKDAAPERDEESGLAYIG  
RQD

## SEQ ID 583

ATGATTATTACAAAATCGGGGTTTATCAAAATAGGCTTGTCCGCCGAGGGGAGCGCGCTCAAAAATATTTTTCGCCGACCAAGGGTTTGTTCATACTGCCGAACCTGCCGGTTTTC  
CATCC

## SEQ ID 584

MIITYKIGVLSNRLVGRGSRSKNIPAGHQGFVHTAEPAGFAS

## SEQ ID 585

ATGGAACCTTCCTCTACGCGGCAGAAAAAGGCAAAAGCGGCATCAGCGCGTCATCAACGCATTCCGCTATTTCGATAGACGGCATCGCGCGCTACCGTTACGAAGTGGCATTC  
GTCAGGTTTGTGGTGAACCGCGCTGCTGCTGTCGCGGCATTTTTTGGGTTTCGAAACCGCGCTCCGCTGCCGTGATTATCCGCTCTTTGTGTGGTTCATTGTGCAACTGTTCAA  
CACCGCGTCGAAACCGCGCTCGATCATCTTCGACCGGAAAAACAGAGCTGAGCCAAACCGCGCAAGATGACAGGTTTCGCCGACAACTGGTTGCCATGCTGATGTGGCGCGGTTTCG  
CTGTCCGCCCTGTTCGGG

## SEQ ID 586

MEPSSYAAERKKGSGIRRVINAPGYSIDGIAAAYRYEAFRQVLNALLVCAAFVWSETAVRLPLIIASFVSVIVELFNTAVEAAVDHTSTKHELAKRAKDAGSAAQLVANMLAAVH  
LSALFG

## SEQ ID 587

GTGCTGATTTCGCAATCGATACCGCCCGCCGCAACCAACAGCCGATGCGCGCGAAGATGAAGGAGAGAGGCAITGCCCGACAFAT

## SEQ ID 588

VLISAIDTAAPNQTSPMAEDGGEALPDI

## SEQ ID 589

TTGGCGTGGCAGCGCGTCTGGCGGCCCTGCTTTTGGGTGATGCCGTCGGCGCGCGCTGTTTTTTCGCCGCGCGTATATCGCGCACTGACCGGACGAGCTCGATGGAAGTGTGGCGC  
TGTGCTTCGGCAATATCGGTTTCAGTCTGTTTTCCGTCGGCAATATGCTGCACTGGCGCGCTGGACGGCGGTGATGATTTACGTGGCGCAACGGTCAGCTCCGCTTTGGGCAAGTGT  
GTGGGACGGCGAATCTTTGCTGTGGTGGCATTTGGCAAAACGGCGCACTGATCGTGTGCTGTGGCTGTTTTTCGCCGCGCAGCAGAACGGCGCGCTGAAACCGTTTCGATGCTGCTGATGCTG  
CTTGGCGGTGTTGTGGTTGAGCGTGAAGTGTTCGCTTCGTCGGCACAACCGCGCGCGCGCTTTTCAGACGGCATGACCTTCGGAACGGCAGTTCGAATGTCTGCCGCTCATGCCGCTTT  
CCTGGCTGCCGCTGGCGCGGCTACACGCGCAAGCAGCGCGCGCTTTTCGGCAACCTGACGGCAACGCTCGCTTATACGCTGACGGCGCTGCTGATGTATGCTTTGGGTTTGGCGCG  
GGCTCTGTTTACCGGAGAAACCGACGTGGCGAAATTCCTGTTGGCGCGCGCTTTGGGCAATACGGCGCATTTTCGCGAGTCTGCTCTCCACCGTTACCAACAGCTTTCTCGATACCTATTCC  
GCGCGCGAGTTCGAACAACATTTCCGCGCGTTTTTCGGGAAATACCGTCTGCTGTCGGCGTTTACCTGATCGGACCGTGTCTGCCGTATGCTGCCCGTTACCGAATATAAAACTTTC  
TGCTGCTTATCGGCTCGTATTTCGCGCGATGCGCGCGCTTTGATTCGCGACTTTTCTGCTTAAACCGCGGTGAGGAGATTGAAGCGTTTGACTTTTCGCCGAGTGTCTCTGCTGCTGGC  
AGGCTTCATCTCTACCGCTTCTCTGCTCTGCTCGGTGGGAAAGCAGCATCGTCTGACCGCGCGCTTAATGCTGCGGTGCCATTGCCACCGTATCGGTACCGCTTTTCTTAAAAAA  
ACCCAATCTTTACAAAGGAACCGTCA

## SEQ ID 590

LGWQRGLAALLLGHAVGGALFFAAAYIGALTGRSSMESVRLSFGKCGSVLFSVANMLQLAGWIAVMIYVGATVSSALGKVLMDGESFVWALANGALIVLWLVFGARRTGGLKTVSMILLHL  
LAVLWLSVEVFASSGTNAAPAVSDGMTFGTAVELSAVMPLSWLPLAADYTRQARRPFAATLTATLATTITGCMYALGLAALFTGETDVAKILLGAGLITGILAVLSTVTTTFLDTYS  
AGASANNISARFAEIPVAVGVTLIGTVLAVMLPVTEYKNFLLLIGSVFAPMAAVLIADFPVLKRREBIEBGFDFAGLVLMLAGFILYRFLSSGWESSIGLTFAPMSAVAIATVSVRLPFAK  
TQSLQRNFS

## SEQ ID 591

ATGCCGATATAATCAAGCCCTGATTTTTTATGCGCGACACTATGCATCCGACCTATTCGCCGCTACAGCGCGCGCTGCTCGAAGCCAAACCGCTTTCCCGGAACTGCTCGCCAAAGCC  
TGTGCATCATCGTGGCGCAACGTCGATATATGCGATATCTACTGCCAGCGCACCGCTTATGAAGCTGGCATTTGGAAGAGGCGATGCTCAATCGGGCAGCTTCCAAATCGATCAGG  
TGTGGCGTGGCGCGCTTTTCGGGCGACAAACCGCTTTGCTACGCCGACACCTGTGTCATCGATTTCGATAAACCGTTTCGCCCGCGCGCTGCCCGGATTTGGGCGGCGAGCGGCAAG  
GTGTCGCCGCAAAATGCGCTCTGAAACCGCGCGGCAAGCGGTTTGTTCGATTCGACCCCAATTGCCCGGCTCGATTTCGCCGCGCAAGCTGCGCGTGTGAACAAAGTGGAAAGCAATCGCCA  
AAGCCGCGCATTCGCCCATCTGCAAGTATGGCGGTTTGAATCGCAATACGATATGGTTTACCTCGCCGCTGCGACGCGCAACACGCGCGGACATCCGCCGATGCTGCGCTGAA  
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AAACAGCCCTGACCAATTCGAATCCCGTCTGCGCTGCGCGCGAGATGACCGTCTTTTGGGCAACGTTTGGCGCGCGTGTGCTGCAAGAGCGGTTCGGACACGTTTGAAGGG  
ATTTCAACCGCAAGGGGACGCGCTTTTCCGGCGGATCGCGCAACCGCTGCGCGCAAAAGCGTTTACCGTCTGATCAGGGCGATTTGCCCGCGCGCGGTTTCGCTCAACATCGA  
CGACGAAGGCAACGAAACAGCGCGCACCGTATTGATTGAAGACGCGATCTTGTGCGCTATATGTCAGGACGAAACCAACCGCGCGCTGACGGGTACGCAATTCGACGCGCGCGCGCG  
CAAGCTACCGCTTCGCTCCGATGCGCGGTATGACCAACCTTTATGGAACAGCGGACGCTACGAGCGGCGGAGAAATCATCGGCTCATCGACAGGGCATTACCGCGTCAACTTCGGCG  
GCGGACAGGTGGACATCACAGCGGGAATTTGCTTTCGGCGCGTCCGAAGCGTGGTGGTGGAGGCGCGAGGCTGCAATACCCGTCAGAGGCGGCAACATATCGGCAACCGCGCGCGA  
AGTGTGAAACACGTTTCGATGATAGGCAACGATACCGCGTTCGACAGCGGTGTGCGCGTGTGCGGCAAGAGGCGAGCGTCCCGCTGCGCGTGGGCGAGCGGACCTGCGTATCGAT  
GCCGGCTGACCGTCCGGCGCAGCGCAATC

## SEQ ID 592

MPYQAPDFLCADTMHTYSAVQARLLEANRLSPELLAKSLCI GAHHVDYADTYQRTAYESWHLKEGIVKSGSFQIDQGVGVRAVSGDKTAPAYASLCTDSINRSARAVRAIGAAGKK  
VSAKMPSETRGKPVCSASDPIAGLDSAAKVALANKVEALAKAADPRIVQVHAGLTCEYDMVYLARLDGKHAADIRPMVRLNVTVIARQGERRECGGAGGGGRYDLAYPDETIVRQFVDAV  
KQALTNLESRPAPAGETTVVLGNWPGVLLHEAVGHLEGDENRKGTSVSGRIGERVAAGGVTVVDQGLDLAGRRGSLNIDEGNETRRTVLIEDGILVGMQDETNRALGTQSTGNRR  
QSYASVPMRHTWTFMENGSTYEPERI LASIDKGIYAVNFGGQVDITSGKFPVFGASEAWWEGGRLQYPVKGATLIGNPEVLKHSVMI GNDTALDSGVGVCKRQSVPVGVGQPTLRID  
AGLTVGSAI

## SEQ ID 593

ATGCCGCTGTAACAACTTTACAGCGGCATCGTCCCGGATTCGCGCTCAGATTGCGCTGCGCGCGCAGCGTTCAGCCCGCATCGATACGAGGGTGGCTGCCCAACCGGACGCGGACGCTC  
TGCCCTCTTTTCCGCCACACGCGGACACCGCTGTGCGCGCGGTATCGTGTGCTTATCATCGAAACGTTGTTTCAGCACTTCGGGCGCGTTGCCGATAATGTTGCGGCTTTGACGGGTATTT  
GCAGCGTCCGCTTCCACCCACACGCTTCGAGCGCGCGGAGCAAAATTTCCCGCTGGTGTATCCACTGTTCGCCCGCGAAGTTGACGGGTAAATGCCCTTTGTCGATGGAAGCGAT  
GATTTCTTCGCGCTCGTAGCTGCGCTTTTCCATAAAGGTGTTGTCATACCGCGCATCGGACGAGGCGTAGCTTTGCCCGCGCGGTTGCCGCTGATTTGCTACCGCTCAGCGCGGCG  
TTGGTTTCTGCTCTGATATAGCGGACCAAGATGCCGCTCTTCAATCAATACCGTCCGCGGTGTTTCGTTGCTTCTGCTGATGTTGAGCGAAGCGCGCGCGCGCAATTCGCCCTGAT  
CGACGAGGTAAACGCTTTGGCGGCGAGCGCTTCGCCGATCCGCCGGAAGAGCGTGGTCCCTTTCGGTTGAAATCGCCTTCCAAACCGTTCGACCGCTTCGTGACGCAACACGCG  
CGGCCAACCGTTGCCAAAACGACGCTCATCTCGCGCGGAGGCGAGGACGGATTCGAGTTGCTCAGGCTTGTTCGACGCGCGCATCGACAACTCCGCGACCAAGGTTTCATCGAAA  
TAAGCAAGTCTGAGCTCTTCGCGCGCGCGCGCGCGCGCTTTCGCGCGCTTCGCCCTGTTTGGCGATGACCGTAAACGTTTCAGGCGACCATCGCGCGGATGTCGCGCGGTTCGCCGT  
CCAGACGGCGAGGTAAACATATCGTATTCGAGGTCAAACCGCGCATCACTTGACGATGCGCGGATCGCGCGCTTTGGCGATTGCTTCCACTTTGTTCAACAGCGCGACTTTGGCGG



GGAATCGAGCGCGCAATGGGTCGGATGCGAACAACCGCGCTTCCGCGCGCTTTCAGACGGCATTTCGGCGGACACCTTGCOCCTGCCOCCCAATCGCGCGGACGCGCGCGGAA  
CGGTTTATCGAATCGATGCACAGGCTGTCCGCGTAGGCAAGCGCGGTTTGTCCGCCGAAACGGCGCGCACGCCACACCTGATCGATTGGAAGCTGCCCGATTGACGATGCCCTCTT  
CCAAATGCCAGCTTTCATAAGCGGTGCGCTGCGCAGTAGATATCGCATAATCGAGCTGGTGGCACCAGTAGATGCACAGGCTTTTGGCGAGCAGTTCGCGGGAAAGCGGTTGGCTTCGAG  
CAGCGCGCTGTACGCGGAATAGTTCGATGCATAGTGTCCGCGCA

**SEQ ID 594**

MPSENLSGIDVPSASDCAADGQPGIDTQGRLEPHADGDLFFFAHADTAVERGIVAYHRNVQHFQAVADNGRAFDDGLQPAAFHPPRFGRADKFPAGDVHLSAAEVDGVNLDVGRD  
DFFRLVAAPHKGVGHTRHRRDGGVALAAAVAGRLRTRQAGVGFVLHIADQDAVFNQYGAACFVAFVVDVERTAPAGNIALIDGNAPGGDAFADPAGKDAGLAVELAFQTVSDRFVQQA  
RPTVAQNDGHLAGRRRTGFEIGQLFDGGIDKLPHQGFIEISQVVAASAARAALFAAFALFGDDGNVQAHHRADVGCVFVAVQTGEVNHIVFACQTGHHLDARIGGGDCPFHVQQRDPGG  
GTEAGNVGVCRTNRLAARFRHRPFGHLLAACRPNRADGAGTGVYRIDAQAVGVGKGGFVARNGAHAHTLIDLEAARFDDALFQMPAFISGALAVDIGIIDVVRTDDAQAFGEQFGKAVGFE  
QPRLYGGIGRMHVSVA

**SEQ ID 595**

ATGCCGCTCGAAAGGTTTTTCAGACGGCATCGCCTTATCTTTTTCCGATGTTTGATATTCCTAAGCATTCTTTAACATTATCTTACAAGTTTCATTAATAACCGCCTTTTCGTTAAGCTGA  
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CGGTGTAACGGCATACCGCATCCGCCCTTCTACGCATTGGCGCGCGCTTATATCGAGCTGTGCGCAATACGCCCTGCTGATCCAAATTTGTTTTCTATATACGGTCTGCCGAAAAAT  
GGGCATCAAGTAGGRCGTTTACCTCGCGCTAATCGCGCTGGTTTTCTTGGCGCAAGCTATATGGCGGAAGCTGTCCGCGCGGCATCTCCCGTCCCAAAGGGCAGGTTCGAGCG  
GGCAAGGCAATCGGTTTGGCGGCTTTCAAGTGTTCGCTATGTGCAATTCGCCGAGGTTTGGCGGTCGCCGTTCCCGCATCGCGCAAAATATATTGTTTTAATGAAAGAACATCCG  
TCGTGACAGCGTGGCATTCGGAATTTGTTATTTGTACCAAGACGTCATCGGTATGGACTACAAAACCAA

**SEQ ID 596**

HPSEFSDGIALFFPHFDIPKHSLSYKPIKIPFVKLISDELALPNRCRTQIRRCGKADAGIVLRRCFVAVRPARRRNGIHPHPLLAIGARLYRAVAQYAPADPIVFPILRSABN  
GHQGRPHLRNRAFGLRKLKLYGSGCPRRHRPRPQAGRSQGNRFELSSVPLCLRLAAGLGRSRHRRKTYIVFNERNIRRHGRHRCGIVICYQRHRYGLQND

**SEQ ID 597**

ATGAACCTGGCTTATTTAATCGATGCCGTACCCAAATTCGCCGATGCCGCAAGCTGACGCTGGAATTTGTCGTTTACGGCGTTGTTTTGTCGTTGTCGTTTTCGCCCTGCCCGTGG  
TAAOCCGATACCGCATCGGCCCTTCTACGCATTGGCGCGCGCTTATATCGAGCTGTGCGCAATACGCCCTGCTGATCCAAATTTGTTTTCTATATACGGTCTGCCGAAAAATGGGCAT  
CAAAATGGGACGGTTTCACTCGCGCTAATCGCGCTGGTTTTCTTGGCGCAAGCTATATGCGCGGAAGCTGTCCGCGCGGCATCTCCCGCTCCCAAAGGGCAGGTTCGAGCGCGGCAAG  
GCAATCGGTTTGAAGCGCTTCAAGTGTTCGCTATGTGCAATTCGCCGAGGTTTGGCGGTCGCCGTTCCCGCATCGCGCAAAATATATTGTTTTAATGAAAGAACATCCGTCGTCA  
GCACGCTCGCATTCGGAATTTGTTATTTGTACCAAGACGTCATCGGTATGGACTACAAAACCAATGAAGCCTTGTCTCGCTGTTTTGCCGCTTATTTGATATCTGCTGCTGTTTC  
TTGTTTGGCGCGCGGATTTGAAAACCGCTACGGAGTGCGAATATGCGCT

**SEQ ID 598**

HMWPLYLIDAVPKFADAAKLTLELSVYGVVLSLFGLPVAVVTAYRIRPFYALARAYIELSRNPLLIQLFFLYYGLPKMGIRKWDGFTCGVIALVFLGASYNABAVRAGILAVPKQVQAGK  
AIGLSRFQVFRYVELPQWAVAVPAIGANILFLMKETSVSVTVGIAELFLVTKDVGIMDYKTNEALFLFAAYLIILLPVSLARRIENRVSAYKV

**SEQ ID 599**

TTGGCGCAAGGCTGCTCTTAAACGGCACAAATTTCTTTAATCTCTGTTGCGGCTTCTTGCCTATTTGGGCAAGCTGTTCGGCTTGGTTTTGCGTTTCGCCCAACCGGCTTGTCCGCTTTGTG  
GACGGTTTTATCTCGAACAACATCGAATCGTCCGATTTTGGTGTGGCTGTTCGGCTGTATTTCCGCTTATCCGCTGAGCAGGCATCCACATCGCGGATTTTGGGTCGCTGCTGGGT  
ATTTTCCCTGTGGGCGTTGCCGAAATGGCGACTTGGTGGCGCGCACTGGAATCGATTGAAAAACACAGGTGGAATCGGGCTTGGCGCGGCTTGAAGCGGGGCGAGGTATTCGCG  
TGCATCGAGCTGCCGCAAGCATCCGCCGCTATTTGCCCGCGCGGTCAACCTGTTCACGCGCATGATCAAAACAGCTCGCTCGCTGCTTATCGCGCTGATCGAAGTGTCAAAGTCG  
GGCAGCAAAATATTGAAAACCTGTTGCTGACGACGCGCAATGCTTCAATTTGGGTTTACGGCGTGAATTTTATGCTGATTTCTCTGTTGCTGCGCGCTATCTCTACTGCGCGCAAACT  
TGAACAAAAATGGGAACAC

**SEQ ID 600**

LGBGLLLTAQISLISVAACVLGTLFGLVLRNRNLRVVRGFFLETIRIVPILVWLFGLYPLSVWTHIGHIGFVWCVVPSLWGVAMGDLVRGALESIEKHQVESGLAPGLSRGQVFR  
CIRLPQSRRLVPGAVNLFTMRKTSIAWILGIVBVVKGQIIENSLTQPNASFWVYGLIFLHYFPCCWPLSLLAAKLEQKWEH

**SEQ ID 601**

TTGCAACACTGCCGGAACGGATAAATCCGATTCACCCACTTCGTATTCGCCGAAAGCGGAATCCGTTGCGTTGGGTTTCAGTCATTTCCGATAAATCTCGCCGATTTGTATTT  
CTAGATTCCCGCTTTCGCGGAA

**SEQ ID 602**

LQTLPERINPDSHPLRHSRESGNPVRWGSVIDKLLPHCISRFLSRE

**SEQ ID 603**

TTGCATCTGATTGGGTGTATCGCTTTTTCCTTTAATGCGCCATTTATATTTGCCACTTTCGCGATGAAGCCGTTTGGCGAAAAATATCCCCACAGCTTTCGCGCAACTGCGCG  
ACGAAGCCCTGCCCGCATACGCTAGATTGCCCGAATGCGCGCTGCGGTACAGACGTCGCCAGTTGGACAAGGAGAGGCGGCTTCTGTCGCCGTTGCGGACACAACTCTTCAGGGT  
GGCAGCCACCTTTTTCGCGTCCGCCCTATGCGCGCGCTTCGCTGATTGTATGAGGCGTTGCTTACAGTATGACGTATATCGAGGTGCGGATACCGGGTCCGCGATCCGCTCTTCG  
CTGCCGAGATGATCGCTGATGTTTTCAGGATTATGGTTTTTGGCGGAAGTGTGTTTGTGCTGACTTTTGGCGCGCGGCTTCTGTTCTGCTGCTGCTGCTGATGCTATGCGG  
CGCTGATACGGAACAGCGTATCTGCGCTGCGTTTGGCAACGCTGTGATGTTGCGCTTGAAGCAGGCGATGATGTTGATGTTTGTGTTTCCACTCTGTTGGCTATATCAAGCT  
CTGCTGTTGCGCAAGGTTTCGCTTCCGCGCGGCTTTATCTGATGTTGCGCGCTGCTGTTATGCTGATTCGAGCTTCGCTATCGGTTCCCGCAGATTTGGTGTATTTCCAAATCGCGCG  
CTGACGGGAATAATCGGTTTCAGACGGCATCGGAAGGCAAACTGTTGACGCGCTGCTGTTATTTCCGCGACAGTCCGGAATCCCTTCCGGGGTGTGCGGCGCGGAACGTACCGCC  
GACGCGCAAAAGTCTGATATTTGTCGCGCTTTCGACGCGCGCGGTTGTTTGTATTTCCCTGCCAATATCTGCGGATTTGATTGCTGCAATCTGCGCGCACGAGGCAACAC  
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CGGCGAGGTTGCTTTTCCGCGCGGCGCAAGAAATGTGCGACCTCTACGCGCATCAGCAAGCGGTCGCGCGCTGGTTCGATGATTGATATTTTGTGATTATTTTGTGATTGTTTCGT  
TCCACACTATGCGCGCGCGCTTATCCGCGCAGTGGCGAGTCTATTTGCTGCTGCTGATTTCGACGATGCTGTCGCCCTATTTATTCGACCGCGCGCTGCTTTGGGACAAACGCG  
TTCAGACGGCATTCCTTCAACGAAACGGAATAATGAC

**SEQ ID 604**

LHPDMVYRFPSPIMPPIFATFPKMPAENIPHSLEGNCRDALPHTVDCPECGCRTDVPQLDKGEAARPCRGHKLFRVGSHPFSGPPAYAAASLILMAFAYSMTYIEVIGPAAASVLS  
LPEMRLMWPDYGFLEAVMPLVFGAPVLFLLCLVYAALIRKQAYPALRLAFTVRMVRRLQAMMVDVFPVSTLVAYIKLSSVAKVRPGAPAFYLMFALSVMILRTSVSVQHWVYPIGR  
LNGNNAVOTASEGRTCCSRCLYFRDASPCGVCAGELVRRRPSLSISSAFLTAADVLYFPANILPIMISSNPAAETANFIPSGIAYMDEGDRLLAAVIPSASILVPLKIAAMSVLIA  
AARFALPAGAKLSHLYRTAAGVRWSMIDIFVIIILMCSFHYYAARVPGSAAVYPLVILVILMLSAYYFDPRLLDKRAADGIAFNETEKYD

**SEQ ID 605**

TTGTGGCGCAAGCTGCACTTTGGCGCGTTTGGCGAGCTGCTGTTTTTCGGTCGAAGTATGATCGACGCGCGCTTCGACGCGGTTGTGAACAGTTCGACAATGACCGACACAAAGAC  
CGGATAATCAACGGCAGGCGGACGCGGTTTCGGAACCCAAAAAATGCCGCGCACACAGCAGCGGTTTCAGCCACAAACCTGACGGAATGCCACTTCGTAACGGTAGGCGCGCGGCA  
TGCCGCTATCGAATAGCGGAATGCGTTGATGACGCGCTGATGCGCTTTTGCTTTTTCCTGCGCGTACGAGGAAGGTTCCATCGGTATCTTTCAAAATGCTCTCAATATATGCG  
GTC

**SEQ ID 606**

LCGRCTCFGAFGQLVFFGRSLMDGGFDGGVEQFDNDRHKRRDNQRQADGGFGNPKKCAHQQRVQPNLTCHEFVTVGSGDAVYRIAECVDDAPDAAFAPFFFCRVGGRFHRYFPKMSSTIYA  
V

**SEQ ID 607**

TTGAACAAAATGGGAACACTGACATGGCTTTACTGAGCATCCGCAAGCTGCACAAAANTACGGCAGCGTAACCGCCATCCAATCCTTAGACTTGGACTTGGAAAAAGGCGGAAGTCATCG  
TACTGCTGGGCCCCGTCGGCTCGGCAAAATCCACCTCTTGGGCTGGCTCAACGGTTTGGAGCGCACCAAGCGCGCAGCATCGTGATGGACGGTGTGCGCGAAATTCGGCAAGACGTTTC  
CTGGCAAAACCCCGCGCAAAAAGTCGGTATGCTCTTTCAAAGCTACGAACCTGTTTGCACCACATGACCGGTATCGAAAACATCCTCTTTAGGCCCCGTAAAGGTTACAAAACCGCGACCGTGC  
GAAGCAGAGGGCGCAAGCGGCAAACTGTTGGAACCGGTGGAGCTGCTAGACCGCAAAAAGCCCTATCCGGCGGAACCTTTCCGGCGGTTCAGAAACAGCGCATCGCCATCTGTCCGCGCCCTGT  
GCTTGAATCCGGAAGTCTATCTGCTGGAAGCAAATCACCGCGCACTTGACCCGGAATGGTGGCGGAAGTCTTGAAGTGGTTTGGAACTCGCCCGCGAAGGGAATGAGTATGCTCATCGT  
ACCGACGAAATGGGTTCTCGCAAGAAAGTTGCCGACCGCATCGTCTTATGACACAAGGCGGCATCGTGAATCGTCCGACCCGAAACCTTTTTCGCAACAAAAGCGCAACGGCC  
CGCAATTTCTGCGCAGGTATGGACTAC

**SEQ ID 608**

LNKNGNTDMALLSIRKLKHQYGSVTAIQSLDLDLEKGEVTVLLGPSGCGKSTLLRCVNGLEPHQGGSIWMDGVGEPKDVSRQTARQKVMVFQSYELFAHMTVTIENILLGPFVKVQNRDR  
EAEQAQAGKLLERVGLLDKRNAYPELSCGQKQRIATVRALCLNPEVILLDEITAAALDPEMVRVLEVVLELAREGMSMLITVTHEMGPAKKVADRIVFMDKGGIVESSDPETTFVSAPKSE  
RQPLAGDY

**SEQ ID 609**

ATGTTTGCTTGGGATGTTTCAACACACAGGACGACACATAAAGCACTGCCCTATGAAATGCCGTCTGAAAAGGGTTTCGGACGGTTTTCGGG

**SEQ ID 610**

MFANDVSTHRTTHKALPYEAPSEKGS DGLR

SEQ ID 611

ATGAATTGAACGCCAAACTCAAAGCCCTTTTGGCTCCGCCGCCATCGCCGTCGGTGTGACCGCTTCGGGGGGCGGCTCCGGCGATGCCAATCTTCACAAAGCAGCGGTGCGGCAACCG  
TTGCCGCCATCAAAGAAAAGCGCTTATCGCATCGGGTATTTCGGGCACAAACCCCGTTTCGGCTATGTTGACGCAACGGCAAAAACCAAGCGTTTGACGTTGAAATCGCCAAAGACCT  
GGCCAAAGACCTGCTCGGCAGCCCCGACAAAGTCGAATTGCTCTGACCGAGGCGCCAAACCGCGTGGAAATGCTCGCTTCGGCGAAAGTCGACCTCATCTCGCCAACTTTACCCAAAC  
CCCGAACGCGCCGAGCCGCTGATTTCCGCCGATCTCTACATGAAAGTGGCGTTGGGCGTGGTTTCCCCCAAACCAACACCGATTACCGCATGCGCGCAATTGAAAGACCAACCCCTGCTGG  
TCAACAAAGGCACCAACCGCCGACGCTTCTTCAACAAAGCCATCCGGAAGTCAAGCTGTTGAAATTCGACCAAAAACACTGAAACCTTCGACGCGCTGAAAGACGGTTCGGCGGTAGCACT  
CGCGCACGCAACGCCCTGCTGTGGGCGTGGCGGAAAGAAAACCGCAACTTTGAAGTCGCCATCGGCAATCTCGGTCTGCCGAATTTATCGCCCCCGCGTTCAAAAAGGCACACGCGAC  
CTCTCGAATGGGTCAACGGCGAAATCGCGCCATGAAAAAGACGGCCGTCGAAAGCCGCCATTGAAAAAACCTCTCTGCCCGGTATGCGGAGAAAGTCAAACCGAAGCATTTGTGG  
CCGAA

**SEQ ID 612**

MKLNAKILKALLASAAIAVLGTACGGSSGSDAQSSQSSGAATVAAIKKGVIRIGVFGDKPPFGYVDANGKQGFVVEIAKDLAKLDLGGSPDKVEFVLTEAANRVETVRSKGVDLILANFTQT  
 PERAEAVDFADPYMKVALGVVSPKNNPITDMAQLKDQTLVNNKGTIADAFITKSHPEVKLLKFDQNTETFDALKDGRGVALAHNDALLMAWAKENPNFEVAIGNLGPAEFILAPAVQKGNAD  
 LNNVNGEIAAKKDKRLKAAVEKTLIPVYGEKVKPEALLAE

SEQ ID 613

GTGGCGGATTTTTTCAGCGCGCGAAAAATATTGCAAATTCAAAGGAAAAATCAACTATCTCATCGTTTTATTATTATTATTATTCTTGCGCGTGGCGGAAATCAAGTTCTGTCGGGTTTTCGCT  
GTTT

**SEQ ID 614**

VRIFFSRRKYCKFKGKINYLVLFILLFLRVRKSSSSGFACF

SEQ ID 615

ATGACGATTTGGAAGTTTCCCGAAATTCAAAAACAGGCAAAACCGGACGAACCTTGATTTCCGCACGCCGAAGAATAATAAAATAAATAAAACGATGAGA

**SEQ ID 616**

MTIWKFPRIKOAKPDELDFRTRKNNKINKTFR

SEQ ID 617

TTGACAGAGAAAATCCGATCCGCATTTGAAGCGGGTCGGGATTTTTTTCAGCCGCCGAAAAATATGCAAAATTCAAAGGAAAAATCAACTATCTCATCGTTTTATTTATTTATTATCTT  
GCGCGTCGGGAAAATCAAGTTCGTCGGTTTTGCGTGTTTTGAATTTCCGGGAAATTCACAAATCGTCATTCAGATAAAAACGCTTCAGCTTATGTTTCCGATGACCGTTTCGCGGGA

SEQ ID 618

LTRKSVSAFEGGCGFFSAAENIANSKEKSTISSFYLFYYSCACGNOVRPVLVVFEPRETSKSSFOIKRPSLMFPMTVPAG

SEQ ID 619

TTGAAACAAGCGTGGCCGAAAGCCGAAAAAATGTTCAAGCCGATCGCGGCAGACGGGACGAAAAATGACGTTTGACGAATGTTGGGCTTGTCAAATCGCTAAAAATTGAAGCAAGGA  
TGCTGCTGCAATATGTTTCGGAATATACGCGCGTCAGATTGTTGACGCGGGGCGGGGAAGAAATGCCGGACGAAATCCGACAGCGGGCGGACAGGCTGGCGCAACCGCGCTTGAAACGGCGA  
GCCGGTGCCTATATTTAGGTGTGCGCGAAATTTATGGCAGACGCTTTACAGTCAACCCGAACGTGCTGATTCCGCGCCCGGAAACCGAACACCTTGTTGGAAGCGGTATTGGCGCGCCTG  
CCCGAAAACGGGCGCGTGTGGGATTGGGGACGGGACGGGCGAGTTGCCGTAAACCGTTCGCTCGAAACGCCCGATGCGTTTGTGCGCGCATCCGACATCAGCACGCCCGCCCTTTGAAA  
CGGCGCGGAAAAATGCGCGGATTTGGGCGCGGGTCAAAATTGCACACGCTTCGTGGTTTCGACACCGATATCGCTCTGAAAGGCAATGGGACATCATCTGTCCAAACCCGCCCTATAT  
CGAAAAACGGCGATAAACATTTGTGCGCAAGGCGATTGCGGTTTGAGCCGCAAAATCGCGCTGACCGACTTTTCAGACGGGCTAAGCTGCATCCGAACCTTGGCGCAAGGCGCGCCGACCGT  
TTGCGCGGAAGCGGGTTTTGTTGTTGGAACACGGTTTCGATCAGGCGCGCGGTGCGCGGCTTGGCGAGAAATGGTTTTCGGGATGGGAAATCTCGCGGATTGGCGCGTTTGG  
ACGGGTTACGCTGGGGGATATGAAATTTGAAA

SEQ ID 620

LNKRAAKPEKMFPHRRQTGRKMTFDZWLGLSKLPKIEARMLLQYVSEYTRVQLLTRGGEEMPEDEIRQADRLAQRRLNAGEPVAYILGVREFYGRRRFTVNPVNLIPRPETEHLVEAVLARI  
PENGVRWDLGTGSGAVAVTVALERPDAPVRASDILSTPALETARKNAADLGARVEFAHGSWFDITMPSERQWDIIVSNPPYIENGDKHLSQGDILRFEPQIALTFPSDGLSCIRTLAQGAPDR  
LAEGGPILLLEHGFDGGAAYRGVLAENCFSGVEILLPDLAGLDRVTGLKYNKHLK

SEQ ID 621

ATGAATGACGCTAGTGTGCCGTAATCGTTATGCTGGTGTCTGCTGCTGCGCGGTGCACTGGTATTGAGCCTGACCGTGCGGCGCTTTGTCGGGGCGCGGTGGCGGGTATGCCGCTGC  
AAAACATTGCCGATGCGCGGGGACAGGTCACTCAGCGCGGGATTATCCCGGTGTTCAACAAGGTTTGSAGGCGCGCGGAAGATTGCGCTTCTTATGCGATGCTTGGTGCGTTTGGCAT  
GGCGATTACCAATTCCGGCTTCCGCGACAGCTTCCGGCGCGGTCTGTCGCAAGCTGAACCGGGCGGTATGCCGACAGCGTGCTGGGCGGAGGGCGCGGTCAAATGGCTGCTGCTT  
TCCATCATCTCTTGATGGGCAATATAGATCAGAACGTCATACCATCCATCGCGCTTATACCGATGATGTGTCGCGCGCTGCTTTGGGTGTTTAAACGCGCTGAAAATTCGACCGCGCC  
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GATACGCGCGGCAACGCGGATGCGCGAAACCGTCCGAGCGCTCCGCTCATCCGACGCTGTTTCCGCGCGCGCGCATTCGCGGTATGCTTGTGCCATTCGCGATGTAGAGATTGCGTGG  
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TGCCGCGCAGGGTTTTCGCCCGTGATGAATGCGACCGGGCATATTCAGCCGCTGGTGGAAAGCAGTATGCGCATATTCGCGCAACAGCAAAAGGTATGGCGGCTTGGCGATGTCTGGTGTG  
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GCACGCGGGGGGGGTGTGGGCGATGCCGGTTCCGCCGCGTCCGATTCCACGCTGGGCCCGACGATGGGGCTGAACGCGACGGGGCGCACGACCATATCCGCGATTCCTGTCATCCGACCTT  
CATOCACTACAACATCCCGCTTCTGATGCCCGCTGGATTGCCGCGATGTTGCTG

**SEQ ID 622**

SEQ ID 622

MNAVVVAVIVMLVLSRVRHVLSLTVGAPVGGAVAGMPLQNTIADAAGQVSQAGITPVFNKGLEGGAKIALSYAMLGAFAMAIHSGLPQOLAGAVVRKINRGGMPDSVRSGECAVKKILL  
STILVMGTISQNVPIHIAFIPMIVPPLLIVFNRKIKIRLLIACVITFGLVTTYMFLLPYGFGAIFLNEILLGNTHSAAPQOLVKNINVMAMAIPALGMLAGLLPAVHYRKRPLQYSNA  
DTAGNADAANRRPQPSAYRSLVAAAAIAIVCAIQLMYEDSLVLGAMLGFAVFMGLGVNRDKANDVPFGEIGKMAVGVFTIIAAQGFPAVMNATGHQIPLVRESSMAIFGNSKGMRAALANLVV  
GLLVFMGTGSSFTSLPIIAITYVPLCTGLGFSPLATAAIVCTAGALGDAGSPASDSTLGFTMGLNADGRHDHIRDSVIPFTFYNIPLLIAGWIAANVL

**SEQ ID 623**

SEQ ID 623

TTGCTTTTCAACGAAACGGAAAAATATGACTGACAAACAGCCCTTCTCCAAACGGACAGCGCTCAAGCAGCGSTCCGCAAAAACAAACCTTCTCTCCGCCGTCTGGCTGGTCCCGCTGATCG  
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CATGATGTTCGACGCGGTATACCGCAATCAAACTGCGCAGCAGCAAAAAGGCGTGAAGTTACTGCCAACTCAATCGCGAGGTATCCGGCCTCATCCGACGCGATACCCAGTTTGGGTG  
GTCAGAGCCGCGTATCGACCAAAGCGCGCTAACCGGTTTGGGTACGCTGCTTTCCGGGTTCGTACATCCGCTTTTACACCGCGCAAAAAGCGCGGAGGGCAAAAGACGTGTTCCAAGTCAGGACCA  
TTCGCCCGCTTACCGCATCGGGCAAAAGCGGGCTGCGCTTGAAATTGATTTGGTAAAAACGACCGCATCTTCAACGCTCAACGACCGCTTGTGTGTAAGAACTTTATGGTTCGGGCAAACTGCA  
AAGCGCGCATTTGACACCCGTCGACCAAAAGCGTGCTATTAACCATCTTCAATCCAAAGCGCCAAACGACGATGATTCATCTCCGCAACCGCTTTTGGCTGGAAGCGGCATCAATATCGAA  
ACCAACAGCAGCGGCATCAAACTCAATTCCGCCCTTGCTGCTGCCCTGTGTCAGGCGCGATTTCTATTGATTTCGCCGGAACCAAAAACAGTAAAAACGTCAAAAGCAGGACAGCTTCA  
CGCTTTAGCAGACGCGCAGCAAGATCGCCAACTGCTGCTGACGACCGCTGCTGCTACTACACCGGTTTTTCAAACAATCCGTGCGGGGATGACCGCTGGTTTGCCTGTGCGATACAAAGG  
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GCCGACGAGCAAAAGCAAGAGCATTTGGAACAACAATTCACAGCGGCTTAAACAAAGGCTGACCGCCACCTTCCGACGAACAACCTGCTGACCGCGCGAAATGATTGATTTGAACG  
ATCAGCCTTTCCGCTTCGCCCAAGCTGCGACCGTACCGCTTTATCGAGCGGATACCGTCTACCGGCGGCTGGTTTGAAGTATCGAGTTCGAGTCCAAATTTGGCGGATTTGCTGGACA  
ATTCAACAATCTGCCATTGGATAAAACCTTGCCCAATTGAACGGCTGCTGCGCTACCGCTCAAGTCCGCACTCAAAATCCGCAATGCCGCCCTAAGCTCCATTGACAAACTGGTCGGCAAT  
CCGACGACGCAAAACATCGGACGCAACTGAAACCAAACTCTGAAAGAGTTGCGCGATAACCTGCAAGCGGTATCGCTCAATGCGCTATCTACGGAGAGCTACAAAAATACGCTGCGCAAGTT  
TGGACAAAACCTTAAAGACGTTTCAACCCGTCATTAAACATTTGAAAGAAAAACCAACGCATGATTTTCAACAACAGCAGCAAAAGACCTTATCCGAAAGGAAGCGCA

**SEQ ID 624**

SEQ ID 624

LLSTRKKRNKNTNSPPNGHQAQRVRKNTFTLSAVWLVLPLIALIAGGWLWVKETNRNGFVVTTLMDSAEGIEVNNTVIKVLSDIVGRVTRIKLRDDQKGVEVTAQLNADVSGLIRSDQFWFV  
VKPRIQDSGVGTGLCTLSSGSIAPFTPGKSGEAKDVQVQVDIPPVTAIGQSGIRLNLIGKNDRLHNVNSPVLVYENFMVQGISAEHAPDSDQSGVHYTITQISPNQDLIHSARFGLRESGINT  
TTGSGIKLANSAPILPALLSGATISPDSPKTKNSKVKSKDSFTLYDNRSEIANLPDDRSLYTTAPFGQSVRGLTVGSGPBYRGLKGVMHNSVDVEYFTRINDSLHLFENGWIPVRIRIPEPSLEIN  
ADEQSEKHWNKQQPQTALNKGITATISNNLLTGGKMIELANDQFASPKLRPHETVYAGDTVIATRGQKGLDLQVGLSADLIDKFPNNLPDKTVARLNGSLAELKSALKSANAALSSIDKLGN  
PQOTNIPENLQDITKELRIGTLQGVSPQSPITGYDQVNTLQSLDKTLKDVQPVINTLKEKPNALIPNNSKDPITPKGR

SEQ ID 625

SEQ ID 625  
GTGGTCGGTACGTTAAACCGATGCCGCTCTGAAAGGCTTTTGCTTCGTAACCGCTTGGTTGTTCCGGCAGGCAGGGGTTTCCCTCAGCCGGCAGGGATGCCTTAATGCCGTACGGACAC  
CCTCCGCCCCCTTTTCAGACGGCATATAT

SEQ ID 626

SEQ ID 826  
VVGTLNRCRLKGFCFVTAWFVRAGRVPQPAGMRLMPYGHPSAPFSDGIY

SEQ ID 627

SEQ ID 627  
TTGGAACGCCGTATTGTGCGAACTGGAAATCCAAACCGCGCTTCAGGAGGACGTAATCTCCGGTCTGAACGCGATGGTGGCGGAATTGCGGCAGACGTTGGATTTCAGCAGGCTCAGTTGA  
GGCTGCTGTATCAAAAAATGCAGGACAGGAATCCCGACGGCGAAGAGCCGTATTCCTGCGCGACGAGATTCCGCCGCATTAT

SEQ ID 628

SEQ ID 628  
LERRIVELEIQ TALQEDVLSGLNAMVAELRQTLDLQAQLRLLYQKMODRNPDAQEPYSLRDEIPPHY

SEQ ID 629

[illegible]

SEQ ID 630

SEQ ID 630  
LNRVHLQHRHGNFAGNQKRDVVVDEGRDGIADMVVPFVGVPHRRQAQGI GRGTGLAQPRRADGGGGKRRKAQTGTQRHNRGNNRQSGKGRTHDAHYRQKPHQHQRHRTFAVAEY  
RHTAFAPHQRNLCRIHHGGKTLAGHNNEADHRHHLDAFAEYTVCLVAVNDPQHKKYGETEHRQAQQRITITQLYKAYGDDGGGNQAAVGGRLRTVCRIGVARRIIGTIALVQPSRFVAVDKR  
QQESGQHSQCGNHRCHRHVDVFHILKLRRGGMDVAQQDPVQKNRAEAVRQEHISRNQPESSDARNQAAVDPAVKHKQKRRNRNRDRGDDVGYDVLTHNAHHKDDGKQGFQFORALATHTAVG  
HTAFVQLADDRAGKLLRQAGMGNHRHKKRTKRTIRKKNLRAAFQTFVHSGDNPLTDLSSRI GNVLQRTHREAADKRADRAQYHVHARQHQHNDYGNYDCIHLSQLTYKCLHIKTHH  
NPITENPPILOTILNSTHNSPA

SEQ ID 631

SEQ ID 631  
ATGAACCGGTTCTGTCCGAACGGCGATGAGCGGCTTCCCCCGCTGCAAAACAGATAAAACCAACCGGTATTCAAACACAGCCAAAAAAGCCGTCGGAACCCAAAGGGACAGACGGCT  
AAACACATTACGGGGAACAGCTTACTCAATGAGTCTCGAAACAGACATTGCTAAACCAACTGCAATTA

SEQ ID 632

SEQ ID 632  
MKPWLVRTAMSGFPRCKOIKPTGYSNTAKKSRPNPKGTDGQTHYGENVLLNESAKQTLKQLQL

SEQ ID 633

SEQ ID 633  
TTTGACGAAATCGGCATCGAAGGCAGCAGAAGCTTTCCGCGCGCATATTTTGGTCGTGGCTGCGGCGGATGGGCGCGCGCGCCCTGCCCTATCTCGGGCCTCGGGCGTGGCGACGC  
TGACCATAGCCGATTCGCACACCGTGCAGCTGCACAACTGCAACGCCAAGTCCCATTTGACGAGGGCCGATGTGCGCAAGCCTAAAGCCGAAACCTTGCGAGGCCCTGAAACGCATCA

CCATATCTGTGCGATGTCGCCGCCGCTCAACGAAAACTCGACGGCTGCCGCTGACCGGTTTGGTTTCAACCGCGGCACATCGTTTAGACTGCTGGGCAACTACGCCACGCCGCGAGGGCGTCAACCGTGCCTTCGCTGCAACGAAAAACCGCTGGTTTCAGGGCGCGGGTATCGTTTGAAGGACAGCTTGCCGCATACCGTCCCGACTTGCCCGACTGCGCGTGTATAGCGCTGCTGTTTGGACGGCGGATCGGCTTCAGACGGCATCTGTTCCTCTTCGCGGTGCTCTCGCCGCTGGTCGGCATCTGCGGTGCACACAGGCGCGGGAGGCTCTGAAATCTGCTGGAAGCGGGCGAACCCTGCACAGCGCAGGCTGGCGGTTTACCGTGCTTGGAAGGGGGCTGGCAATATTCGACCTGCCCGCAACCCCGAATGCCGGTTTGGCGCGCGCACGG

**SEQ ID 634**

LEDETGEGQKLSAAHILVVGCGGLGAAALFYLAASGVGTLTADSDTVELHNLQRQVAFDEBVGKPKAETLAGRLKRINHIVDVRVAVNEKLDGCRITGLVQYTDITVLDDCCNYATRQAVNRACVQTKFPPLVSGAAVRFEGLQAAAYRFDLPDPSCYACLFDGGSASDGTCSLFGVLSPLVGVIGVCTQAAEBALKITLLEBAGEPSHGRLAVYRALBGGWQYFDLPFRNPECPVCGAAR

**SEQ ID 635**

GTGGCGGCGTGTACCGCAGCAGGAAGTCGTCGTCGTTGTCGTGTCGCTCGCGGTCATGATGATGTTCCGAAAAAAACAGTTGCGGGCGATTGTAACCGCCGCGTCGGCGGCGGTTCAACTT  
CAGACGGCATTTTCGGGACATGAGTGGTTAAAGTGTGAACGGTTTGGCACCAGTACGGCATTTGAGGTACATTTACAGTATTTACGGCAA

**SEQ ID 638**

VAAPFOOECVVVVVFGRGHDDVRKKTAVAGDCNAVGRRSTSDGLSGHEWLKCRFGTDAAFEVHLQYLRO

**SEQ ID 637**

TTGAGGTACATTTCACGATATTTACGGCAATGAGAGGAAAATCATGCAACTGCATATCTCGAACAACTCGAAGGACGCGGCTTTGGCGGCGGACGCGGAATTTTGAACAGTCCCTGTTCA  
ACTCTCTGCAACGAAGAAGCCTCGCCGTTGGTTGTGCGAAACGGTCAAACTCTGTGTCACATCCGACGACAGCGCGGCATTTGATTGAAAAGATTTGCGCGCAATTGGACGAACGGCAGACCTA  
CGATCTGACGCTTGCCCTGCGGGCTGTTCGCCCAGATTTCTGAATATCGCCGAAGACGTGCACCAACGAACGCGCGCGCCAAATPCACGAAGATGCCGGCCACACGACGCAAGAAGGCAGCCTG  
ACGGAACACGCTCCGCGAGGCTCAAAAGCGGGGAAAGCGACGGCAAACTCGGTCAGCGGCGAGTTGGACAATACGTCGGTTACCGCGCGTTTTCGACCGCGCACCCGACCGAAGTCAACGCAAA  
CCGTTTGTGAATTTCAACCGCGGCATCCGCGCGCTGCTGCGCGCAACGCGAACGTCACCAATCGGAAGCGCTGAGCAGCTGTCGCGCGGCAATGCACAGCTGCTCTGGCTGTGGGCA  
GACCAGCGAAACCGCGCGCCACAACTCAGCTCAGCAGTCAACGATCAACAGCGGCTGTCCTATTTCCGATGAGCTTTTGTGAAGCCGTCGCCCAAATCTTACCGCAAGATGGAACACGAC  
TTTCAAGCGGCTATCCGATGTCGCGGTTTCGATATGCTTAAATATCGCGCGTGGATCGCGCGCGACCGCGACGCGCAATCCGTTTGTGTTCTGCGAAACCCCTGCGCTTTGCTTTCGCGC  
GCCACGCGGATGCCGTGTTCCGTTTTCACGCGAGCGAACTCGACAACTTTACCGCGAACTGCGCTTTCCATTCGCGCGCTCAAAATCAGCAGACGCTAATGGCACTGGCAGCCCTCTC  
GCCTGACGAAGAAATCGCCCGCACCGAAGAACTTACCGCGCGGCGATTTGCTTACATATGGCGCGCCTATGGGCAAAAGCGCGCTCGCTCGGTTTGGCATGGGCTGCAAAATTCGGCTTT  
CTCGAGCCTTTATGCTTTCGCGCCAAAATTTCTCGATGATTTGAAAAAATTCGAACGTTCCCTTTATCGACAACGCGCGCGCTGCTTGGCCGAAGGCGGCTTTGGCAGACCTCATCCGTTCCG  
TGTCGGTGTTCGCTTCCACATGATGCGCGCTCGACCTGCGCCACACGCGCAACACCGCCGATGTGGTTGGGAGCTTTTCAACACGACGAGCTTGGAAAGCATACACGAGCTGGAACGA  
ATCAAGAAAAACAGCGCGCTGTGTCGGAGTTGGGCAACAACGCTCGCTGTATCAGACCGGCTTCATCATATCAGCAGACCATACCCGCGCGGAATTTGGCGATTTTCAACGAAGCGCGCAAA  
ATCAAGAGCAATTTTGGCGAGATGCGGCTTAACACAAAGCATTATTTCCAATTCGGAACAACCCGGCGACCTGCTCGCTTGGCATTGCTGCTGAAAGAAAGCGCGCTGTGGCGGTGGA  
ACGGCAACACGCGCAGCGCATCAACATCGTGCCTCTGTTTGAACCAATCGAAGCGCTCGAAATATGCTGTGTCGGGTATGGAACACATGTTCCGCGCTGACGTGATGATGATGCCCTGCTCA  
AAGCGCGGCGACATCTCAAGAAATCATGCTCGCTATTTCGACTTCAACAAGAGACGGCGGCTACGTTACCAAGCTCATGTTGTCATCAGGCGGAATTTGGGCTTTGGTGCAACTCTTCTCAA  
AAATACGATGTCGCGCATGCTGTTTTCACGCTGAGCGCGGACGCTGGAAGCGCGCGCGCGGCTTCTACCAAGCCATCTTGGCGCAACCCGCGACGCGAGCTGTCGCGCAACATTCGCA  
TTACCGGACGATGAGCGAGTCTACCTCCGAAATACGCTCGCAACCGCCGCAACGCCCAACGCAACTTGAACAACTTGGTTGTGCGGCGATTTGAAGACGCTTCCGCGCAACATTCGCA  
TGAATGCGAACTGAGCGAGCAATTTGTCGAGCATATGCTGCTTCAATCATACCGGCAACTGATTAACCCACCCGACTTTCATCGACTACTTCTCGCAACACGCGCGATTCAGGAAATCGCCACC  
CTCAACCTTCGGCAGCGCTCCCGCCAGCGCGCAAAACCCCTGGCGCGAATTCAGGATTTACGCGCATTCGTTGGGTATTTCTCTGATGTCAAACCCGCTCATGCTGCGCGGCTTGGTACGGFT  
TCGGCAGCGCGGTGGAACACTTTGTGCGAAGGCGACCGCCGAAACCTTCGCGCGCTTCGCGGACACGCGCCAAAACCAACCCCTCTCTTCCAAAGCATGCTCTCAATATGGAACAAAGTATGATGGC  
GAAACCGCATCACTTTCGCGGGAACATACGCGCGTTTGAAGCGAATCAACCCGAAACAAAGTCACTTTCGACATGATTAAGGAAGAATACCGACGCGCGCAACCGCCCTGCTCGAC  
CTGCTGCAAAACGAAGAACTTTTTCGCGGACACCGCGACCTCTCGCCGCTTCGCTGCGTTTGAAGATTCCTATCTTGCACGCGCTCAACGAGTTTGAAGATGCGCATTCGCTCAAGCGCA  
AAGAAACCGCAACTTCGCGACCGCTCTGATGCTGATGTCACCTGACCATCAACGCGGCTGGCGCAAGGTTTGGCGCAATACCGCG

**SEQ ID 638**

SEQ ID: 638

LRVYTSYIGNERKIMQLHI LNPDPDAALAAADAEFLKQSLFNLLHEEASPLVVTVKLLSTSDSAALETKVLPLQDERQTYDITLACGLFAQIILNIAEDVHHERRRQTHEDAGHNAEBGSL  
TEVVRRLKAGKADGKSVQRQLDNTSVTAVLTAHPTFVQRQTVLFNFRRI RALLPQRERCTNADALARLRREIDTVLLGLWQTSETRHRKLSVNDEINNGVSIFPMSFFALPKLYRKHED  
PQTAYPDVRVPNILKIGWIGGDRDGNFPVSGETLRPAFRRHADA VFRFYRSELDKLYRELPLSTRRVKVNDVVMAALASPDEIARTREPTRYRAIAYTAMARAMKARSLSGLGMCKPGF  
LEPYASAQKFLDLDKFLQSLINDNGSRLLAEGRLADLIRSVSFVGFHMPMLDLRQHAGKHADVVAELFQHAGLEDVYNLNEBQQAALLRELGHQRPLYSPTFYTSWHLRRLALFNEARK  
IKDFEPGEAVTQTSIISNCEBQPGDLLALLLKESEGLLAVENGKPHSRINTVPLFEITALEACNCFVMTPEFLWDYDLALLSREGNITQIMLGYSVSDNIDGGVYTSXDLRQLRGLLWELFK  
KYDVRRMLFPHGRGGSVGRGGGSPSYQAILAQPAGSVAGQIRITEQGEVITAKYADPGNAQGNINLETVLVAATLESLILPKDKPDQAKMLQSGVDSFVKYITLITHPDDIDYFQTSPTQEIAT  
LNLGSRPASRKTFLARIQLDLRAIPWVSWNQNRMLPAWYGFPGSAVETLCEGSPETLALALBGHAQNNPFFQAMLSNMGEQVMKATDITLAEANYAGLSPESEKAKVIFGMKIEEYRRSRKALID  
LLOTELLRLDNESRLASLALRIPYLNALNGLOVANLKRKRKEPNPHALLMHLTITINGVAQGLRNTG

**SEQ ID 639**

SEQ ID 639

ATGATGAAAGTCTCTTTATGCGGACCGGATGGCAAGTTTCAAACCTACAAAGACACCCTACGCGATGATGCGGGAATGGCAAAACGCGGCTGGGCGTGTGTTTCATACCTTGAGCG  
GGGAATTTGCTGTAAACGGCGGTTTGGTAACGGCACAGGCATCGGCATTGAAATTTTCGGGTGCAAAAAACGATGATGACCATGAATGGTTTAAAGCGGGGACAAAGTTCAGACGGCAATT  
AAAAGAATTTGATGCCGTGATTATGCGTACCGATCGCGCGTTGATATGCAATACCTTTACTCACCCAAATTACTGACGCTGGCGGAACAGCAGGGCGCCAAAGTGTCTAACACGGCGGACGG  
CGCATGCGCGACTTTAAACGAAAACTGGCGATTTTGAATTTACGCGCTTTACCGCGCCACGCTGGTAAACGACCCGTTCCGCGCATGTCCGCGCATTTTGAAGAAGACCGGCGACATCA  
TCGTCAAACCGCTCGACCGCATGGGCGCATGGGCGATCTTCCGCTGACCCGAAAAAGACCCCAACATCGGCAGCATCTCGAAACCTTGATCGCGGTTGTAATCCCGCACCAATTCGCGCGCA  
ACGCTACATTTCCGGAATCTGTACACGGTGACAAACGCATCTTGATTATCGGCGCGGAAGTCGTCCTTCATGCTTTGGCGCGATATCCCGCAAAACGGCGAACAACCGCAATTCGCGCGCA  
GGCGGGCGCGGTGTGGCGCAGGAATTGGACGGACGCGCGGAAATTCACAGAGATCTGGCTCCCGCATGCTTTAAACGAGCGCGGCATCTCTGCTGGCGCGTTTGGACGTTATCGGCAGCAAC  
TGAAGGCTTAACGTAACGACCGCTTACCGGATTTCAAGAAATATGCAAGAAATTTGCAAGAAATTTTCGACGTTGGCGCGCAATGTTTGCGCATGCCGTTGCCGCGTGGTGGTACG?

**SEQ ID 640**

MMKVLFIADPMASFPTYKDYKDTTYAMREMARKGWRLFHTLSGELSVNGGLVTAAQASAFESGAKNDDHWFKAADKVQ TALKEFDVIMRTDPFFIMQYLYSTQLLTABEQGAKVFNSGR  
AMRDFNEKIALILNFSRPTAPPLVTITRSADVRAFLKHEGDIIVKPLDGMGGMGIFRLTEKDPNIGSILETLMRFDSRTIMAQRYIPEIVHGDKRILLIGGEVVPYALARI PQNGETRCNLAA  
GGRGVAOELDGRDRETAFTLAPELKRS GILLAGLDVIGSNLFEVNVITPTGPQELMKQKSFUVAAMFADAVAAWSVR

SEQ ID 641

ATGCAGGCGGAGGGCGGTACCCACGAACCTGCGCCGATACCGGTAATTTTCATTGGTCGCTCTTCAACATATCACTGCCGTTCACTTTAAACAATCGGTGTTCCTCTGCAAGTCCGGTC

SEQ ID 642

MOGERRTPTCADNGNFHWSFNISLPFTLKQSVFLCKCGQVNAV

SEQ ID 643

ATGCAGGAGAGCGCGTGAAACAAACCGCGCAGTGCOCGGCTTTTCTTTCCCGAAACCTTGGAGTGTGTGCGGATTGGCAGAGGCGCTCAAGACAGCGGACTTGTCTTATCGTAACCT  
CCGTGTTCGCGGATTGAGAAGCAGCGCAGAGCTGCTCAAACAGTACGGCGCGGGACAACCTCCCGCTCTCGCGCGCTGCAAAAGCTTCGAGCAGGATACAGGCTGTGTGACCTTCCAAGTCTT  
GAAAGAAGTATTGCCGACAAATAAGAAAATCGCGGTACTTTCCGGTCCGAGTTTGCA CAGGAAC TGC CAAACAACTGCCCTGCGCGCTGCTCTGCTCCGAAAACCAAGAGTGGATT  
GAAGAACTCGTACCGCAGCTCAACACGACGCTCATGAGGCTTTACGGCAGTACCGAGTTATCGCGCTGGCAGTAGGCGGTTTCAGTCAAAAACGCTATGGCAATGCTACCGGACTCTCCG



ACGGACTCGAATACGGACTCAACGCCCGTGCAGCACTGGTTACGGCGGACTGGCCGAANTACCCGCTTGCTCCGCAATGGGCGCGCAGCCAAAACCATGATGGGGCTTCCGGCAT  
 CGGCGATCTCATCTTGACCTGTACCGGTGCACCTTTCGCCCAACCGCGCTCGGCTTGGGTTTGGCAGAAGGCAAGGAATGCATCAGGTCTGGTGGAAATCGGGCAGCTTCCGAAGGG  
 GTCAGCACCATAGAAGAAGTCTTCAATACCGCTGCAAAATACCAATCGATATGCCGATTACCCAAACCTGCTGCAACTCATCCGCAAGAAATGACCCCTCAGCAGGTCTCGAAAGGC  
 TGATGGAACGACGCGCGCTTTCGAA

## SEQ ID 644

MQEARENKRLGPFSPFETLEVCAADLAEALKDSGLVLIVTSVAGLRSSABELLKQYAGHLFVLAACKGFEDTGLITFQVLKEVLPDNKICIVLSPGSPAQELAKQLPCAVVLASENQEWI  
 ERLVQQLWFTVMRLVGSVDVIGVAVGGSVKNVMAIATGLSDGLEFGLNARAALVTRGLAKITRLASAMGAPKTMMLAGIGDLILITCTGALSRRNRVGLGLAEGKELHQLVREIHRVSEB  
 VSTIEVFNPACKYQIDMPTTQTLQLIRKENTPQQVVERLMERSARFE

## SEQ ID 645

ATGCCCTCTGAACCCCGACAGCGCATACAGACAGGTAAAGTCATGAAACAAATAATCGAAAACTCGAAAGCAGCGTTTATACGTTGGTACAAAAATCGAAACCTCGTCAGCGAAAAAC  
 GCCGCTCAAAGAAACCGTCCGCGAACTCGAACGGGCGCAGAGCGGCAAACTCGAACGACGAGACCGCGCTCGACGAACTCAGCGAAGCCCTGCTCGTCAAGTCGGCAAACTCAAAGA  
 AGACCTGCAAAACAAATCGACAGCCTGACGGAAGAAATGACGATACCGCGCCCTGCTCGAACAGAGCAGGAGAAAAATCAGCGCACTGGCAGCGGCTCCCCCAACGGCAGGAAACG  
 CAGCAA

## SEQ ID 646

MPSEPPDGIQTGKVMQNIKLESSVYTLVQKPFETLVSENRRLKETVAELERAHERQKLEHETAVDELSEALLVQVVKLEDLQNKIDSLTEENAKYRALLEQSRKISALAARLFQRQET  
 QQ

## SEQ ID 647

ATGAACATCGAACAAGTCTACATCGAAGTCATGACGCCCGCTGACCGTCAACACGCGCGCAGAGAAAAAGACACACTGTTGACAGGAGTCGGAATGCTCAACGGCAAGCGGAGCCA  
 TCCCGCAGGCGCGCGCTCGCGGACAGCGGAAAAATCGTCATTATGGCCGCGCTCAACGTCCTCCAGACCTATTGAAACCTCCCTGAACGGCGCGGATTGGCAATCGGCGATTGTC  
 CGGTAAATAACCGATATGGAACAACGCTGCCAAAGGCACTATCCCGCTTGGGGCAGGAA

## SEQ ID 648

MNIQVYIEVMHARLTVMTPAEKDTLLQAVGMLNGKAEAREGGRVADSEKIVIMAALNVHDLRLKTSLNGDLAIGDFARKITDMDNACQKALSRLQGE

## SEQ ID 649

TTGCTGACAAGCGCGCTGCCCGGGTAGTTTCGGGTGCGTCCGCAAAAGGACGCTCGCGCCCACTACTGCTCCCGCAACCTTAAGCGAACTTATGCTTCAAAGGAATATATGCCTTCGC  
 GGACACCGCAGGGAAGGAGGGTTATCTCGCCCAAGCGGATAGTGCTTTTGGCAGGCGTTGTCATATCGGTTATTTACGCGCAAAATCGCGAATGCCAATCGCGCGCTTCAG  
 GGAGGTTTCAATAGGTCGTGGACGACGTTGAGCGCGGCAATATGACGATTTTTCGCTGTCGCGACGCGCGCCCTTCGCGGATGGCTTCGGCTTTGCGGTTGAGCATTCGACTGCC  
 TGCAACAGTGTGCTTTTCTTCTCGCGCGTGTGACGGTCAGCGCGCGCTGCATGACTTCGATG

## SEQ ID 650

LLTRRLPRVVSAGASGRSRPLPATLSLIGSKEYMPSRTPGKRGYSCPKRDSAFWQALSISVILRAKSPIAKSPFPREVFNRSWTLISAAMTIFSLSATRPPSRMASALPLSIPTA  
 CNSVSFSSAGVLTVSACMTSM

## SEQ ID 651

ATGAAACCTTTTCAGGAAACCCACAGGTTGAAGCGCAATGGTTCGTCATCGATGCCCAAGACAAAGCTTGGGTCGCGTTGCAACGGAAGTCCGACGCGCTTCGCTGGCAACACA  
 AACCTGAATACACCCCGCAGTCGATACCGCGGATATCATCATCGTCATCAATCGCGCAAACTCGCTGTAACCCGTCGCAAAATCGAAGATAAAAAATCTTCGCGCATTCGCGTTTTC  
 AGGCGCATCTACGACGCGCATTTTCGCGGAATGCAAGATCAATTCGCGCGCGCGCTTGGAGCAGCGCTGTAAAGGTATGCTGCCAAAGGTCGCTGGGTTACGCCATGATTAATAAA  
 CTGAAAGTGTACGCTGGTCCGAGCATGCCATGCTGCGCAACAACCAAGTTTGGAACTGAAA

## SEQ ID 652

MKTFSAKPEHVKREWFIDAQDKVLGRVATEVASRLRGKRPETTFHVDYIIVINADKLKVTGAKFEDKKYFRHSGFPGGIYERTFREMDDQPPGRALEQAVKGNLPGPLGYANIKK  
 LKVYAGAEHAAQPKVLELK

## SEQ ID 653

GTGTCTTATTATTTCAGTTCAAAACTTGGGTTGTTCGCCAGCATGGGCATGCTCCGCCACCGCTACACTTCAGTTTATTAATCATGGCGTAACCCAGCGACCTTTGGGCAGCATA  
 CCTTTTACAGCTCTCTCAAAGCGCGCGCGGAAATGATCTTCGATTTTCGCGGAAAGTGGCTCGTAGATGCGCGCTGGAACCCGGAATGGCGGAAGTATTTTATCTTCGAATTTGG  
 CACCGTTACAGCAGTTCGCGCATTTTCGCGATGATGACGATGATGTAATCGCGGTATCGACGTGGGGGTGATTCAGTTTGTGTTTGGCACCGCAGACGCTGGCGACTTCGGTTGCAACGCG  
 ACCCAAGACTTTGTCTGGGCATCGATGACGAACCATTCGCGCTTCACTCGTGGGGTTTCGC

## SEQ ID 654

VSLLPQNFGLLRSMGLRSTSVHFQPFNHGVTQRTFQHTFFYSLLSAARELILHFAESALVDAWKTGMAEVFFIFEFGTGTTQFVRIDDDVLAGIDVGGVFRFVFATQTAGDFCNA  
 TQDFVLGLDDEPFAHLVGF

## SEQ ID 655

ATGAACGATAAATACTACTACGGCAGCGCGCGCAAAAGTTCAGTGGCTCGTGTATTCCTGACTAAAGGTACGGGTCAAATCATCGTAAACGGCGCTCCGTTGACGAATCTTCGCAC  
 GCGAAACAGCCGATGATGTTGTCGCGCAACCTCTGCTCTGACTGAAAAACCGCAATCTCTCGACATCAAGATAAATGTTGTCGCGCGCGCGGAAACCGCCAGTCCGCGCGCAATCCGCCA  
 CGGTATTACCGCTGCCCTGATTTGATTTGACGCTGCTTTGAAACCTGCCTTGTCTCAAGCGGTTTCGTTACCCCGATGCGCGGAAAGTCAAGCTGAAAAACCGGCTCTGCGCAAGCA  
 CGCGGTGCAAAACAAATTCACCAACCT

## SEQ ID 656

MNGKYYGTGRKSSVARVFLTKGTQIIVNRPVDEFFARETSRMVVRQPLVLTENAESLDIKVNVVGGGTGQSGAIRHIGITRALIDFAALKPALSQAGFVTRDAREVERKKPLKKA  
 RRAKQFSKR

## SEQ ID 657

TTGATTTTGGAAATCAAAAAACCTGCTTATCGCAGGGTTTTTATTGTAACAGCGGTTTCCCATTTGGTAATCTAAAGATTACGATTTGGGCAAAAAATCAAAACAGCAGCGGTATCG  
 ACTACAGGACGAAGTACCGCTCAGGATGGCTGTACTGAGAGGACATCGTATTCTACTTTG

## SEQ ID 658

LILEIQTLIAGFFICNRRFPIGNLKITDWAIKINSTGIDYDTELVRDGCYWRGHSITL

## SEQ ID 659

ATGCGCTTTTCCCCATCGCGCGCGCTGACGCTTGCCGCTGCGGTACTGTGCAAGACACAAATATTCGTTGTCGCGACGCGCTACATCGCTCTGCAACCGCAAGGGCGGAA  
 CCGCGCTGCAAGTCCGCTTTCGCGAACCGCTCAAACCGCGCGGACTGTCTATCAACAGCAACCTTACCGCATCAACACCGCAAAACCATGTTTGGCGAGACCTTGGACGATATGCT  
 CGAAGCGCGCTTGGACAAATGCAATCAACCGTTTGGACAGCACAACGACCTTTGTTCTGCTCAAGCAGCGGAGTACCGCAAAATGGAGGCTTATATGACGCAATTCGAAGCAGCTAC  
 ACGGGCAAAACCTCATCAGCGGCTACGCGCTCTACCGCAGGTACGAACAGACCTTCAATATCGAAACCGAACAGCAGGTTGACGCTACGCGCATGACCGCGCACTCGAACAGG  
 GACTGAAACAGCGCGCAACAGATGCTCAG

## SEQ ID 660

MRLPPIAALTLAAGTVQSTQYFVLPDSYIRPATQGGTAVEVRLAEPLKRGGLVYQTDPIRYNTAQNHVWADTLDMLAALSNAFNRLDSTRTPVPSRSGSTDKWTVYIDAFQGSY  
 TGTILISGVAVLPDGTNRPHIETBQQGDGYAAMTAALQGLKQAAQQWVE

## SEQ ID 661

ATCCGATTGCGACACGGTAACCGGTATGCCGCGCAAGCGCGCAAGCAGCGGTCGCCCTTCGTGTTCTGCGCGCAACCGCGCTTGTCCGCTGCGTCAATTCGGGTGTCCGCAATGCG  
ACCGAAACAGGATTGACCGGCTGCCCGTTGATGCGCGCTCTGTAATGCAAGTGCAGGTCGCGCCCGGTGCAACGCGCTGTCGAACCGCAAAACCGATGACCTGCGCCGCGCGCACATGCGCTTGTG  
CCTGCGAAACCGCGCTCAAGTGGCGGTACAGCGTTTCCACACCGTTGGCGTGGCGTATCATCACCGGTTGCCGTATCCGCCCTTCGCGCTTTAAAGGTAAATACCGCGTCCGCGGAAGC  
CCTGACCGCGCTTCCCTGCGGTGCGGCATAATCGATGCCCGTGTGCGAGCGCCATGTGTCAGGATGGGTGTCATACGGTAGCCGAACCGCGGAAGAAATGCGGTATAGACCGCGCTCG  
ATGTTGAAGCGCGCTTTTCTGCAACACCGTGCCTGCTTCATCGTAATAATGCGCGCCCTCCGCTTCTTCTGCGAAGCGGTAATAGAACCGCTGATGGGTGTGCGCGCTTGTGACAA  
CTTCCGCGCGCAAAATATCGCGCGCGCGCACCTGCTGCCCGTGAATAACAGGCTGCTGTAAGCAGCGCGCACGGCATCGCTTCTTCAAACCGTCAAGGCTGAAGCGCGCGCAAAAT  
CCEGCTTAAGGATTGCGGATTTTCGACGGGCACCTTCCGCGCGCGCGCAGCGAACCGCGCGCGGAGCTTTTGACACGACCGAACGAGTGTGCGCAAAACCTTCATATCCGATCAGAAGCC  
GACCGCGCGCATATGCCGCTTTTTCCAAAGCGACAGATTGCGCTGCGCGCTTCTGTCGTAAGAAACCTGACCTTCCGCGCGCTGCGCTGCGCGCGCAAAACATGAACCGACT  
GGTGGCGACGCAAAATGCGCGCAATCGGCTTCCGCGCGCATATTTTTCGCTGATTGCGGCAATCTGTCGCGCGCATACCGAACCGCGCGCAGCAGTCCGCGCGCGGCTGCAC  
CGCTCTGCAACCAATATGCGCTTGAACCGCGCTGCGCGCGCAAGCAGCGCGCGCAGTTTGTGTCACGCGCTGCGCGCTGACGCGCTCGTCCCTCTGTCGAAGCAATGTATGCG  
CGCGACACCAAGATAATCGAACCGCGCGCGCGCAGCGCTATTTCCGATGTTTTCGCAAGTGGGAAGCAGCCAT

## SEQ ID 662

IRLRHGNRYAAQARKQVRLLFLRGKRLVRLRQFGRQCDNRIDGLPVDARLVQVRPGRTPCRTDKTDLAAAHIALCLKRAQVRVQRFHTVGVYHHRVAVSALPAFKGNHVGGS  
PDRSLRCGIIIDARVQPPCVDQVHTVAERRRNARIDQLDVEAFLQHPAVTIVILAPSAFLVTVIERLMGCAALNFRQNIARRHLLFVEIQAVVKQARGIAFLQTVKAEAGKN  
PA\*GPADPDGHRPQRRTARRRFDHRTQCRNLHIRIRSRFPFYAAFFQSDQLALAVFVKGKILHARTAVAADQNNRNLVGTQMPQIGFAAIFPRDSGNLVRHRTTRQHVQRVARLH  
RLHLPICRLNAAAPRQRRLFLHALRSDALRPLCRSNVCRRHQNNRNGKRAQVRVPHPCRKHEDSH

## SEQ ID 663

ATGAGATTACGAAATATCCTTATACTCCATAAGAGAGTTAGAAGACTATTATAAACACCTATCAAAATATATTATTTACAGAGGAGGAGAAAGAGATTTATCGATGTTTTATTCT  
TTTCTTTTATAAGAATTCAATATAGGTATTGGATTAGCTGTTCTTGCATAAGTATCCCCCAAAAGTATTAAATGCTTGATGATAAAATATTTTATCGGATTGATTGATCGCTTTT  
TTGATTTCATATAAAATCAAAAGTTAACAATAATAGATGAAATAGTTTGTATATTATTTATGGAATATCAAAATTTGTATTTATTCATGATTGGGTGCAATTAATACATA  
GATAAAATTTATAAGAGAGAAATTCAGTATCTACCGATATAATATCAGACTGGGAAATAGATAAAGTTAATAAGTTAATCATATTAAGAGATTAGACTCTGAAAAATAATTTCTCTAA  
ATTATGAT

## SEQ ID 664

MRLLKYPYNSIRELEDYLINFYQKYIILQEGGKEIYRCFILSPYKEFNIGLAVSCISIPKVMILDKRNIFIGFDSVVFICISQNSKVNILNDIGVFDIYLLDNQKICIIHELGAIT  
DKNLIRENSVSTDIISDWEIDKVNKLIILKELDSKTIISLNTD

## SEQ ID 665

ATGGATTCCATTATCGAATTGCGCCACCTCAAAACCCCTGCTGGCACTTGAAGAAACCGGCGAGCTCTCCCTTGGCCCAACCGGTTTCTTACCAATCCGCGCTTTCCACCGAGATCC  
GTATGCTCGAAACCACTACCGGCGCGCGCTGTCGAACGCAAAATCCACGCGCTTGAACCGGCGGAGGCTTACCCCGGTGGGCGAAAGGCTGCTGCGCTCGCCACGAACTGATACCTCAAGTGTCTGT  
TGCAGAACGAGATTGGCGGAATCAGCGAAGGAGGCGGAGAGCTGCGGATTGCGCTCGAATGCCATACCTGTTTCGACTGGCTGATGCCCGCCATGGGCGAATTCGCGCGGATGTGG  
CCCCAAGTCGAACCTGATATCGTATCAGGATTCAGCGGATCCCGTGGGCTGCTGCTGCAACCGCGCGGAGCTCGCCATTGCTCGGAAGCGGAAAAACAGCAGCATCAGCTTCC  
ACCCACTGTTGCTTACGAAATGGTGGCATTTGCGCCCGGACCATCCGCTTGGCCCAAAACGTTTGGACGCGGAGACTTTATCGGGAAACCTGATTACCTATCCCGTTTCCCGA  
CGAGATGCTGGATTATCCCAAAATCCGTATTCGAAACCATCAACCGCGCGCGCGCAGCAGGAGCTGACCATCGCCATTATCCAACTGGTTCGAGCAGAGCTGGCATTCGCGCC  
CTTCCCTATTGGACAGTCATGCCCTACCTTGAAGAGGCTATGCTGCTCCACCGCAATTAATGCTGCGGAGGACTGCAAGCAAACTGATGCGCGCATCCGACTGAAGACACAGATAAA  
GTTATCTGAACCACTTTTGCAAAATCATACGTGAACCGCGCTTCCGCGACTTGGCCGATTAAAGTGAAGTTGGAACCGGTC

## SEQ ID 666

MDSIIELRLKTLLEAETGVSLSAARVFLTQSLSHQIRLMLNHYGTPLFERKSTPLRPTVGERLLRLAHELIPQVAVARDLARITEGEAGELRIAVECHTCFDWLMPPANGFEPKZ  
PQVELDIVSGFQADPVGLLQHRADLAIVSEAEQSSISFHLPAYEMVIGCAPDHLAARNVWTAEDFIFGETLITTPVPDEMILDKPKLILPKNINPPRRSELTAIIQLVASRRGLAA  
LPYVTVMPLEKGVVHRQITADGLQSKLYALRTFEDTKSYLNNPQIIRERGFADLPGLSELEPV

## SEQ ID 667

TTGTTTGGAAATGACAGGAAAAATATGGTTTGGCCAGAGATTTTATAGCTGTCGCGAGAAACGTTGCAGACGCGATCGTTTAAAGATTACGCCCCAATGGTTGCGAGTTGAAGGGA  
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GCCGACCGTTACCGTTGGAAAAAGAACGATTCGCCGACTGTTACGGCAGCAGATCAATATGGCAGGCTACCATCTGCCCTGGATGTGATCCCATACTGGGCAACAAATGCCAACTC  
GCCGACAGATTGGGTTTGGCAGAAAAACGTTGCGGCAACAAACCTGCTCAACTCGGCGAGCTGAAACAGCCAGACACTCGCGCATTTGGCGGCGCATATGAACAGATTGTC  
AACGTAAGCCTGTCGCGCATCGGCAATCCCGAACCGCAATCCGACGGTGCATGGTGTACCGCGCGTGCACAGGCTTTTTCAGACGCGCAATAGATGAAGCGCGTGCATCTGTATCTGAC  
GGGTGAATTTCCGAGCCCAATACCACTCGCCCAATGAACCGGTACCGCTTTCATTTCCGCGAGGCGATCACCGACGGAACGTTACCGCGTACCGCGCTGCGAGATTCGCGCGCAGAG  
GTTTTCGGGTTGGAAGTGTGCCATTTTGACGAAAAACACCGGCT

## SEQ ID 668

LFGNDRKNNVLRDLAWCDETLQTSFKDYAPNQLQVEGREYIGKIVTSVTSRAAIDFAVEQKADLLLVHGMFWKSELPTVTGKKERIAALLRHDINMAGYHLPLDVHPILGNNAQL  
ADRLGFATKRFQGNLNSGSLKQAKTLGALAAHITVLQKRPVAINPERIRRVAVCTGGAQGFFQTAIDBGVDLYLTGEISEAQYHLANETGTAIFISAGHHATERYGVRLAESAAE  
VFGLEVCHFDENNPA

## SEQ ID 669

ATGGCACACTTCCAAACCGAAACCTTGGCGCGGATTCTGCCAGCGCGGTACGCGCTAACGTTCCGTCGCGTATGCCCTGCCGAAATGAAAGCGGTACCGCTTTCATTGGCGAGGTGG  
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TCCGATGGCGACAGGCTTACGTTGCAAACTGTTCAATATCGCGCGCAATGCGCGGAGTGTCTTGGCTTGTTCAGCTGCGCGAGTTGAOCAGGTTTGTTCGCGGACCGTTTTC  
TGTGCAAAACCAATCTGTCGCGGAGTTGGGCTTGTGCCAGTATGGGATGCATCCAGGCGCAGATGGTAGCTGCCATATGATGTCTGTCGCG

## SEQ ID 670

MAHFQPENLCRRPQRAYAVTFRVMPCRNRSRPIGEVVLFGNFTROIQIDAFITCRLKALCTAGTTPCDPSDFAFGLADGRLTLQNCFMNRQCAECLGLFQARVEQVLFAPFPF  
CRKTSVGLGIVAQYGMHIGQGMVACHIDVVF

## SEQ ID 671

TTGAGAAATATCAAAACTTTACCTTATTTAAATAATGCTTTGAGTATCACTGCAAACTGGGTAAATGCAATGTTTAAATGCTGCGCATTCCTCAAAATATTAGGACGACTGAA

## SEQ ID 672

LRNLIKLYLILNALSITANWVKLQCLMARHSQNIIRTFE

## SEQ ID 673

ATGGATAATCAAGAAATCAACAAAGCGCGCGCGCTTCTGACACTTGGGACCTGCGCGCGCGCGGAGTGGCAGCATTGGGTGTGCAACCGCGCTTTGTGGCAGTTTTCCTTTCG  
AAAAAGCAAGCGCTCGGTCGCTGCGAGGTGATGTAATAATCGAAGCGGCTGAGCTGCTGACCGCGGAGTGGCAAGGCAACCGATTGGGTGCTCAACCGTACAGATCAGCA  
GCTTAAAGACCTGAAAGCGCTGACGCGGCAACTTACCGATCCCAATCCGATGCGGAACAGCAGCGCGGAGTATGCTAAAGAGAGACCGCTGCGATTAAGCGCAACCTCTTTCGCGCATC

GGTATCTGCACCCATTGGGCTGTCTGCCACCTTCCGTCCCGACATTGCCCGCCGCGATTGGGCGCAGACTGGAAGGGCGGCTTCTCTGCCCGTGCCACGGTTCGAAATTCGACTTGG  
CCGGCCGGGTATATAAGGTGTTCCTGCCCGACCACTGGTGTGTCCGCCATATAAATCTTCTGAGCGACACAACTATCTTGGTGGGCGAAGAC

## SEQ ID 674

MDNQEINNGRRRLFLATCGAGGVAALGVATPFVASFPSEKAKASGAAEVVDVSKI EAGQLLTAEMQKPIWVILNRTDQLKDLKGLNGELTDPRSDABEQPEYAKNETRSIKPNLILVAI  
GICHLGCSPTFFREDIADLADWKGFFPCFCHGSKFDLAGRVYKGVPAFTNLVVPYKYLSDFITLWGED

## SEQ ID 675

TGTGTTGCCATAATATTCGTTCCTTATCTTAGTCTTCGCCACCAAGATAGTTGTGTCTCAAGTATTTATATGCGGGACAACCAAGGTGGTGGGGCAGGAACACCTTTATATACG  
CGGCCGGCAAGTCGAATTTGCAACCGTGGCACGGGCAGAGAAGCGGCCCTTCCAGTCTCGGCCAAATCGCGGGGCAATGTGGGACGGAAGGTGGGCGAGCAGCCAAATGGGTGC  
AGATACCGATGGCGACAAGATGTTCGGCTTAATCGAACGGGTCTCGTTTTCAGCATCTCCGGCTGTGTTCGCGATCGGAATTTGGATCGGTAACTTCGCGGTTCAGGCTTCAGGTC  
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GCTTTTTCGAAGGAAAAAATCGGCCACAAACGGCTTGGCACCAATGCTGCCATTCGCGCCGCGCGAGGTGCGAAGTGTGAGGAACCGCGCGCGGCTGTGTATTTCTTGAT  
TATCCATTATTCAGTCTGTCTAATATTTTGGGAATGCCGAGCCATTAAACATTGCAATTTTACCAGTTTGCAGTGATCTCAAAGCATTATTTAAAAAAGG

## SEQ ID 676

LVCNHYRSLFLVFAHQDSCVAQVFIWRDQVGRGRNFTIYAAGQVEFRTVARAEAAALPVCAQIGGGNVGTGGRAAGMADTDGDKDVLNRTGLVPSILRLIFRIGIGIKFPAVQAFQV  
FKLLICTVEHPNRFALPLGGQQLTRFDFTDILHDSGTGLGFFRREKTGHKRRCHTQCHSARAAGKRCQETAADVDFLIHYSVVLIPWECRAIKHCNFTQFVILKALFKIR

## SEQ ID 677

ATGGCAAAACCAACCAATAGCAAAAGCAATGTTAGGCTGGATGGACGCTCGCTTCCCTCTGTCTAAATGTGGAATGAGCATTGGCGCAATACTATGCGCGAAAAAATTTAAT  
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CTTTACCGCAGTAGAGTACATCATGCGCGAGTGTCCGGCGGTGGATTTATCCGTACATGACATCCACCGCGCATCTTCTCTCTCATTTGTTGTTATCTGACATGTTCCGTGGTTTG  
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TTGGTCTTGTTCATCTTCTCTTATCGGTTTGGGTATTTTGGGCGCGATGGTGGCAACCGATACGCGTACTTTGGTCCGCGCATCTCTGCTCTGCTATTTCCGATCTCTCTCTGGGT  
TGCGCTCTATACCAAGCTGGATAAAAAACAACCGGTTCCGAACCGGTAAACATGACACCGCCAAACAAAAATCATGTTCTTGTGTTACGTCGGCATTACTGCGGTGGGTGCTTACCT  
GTTTGAACCAACATC

## SEQ ID 678

MANQTNKAKALLGMDARFPLSKMWNHQAQYAPKNFNFYYPGSLALLVLVIQIVSGIFLTHNYKPDGNLWAYHLPAFTAWEYIMRDVSGGWIIRYHSTGASFFFIIVYLHMFRL  
IYGSYKPRELUVWIFGSLIFLALMAEAFMGVLLFWGMSFWGAQVLIINLPSAIPVIGPOLSTWIRGDFNVSDVTLNRPFLHVLVAVPLVLLGLVVARIALHEVGSNNPDGVEIKKNKDE  
GIPRDIIPPHYVTVKDLGLVGVFLIVPCAVLFFAPEGGGYLEAPNPDANALKTPHPIAPVWYTPFYAILRAIPSFLGTQVWGVIGMAVVLIALLPWLDORGEVSVRYRGPPIFKTA  
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## SEQ ID 679

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TCTGAAACCGTCCGCTCGCCACCGCGCTGTGGCAAAAAATGGGCTGTCATCAGCAAAATGTGCTGACCGCGGAATATTTGGATGTCGCTACCGATGAACGGAACGGCTCTGCGCGATC  
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GTTGGCGCGGAGCATCAGCGGACGGGAAGACGCGTTGGAATGGCTGCGCGTCCAAACCGAAATCCAAATGTGGCTGAACGCTCAACCGCTCAACCAACCGCAAAAAACCGCGGCTG  
CCCGAATGAACGCGTTATGCTTGTGGACAGTCTGACGGAAGCGCACAAGCGCGCAGCTTTTCCGCGATGAGGTTTGGAGCGGTTTTCACCGCAACCGCGGAGCATTCGCCGACGCT  
TCCGAGCTTATCGGAAACCGCGCACACCTGCGGATACGACACCATCTGTTTATGAGCAGATTTCGCGCTGACCGCGCTGACAGGGGACAGGAGCGGATGCGGCAATATTCGCGCA  
GTGGAAAGACCTGCTGCGACCGCTTTACGAAGCGCTCCGACCGGCAAAATCAACCGCTGACATCGCCACGCGAGCAACACCGCGGTACGCTGACCTTCAACCCACAGACAGG  
CGAAGTTTTCGCGCTGCAAGAAAACTTTGACGGAATCTG

## SEQ ID 680

MYADTRILITASARSAYPRCPAESGKTAFLFDVGVCAESSII SARSSFVRHQTKLTLALPSLNLDDEIRIPLCLPAFNKILQYGSFHRQSCASAFYARYLWCGRLAQRPAQSLNMP  
SETVALATPVWQKMLHQANVLTAEYLDVGTDEAERLCRDLFAFYGDIPWRFVPLPELWLSLPRAYRWGAKPVLIDGLGLGADDQPDGEDALEWLVQTEIQLWLNHNFVNHNRKRL  
PELNLGLWDSLHGAAGGTLFADTVWSRFHPNRRALPDSFRAYETAHLPDTHHILFMDDLRLTALTGDRERYAAILQQWEERWFLPYLZAVRTGKILRLDLATGQHGGLTFKPTDR  
RKFWRCTKTTFDGM

## SEQ ID 681

GTTTGGAAATCAATCAGGCAAGGATTAAGTTGACGCTGATGCTGAAGAAGCGCGAGCGGTTTCAGACGCGATTGGAAGTTTCAGATCGATACGGTCCGCGCATTTTGGCGAAGCGGATA  
TTGAACGCGTCTTACCGATGCGGGTATTTGTCGCAACCGCTCGAAATCGATGCGGCCATTTTCAATGACGCGCAATTCAGCGCTGCAACAAGAACAGGTTCTGTTCAAGAACTGGCT  
CGACGCGCACCATCCGCGAAGCAAGACGAATGGGTCAAACTCTTTAAAAAACATTTCAAAATTCGTCGCGCGGCAAAATCGTCGCGCAATTTCTGATGAGTACCGCTACCTCAAGAGCGG  
CACGCGAAAGCTGTCGGTTTACCGTAAACCCCTGAAATACCAACCGCAATGGCTCGATGCGCTC

## SEQ ID 682

VLEINQAGLSWTLMLKKRQAFQTAFFEGFDIDTVAAFGEADIERLLTDAGIVNRKLIDAAITFNARQIQALQEHGSFKNWLDARHPRSKDEWKLFKKHFPKVGGRIVGEFLNSTGYLGA  
HAESCVPVYRKTLYKHPKWLDAV

## SEQ ID 683

ATGCGCTCTGAAGCCATCTGTTTAAAGAAAACCATGCTCAATAAGACCAATTCGCGGACAACCATTTTCATCCGACCATCATCGAAGACGACCTCAAAAGCGGCAACACGAAGCGGCTC  
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CAACCCGAAAAAGAAAACGAGAAATAGCTCAACGCAATCAAAGAAGATGTGAGTGGCTCGGTTTCCATTTGGCGGGCGAGCGCGTTTCTGCTTCCGACTATTTGACCGGCTTTATGAC  
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 CGTCTGTACGACCGCCTCTTACCCTCGAGCGTCCCGTGCCTGCGCGCGCAAGACGGCGAATACCTGCCGTTTACCAGATTCTCTCAATCCGGAATCCGTTAAGGAAATCACTGCTTACG  
 CCGAACTGCCCGCAAGAGATTGCGCGCGGAAACCGTTGGCAGTTTCGAGCGTATCGCGTATTTTGTACCGACCGCCCAAGACCAACGGCAAAGACACCGCGGTGTTTAAACCGCACGGTGAC  
 GTTGAACATATCTTGTGCGACGCTTAAG

SEQ ID 684

NPSEATCLKRTMLNKDQFADNHFRITITIEDDLKSGKHEAVQTRFPPBPNGYLIHGHAKSICLWFLGLAYITDGLCNLRFDOTNPEKENEYTVNAIKEDVEWMLGFHWAGEPFASDYFORLYD  
YAVGLKDGKAYVDDLPTEEMREYRGTLFEAGNSFLYRDRSITIEENLDLFTMRKNGEPDGSKTLRLKIDMAAGNINMRDPVITYIRIRAAHHHNTGDKKCIYPMYDYTHCISDATEGITTHSLC  
TL&FEAHRPLDYDVLNDNIPALHATRPRQYEFESRLQLTYITISKRDLNQLVERHVSNGDDFPMPTISQMRRRGYTPEGVRLFAKRAIGKSENIVDSNVLEGAIRELEENSAPRLMAVLNP  
LRVLTYNFQAGKTQSRRAAFPHNHEEPTDFRSEVQITIEADPAENPFGKGRLLIPGGEVRLHGVITVKGCEVVRDAGNVVELKCSIDHDTLGNPBGKRVKGVLIHWVSAEHAETKV  
RLYDRLFTPGRPGAVRGEDGEYLLDLPFNPESVKEITAYAREPAKDLPAESRWQFERIGYFVTRDQDHGKDTFVFNRTVTLLKDS&QFK

**SEQ ID 685**

TTGCTGCAAAACCCCAAGCTGCGCGTCATGCGCGTCCATAACAGACAGCGGTTCGCGCGCATTCGCGCGCTCATTTGGCAGCGGACACATTGCCGAAATTCAGGACCTTTTCGCGAGCGGAAC  
GCGGCGAATTCATGGAAATGCTGTACAAAGTCGAAGCCGCTATCGCGCAAGTGTTCCGGCCGGCAAAATCAACCTCGCCAGCTTGGGCAATGCTGTCGCCGCACTGCATTGGCATATTAT  
CGCCCCCTTTGAAAAAGATGCGACTTTCCCTGCGCGGATTTGGGCAAAACCCCGTTCGAAAAACAGGTTATGACCTTCGCGCAAAATGGAGCGGAACAGCTTTAAAAAGCTGCTT

**SEQ ID 686**

LLQTPKLRVIAVHND SGSPAFCRVIWGHGLAEITDLSAAERGELMENVYKVEAAMRQVFRPAKINLASLGNVPHLHWHILARFENDATFFPAPIWANPVRKEGHTLPQNWTEQLKLL

SEQ ID 687

ATGACTGATAATCGGGGGTTTACACTGGTGAATTAATATCAGTGGTCTTGATATTGTCGTACTTGCCTTAAATGTGTTATCCGAGCTATCGCAANTATGTTGAGAAAGCAAAGATAAATG  
CAGTGGCGGCAGCCTTGTAGAAAAATGCACATTTTATGAAAAAGTTTTATCTGCAGAAATGGGAGATTAAACAACATCTACCAAATGGCCAAAGTTTCCCGATTAAAGAGGCAGAAGCCTT  
TTGATACCGTTTGAATGGAATCGCGCGGGGCTTTAGACAGATAAATCATGTTGAAGGCGGTAGCCATAGATAAAGATAAAAAATCCCTTTATTATTAAAGATGAATGAAAATCTAGTAAC  
TTTATTTCAGAAGTCCCGCAGTTCTGTGTAAGTACGGGCTGGATTATTTAAAGGAAATGATAAGGACTGCAAGTTACTTAAAG

SEQ ID 688

MTDNRGPTLVELISVVLISVLALIVYPSTRNYVEKAKINAVRAALLENAHFMKPYLQNGRFQQTSTKHPSLPIKBAEGFCIRLNGIARGALDSKFMKKAVIDKDKNPFIIMNENLVT  
PICKKSASSCSGDLQYFGKNDKCKLLK

SEQ ID 689

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GGGAACAGCAAGCGGTTTCAAGCGGTTTGAGTTGGATGCCAAGGTTCAGCCGGTTATGTTAAAGACGAACACCGCGAGATGAAGCCTAAGCTGTATTGGGAATCTACCGGTTTGCACAGCCG  
CCGCTGCTTCAACCGGCAAGGTGATCAGAAAGTGCAGACGCGATATGTCGCGCATTTGCGCAATTCAGTTTGTGATCATGGCGGAACCTGCACAACTGCAACGCAACGTAATAGGCTATGTC  
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**SEQ ID 690**

MRAVEMQAMKNWPAALLSAPVMSAAPASGGHAYEKVDIDLDRQVSLQORGAQIFTNCLSCHSASGRFNLKDIGLTDERIKKNLHFTTDDNVGVHMSAMNPDKAARWFGAAPPDLTLI  
ARSGADYLYAEMRGFYKDPTPSGWNNTVFDKVGMPHPLWEOQGQVAVELDAKGQPMVKDEHGEKPKPLYWESTGLHSRRLPNGKVIQKEYDAYVRDLVNYLVYHGEPAQLQRKRIGYV  
VMIFLPAVMLPLAYFLKKEYKHVDH

SEQ ID 691

TTGAATATTAGGATGATTGATGGAGCTGATGACTGTTTTCGTCCTTTGGCGGGCTTGGTGTCGGGCGTGTGTTTACATGGTTCGTGATGAAGGGCAGGTTTCAGGGCGAGTTTGGCGGT  
TTGAACGCGCAATTGGCGGAAAAGGCGGCAAGATG

**SEQ ID 692**

LNIRMIDGADDCFAAFGGVGGRVVYINVADEGQVSGRVCRFERAIGGKGGM

SEQ ID 693

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GACTTTCGGGACGGTGGCGCATATTTCGGCGCAACGAGCTTCAGAACCCAAATACGCGCTGCGCATGCGGACAGCGGGAAGCTCAAGCTGTACGACAAAGATTGTGCTGCTGCTGATACAGCGCTCGAA  
AGGCTTCGGCAAAAGGCATCGATCAGGCGCAAAACAGCTTTCAGACCGCAATTCAGCAAACTTCGCGAGGAGCGAGGGAATCTGCTGCGGACGCGCCGAGTGTGCTGTTGGCGTGAAGG  
CAGGCAAAACAGCTTCAACGGGATTTGGTTCGAGCGGTGCCAACGAAACAGACGCGCAATTTGCTTTGGCAAACTTCGGAACAGGAGCGGCTGACGAGAAACCGGAA

SEQ ID 694

LAEKAAACDFTBQAHAEIASELAAALDGKYHQLDQENYALSNRPSAAEQIAHLQKEAESEVRLKQSYDILQKQAQGLAVENERLATQGLQERKAFABQYALERQIRQRVETDLEESRQTVR  
DVQNDLSDVGNRPAAEKQIAYLQKEAEAEERLRQSFTELQKQAQGLAVENERLATQIEQERLASSEKLSLIGBARKSLSDQFPQNLAVITLEEKSRRRFTQNRBQLHQVIANPINERIHGFG  
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SEQ ID 695

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SEQ ID 696  
MFSETHPPFLFGVSRFLFRFPAQSKCRFLFVGTLDQIPLKFLACLHAQQTQFLGASDQIPASLGLLECRLKAVLRLIDAFADAFERLYEADKLVLQLAAPVNRNRQVLVLLVAPNKRHR  
PQSQRQRTGADQHNPFVETLLBQARVILORQQVGRFDRDKHDEIKCVHTTQIGVILQRQAFRERAYAGDIRQOFACRLIRKRLRVAHISRQNRGINDMLLVQGVQDVQNVGLEAARAAV  
FLFSDGCRNLNHTFLPPFLKAGIQPNRPNQMLAPIALNLVLIRAGQRVGGCLCLAVQLRIQLEPPQOFVFSQPLRADFIISLPLQDASTVDPAQRVQNRGINDMLLAVLGKTAARVGRK  
LKLIAQAPARLADQOGLFFRSKAFILDLRCQTVFVNRQTLRLFLQEMRLPQPLRLPFLFIQGNLFFGCGKTVADIGKVLVHADSLLAAFFQIGFDSLADLAFQRTILGKRLPFLFLKRC  
OFTFVNRQTLRLFLQIDIRLLQPNRFLPLQMLGNLFGCGKNTVAQSTIFVLQMLVFPIQSQGF

SEQ ID 697  
ATGACCGCTACGTTACGAAATCTCTCCCGGTTACCCCTCTCCGCCAAAATGCAACCTGATTTTGGGACGACGAAAGCGCGGAAGCCGCTCTGACCGATGTGCGGGCGGACGTCGCGTCTCTGC  
TCGAACGGTTGGCAACCGCAAATCAAGCTCAGCGCAATCTGGCTGACGACAGGTCATCTCGATCAGCGGGCGCGGTGGTGCAGATGCTGGAAACGCATAAAGTCCCGCTCTCGGCC  
GCACCGCGAAGATGAATTCCTGCTCCAAATCGCTGCTGCGCAACACACGCGCAATACGGATTCCCGGCTCTCGCCCGCTTTGCGCGAACCCTTGCTGCTGGAAGAAGCGCAACCGCTCAGGGC  
GGAAGCTATGCTTCCAAGTCTGCATATCTCCGGGACACGCGCCGACAGTGGTTTCTATTGTGCGGAAGCGGAGCTGCTGATTGTGCGGCGAAGCTGCTGTTTACGAAACATGAGCA  
GGACCGATTTCCTGCGCGGCAACACGCGCACTTATCAACAAATATCCGCAACAAATTTATTCGCTTCCCGGAAACCGTGCAAGTTGTGCGCGGACAGGCGTATGACTTCCATCGACA  
CGAAAAACCGCAACATCGTTTCTTC

SEQ ID 698

MTLRYEILFVTPFRQNCITLWDDSEGAVLTDVGGDVPFLIQALANRKLTLTAIWLTHGHLDHAGGVVEMLETHKVPVLGPHREDFLLQSLPQTIAQYGFVSPAPAPNRWLEEGETLTV  
GRYAFQVFLHIFGHTPGHVVVFCAEELLGIAGDVLFIYETIGRTDTPRGNHADLNNIRNKLFAFPETVQVAGHERMTSIGHKRHNPF

SEQ ID 699  
GTGTCCTAAACCGGTTTTCAGACGGCATCGCGTTTGCCGTTTGTTTTATGCCGCTTGCCGCCCTGTTTGATATTGGGGGAATCAGGTGAT

VFLKRFFRRHRVCRLFYGGLPPVLI LGESGD

SEQ ID 701  
TTGGCGTGGGTTTCGGGCGGATTTTCTGCGCAGCGCGTAAGAAGCAACGCGCTGCGCCGAGGAGGAAGGTCTCTGTTCATTGGTTTTTCAGAGGCATCGAGCCATTTCGGGTGGTAT  
TTACAGGTTTTACGGTAACCGGACAGCTTTCGGCGTGCGCCCTTTAGGTAGCCGGTACTCATCAGAAATTCGCCGACGATTTTCGCCGCCGACGAAATTTGAAATGTTTTTAAAGAGTT  
TGACCCATTCGCTCTTGCCTTCGCGGATGGTGCGCCGTGAGCCAGTCTCTGAACAGAACCGTGTCTTGTGTGCAACGCTTGGATTTGCCGTGCATTTGAAATGCGCGCATCGATTTTCAGACG  
GTTCCGGACAATACCCGCATCGGTAAAGCAGCGTTCAATATCGGCTTCGCCAAATGCGCGCAGCCGATCGATGTCGAAACCTTCAAAATGCGCTCGAAACGCCCTGCCCTCTCTTCAGCATC  
AGCGTCCAAT

SEQ ID 702  
LAWVRADFLPQAVRSNAPAPRRKVLVLLIGFSDGIEPFRVVPQGFTVNRATAGVRAFEVAGTHQKFADDFAADEFEMFFKEFDPFVFSRMVRVPEVLERTVFLQLRLDLPCIENGIDPQT  
VADNTRIGKOPFNIGFAKCGDRIDVETFKCRLKRLPLLQHQPT

SEQ ID 703  
TTGCGGATGCCGTCTGAACGCTATCTCAAAGCGCGCAAGTCGGGTACAATAAACACATCATCAAACCGCTTCAGACGGCATACGGAACCGCCCCCANTGCGGTCTGAAGCCATCTGTT

SEQ ID 704  
LPMPSERYVKARKSGTINTSSNRFRHTEPPQCRLEKPSV

SEQ ID 705

GTGATTAAGAAGATAATCGGCGGCATCATACCGATTTTTACGGCGGTTTTCATCCCTGCATCGGCGAGCGCGCGGATTTGATGCTGCGCGCAGGAATACAAAGGCGAGGACATTCGCGGCT  
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TTTGACGCGGCAATTGTATAGCGGCGCGGTCAGTTGCGACGAGATTTCCGCTACCGTCGGTTCGTGTTCTTCAGACTGGCGGGCATCCGCTGCACGTTTTCGATGTACCCAAAGGCGCAG  
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AACAAATCGAAGTGCAGGGCGGCGAGGAGCGTATGCTGCGCCGACCGCGGAATCCCGTTACAGCGGGCGGCGAGGAGCAGCCAAATTATTGAAGCTGAAAGGCCAATACGACGCAAGATGCACGGT  
AAGCGGCATCTATGAGGGCAAAGGGCGAAACGCGCGGACGGCTGGGCGCGTTCGGCTGCAAAAACCGACACGGCGAATTCCGCAATCGGACGCGGTTTCAAGGACAAAGACCGCGACAATCCG  
CCCAAAATCGGCACGCTGATTACCTACCGTTACCGTGGCTTTACGCGGAAAGGCACGCGCAAAATTTGCCACATTTGTGCGCGTGCCTACCGACCGC

SEQ ID 706  
VIKKIIGSIPTIPTAVFIPASAGAADMLAQEYKGGQDIAGWAMSEKLDGVRATWDGKHLISRQGYAFTPPKGFPAQFPFYPLDGELYSGRQCFEQISATVRSVSSDWRGIRLHVFDVPAQ  
GNLYQRLAVATQWLKTHFNAPITPIPIQIKVRDRRHAMDFLKQIEVQGGEGVMLRQPSRYSGGRSSQLKLKLSQYDDECTVTRHYEGKGRNAGRLAGVGCKNRHGEFRIGSGFKDKDRNP  
PKIGTLITYRYRGFTKKGTPKFATFVRVETDR

SEQ ID 707

TTGGTTTATAAATTTCCCTTTTACCGGACCGATTCCGACATATGACCGGATTAGAAAACCAACCGCCTTGAAACACAGGCGATGCTTGAAACGCCGATCTTTTGTTCGACCAAGGCCAATGCC  
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TTTTCCCTTAGATTTTGATTATGTTACAGTTTCCCGTTACGGCGCAACGCTGAGAGGCGCGCGCTTCAACTGGAGCGTATGCCGATGCGGAACAANTCCGGGGCAGGCACTGTGTCGTG  
TTGGACGATATTTTGGACGAAGGGCATACGATGTCGCCATTCAAGCCAAACTTTTGGAAATGGGTGCGGCAAGCTGCCGTGCGGCGGTGTTGCCCAATAAATTAATCGACAAGAAAAAC  
CGGTCAAGGCGGATTAATGTCGGAATGGATGTGCGGAACCGTTATGTTTTCGGTTACGGCATGGATCGCGCAGGCTGCTGGCGCAATTTGGGCGAGATTTACGCATTGGGCGGAAAA

SEQ ID 708  
LVNVPFPTDRFRHMTDLETKRLEQAMLENADLLPDDQQCRAALQKVADEITRDLGDKYPLLLPVMGGAVVPTGQLPLLRFPDLDYVHVSVRYGDKLEGGAFNWKMPDAEQIRGRHV  
LDDILDEGHTMSAIOAKLLENGAASCRAAVFANKLIDKRPVKADYVGLDVPNRYVFGYGHDAAGCWRNLGEIYALGR

SEQ ID 709  
ATGATAGGCGCTTTTAATCATCACACGAAACCATAGCGAAGCCTACCGCAAGCTGGCGCATCATTTTTTCCGGCGGGGTCCTGAAAACGTCGCATATCTCGCGTGCAGCGGACGG  
AAGACCAAGACGACATTATCAACAAGCCATTTCGCGCTGCAAGAGTTTCTGAAAACACGCGTGTTATTGATTATGACCGACATCTTCGGCGGACCCCTGCAATTGCCGCCGCGCGGCT



**SEQ ID 722**

SEQ ID NO 722  
GAGGHTTGTGCAMLELNGLCKCPGGKTVADNCTITVGRGKILAVLGRSGCGKSTLLNMIAGIVRVPDGGETRLNGENTTCMPPEKRRISLMPQDYALFPHMSALENTAFGLKMQKMPKAAER  
LALSALAEVGLLENAHRKPEKISGGEKRLALARALVVRPSLLLLDESPSSLDTHLRDLRRMTAERIKGGIPAVLVTHSPSECAATAEDIAVMHEGKILQCGTTPETLITQTPAGVQVARL  
MGLPNTDDDRHIPQNAVCLDNHGTECLLSLVRLPDSLRLASAVPEHGELTLNLTVGQHTDGISGNGTVRIRKVDGEIRVRF

**SEQ ID 723**

SEQ ID 723

ATGGTAGCTCGTCGGGGCTCATAAACCGAAGTGTGAGGTTTCGAATCCTGCTCCGCAACCAATATCAAACCCCTCGGTTCATATGCCGAGGGGGTTTGTGTTTTCCTGTTTCCTGCCGCCT  
CCGTTTTCGCGGAATTTTCCTCCTCCGCGCAATATCGGAACGGCAGGCCCGCGTCTGTTTCGCGTTGCAAAATTCAGCGGTTTGGCTACAATCTCCGCATTGTGTTCAGAAAGACCGGC  
TATGCCGACCCGTCGCGTTTATCCGAATCCGTCAGCAAAACAGACCTTGATGCCCTGTTTCGAGCGGGCAAAAGCAAGTACGGTCCCGAAAGTGTCTGCGAAAACGCTGTATCTGAACCGTCTT  
CCTTTGGGCAATCTGTGCGCGGAATGGGCTGAGCGCATCAAAAAGACTCGGGAGGCAAGCTGCTCGAGTCTTCAGACGGCAATTTTCTGAATCGCGACGGCTGGCCCGGATATGGCGGAC  
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GGCTGCACAGCTTTCGCCCGCTCAGCGGAGTGTGCAAAATGAAATTCCTGTATGTGTTCGATGCCCTCTGCCGAAACCTTCTGCCTGAAAATCAGGATGGCGAGGTAGCGGGTTTGA  
AAAGATGGCAATGGCGGGCTATTGGATGCCATGTTGTGCAAAAAACATGATGCACGACGCGCACTGGTTACGCTGCAGCGGTTTACCGTTCAGGTCTGATTTGATGCCGCCCAATCCGCTG  
TCCGAGTGGCTGGACGGCATACGTTTA

**SEQ ID 724**

SEQ ID 724

MVARRAHNPKVVGNSNPAPATKYQTTPRFAEGVLFPLFPAASVFCRIFLPAASISERQAACVRLQLQIAVWLQSSALCSRKPAMPTVRFPTESVSKQDLALFERAKASYGAESCWTLYLYNL  
PLGNLSPENWAERIKKDWAGCSESSDIFLNAIDGWPFMGGRLLQHLARTWNKAGLLHGWRNECFDLTDGGGNPLFTLERAAPRPPGILLSRAVHLNGLVESNGRWHPWIGRRSPHRAVDPGKL  
DNLAGGGVSGGEMPSEAVCRSESEAGLDKTLFPLIRPVSRLHSLRPVSRGVNHNIYVFDVAVLPETTFILPENQDGEVAGFEKMDIGLLDAMLKNNHFDALQVTLDAFYRYGLIDAAPHPL  
SEWLDGIRL

**SEQ ID 725**

SEQ ID 725

TTGCGTTTTTCAGACGGCATTGTGAAAACCAATGCCGTCTGAAAGACAGAATCGGTGAAAAC TCCCCACGCAGGTATTATCCCGATCGGGTG

**SEQ ID 726**

LRFOTAFENOCRLKDRIENSPRRYYPDRV

SEQ ID 727

SEQ ID 727  
TTGGTTAAACATCGAAACAGGGGTGCTGCCTGATGTTTCAGGCGGCTGAGAAATACCTTTTACACCGCATCGGGGATAATACCTGCGTGGGGAGTTTTCACGGATTCTGTCTTTCAGACGGCAT  
TGGTPTTTCAAATGCGCGCTGTGAAACGCAAAACGCTCCCTGTTCTTTATTC

**SEQ ID 728**

LVNIETGVLDPDVOAAEKYPLHPIGIIPANGVFTDSVFTALVFKCRLKTONAPVSLF

**SEQ ID 729**

SEQ ID 729

ATGACTACGCCAGAAAAAACCGCCAAAAATTTCGGCGAACGAAGCGCGCGAACTTTCCGACTTGAGCGAAGACATCGGCATCCGCTTCAAATATCAGAACTCGAAACCGGTGTATCTCGAAG  
TCGCGCGCGAAGACATCCGCGTGCTTTTCGCGAAATTCGTCAGGACGACACTTACACGGCGCAAGGTACGGAAGCCAAACCCGCTATTTCGCGTGTACGACACACAGCGCGCATACGGCGA  
CGCGGCGCGCACATCGACCTGAAACAAGGCTTCGCCACATCCGCACGCGCTGGCTGGACGAAACGCGCGGATACGGAATTCCTGCCAAAGCTCTCCACGCGAATACGGGCATCGAAACGTGG  
CACGATCCGAAAAACCGCCCATCTGCGCTTCAACCAAAATCACCCGCGCGCGCTGCCAAAGCCGGCGCGCAATGTAAACCCAGCTCCATTACGCCCGCAAGGCATTATACCGCCGAAATGG  
AGTTCCGCGGCATACGCGAACGCATGAAGCTGGACGCGCTTTTCAGACGCGCTTTCAGCGCAAGCTCTTGAAACAGCACACAGCGCAAGTTCGTCGGCGCAACATCCGACGCCCTCCGGA  
CCAAAGTACACCCCCGAATTTCGCGCGTAAAGAAATCGCGCGCGGACGCGGCTTATCCCGCGCAACTFCAACCAACCCGGAATCGAACCGCATGATTATCGCGCGCACTTCGCGGTCAAATC  
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ACGAAACGCGCGAATGGATTATCCGCAACGCGCCGCTCCCATCGGCACAGTGCCGATTACCAAATTTTGAAAAAAGACGCGCGCATCCGCGAAGATTGACTTGGGATTTGTTGCCCGGA  
CACCTTAATTCGAGCAGCGCGAACAAGCGGTGACATATTTCACCATFACACCGCGGCGTGTGCTCGCTTATGTCGCGATAGCGCCGATACCGGCATCGTATCGGCGCGCGCGGTTCG  
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CCGGCTGCATTTCCGATATGCAACGACGATCCCAATTCGCGAAATPGCACACTTGGGCGAATTTGACGATAAAGCGTGGAAACACGACGTACAAGTCATGATCGAAGGCCCGCGGCATGT  
GCGCGTGCACAGCGCTCAAGAAATAATGACCGGAAGAGTTGCAACACTGCTTTGAAGCACCGTTTACACACTCGCGCCGCTGTTACCGACATTCGCCCCGCGTACGACCATCATCACTTCG  
GGCATAGGCGCGGCCAATATCGGCTGGTACGGCACGCGGATGCTTTGTTACGTTACCCCAAAGAACATTTGGGGCTGCCGACAAAGAAGACGTGCGCACCGGCATCATCACTCAACAC  
TCGCGGCCACCGCGCGGACTTCGCAAGGCTGCGCGGCGCGGCAATTACGCGACAACGCCCTTGAGCAAGCGCGTTTCGAAATTCGCGTGGCGGACCAATTCGCTTAAGCTCGACCC  
CGAACCGCGCGAGAGCTTCCACGACGAACACCTGCCCGCCGAAGGCGGAAATCGCCCAATTTGCGTTCTTAATGTGCGGCGCCAAATTTGCTCTGAGTAAGAAATCACGACGGAAGTTGCGCGAC  
TTCGCGCAAGCAAGCAAAAGCGCTAACGGCAGGTTATGGAGGAAAAAGCGGCTCGAGTTCGTCAAAAAAGGCGCGAAGATTTACAGT

**SEQ ID 730**

SEQ ID 730  
MTPPKTKATKISGNEARKSLDLSIEDIGIRFKYQNSERVYLQGSRDDIRVPLREITRQDDTYTAQGTANPPIPVYDTSCAYGDPAAHIDLQGLPHIRTAWLDERGDTIELPKLSSEYGIERA  
HDPKTAHLRFNQITPRPRAKAGNRNVTQLHYARQGITPEPEFAAITERMKLDLFRPEYAKLLKQHTQGSFGANIPTRPDQITPEFVRQEAAGRATIPANINQPELEPMIIGRNFVKI  
NGNLGNSAVTSSLTEVEEKVWLSLWAGADTIDMLSTGAHITHETREWIIRNAPVPIGTVPVYQTELEKGGIAEDLAWLDFRLTLEBQAEQGVYDFTIHAGVILRYVPMANLRJAGVSRGGS  
INAKWCLAHIRENFLYTHFDEICEIMKAYDVFSGLGDGLRPGCIADANDESQFAELHTLGLKLTOKAWKHHDVQVMIEGPGHVPLRVKENNTEBELQHCFAFPPTFTYGLPVLDTIAPGYDHTS  
GIGAAINIGWGTAMLCYVTPKEHLGLPDKEDVRTGITTYKLAHAADLAKGWPGAQLRDNALSKARPEFRWRDQFRLSLDPERAESFDEITLPAEAGAKIAHCFSCMCGPKFCSMKITQSVRD  
YADKQAKOROGMEEKAVEFVKKGAKIYS

SEQ ID 731

**SEQ ID 731**  
 TCTGTCCTTACCGCCTGCGGCAGAAAAATCGCGCCGAAACCCACGCCAAAATATCCCGAAGGAAGCACCGTGCTTGCTTGGCGGATTCGCTCACCTTCGCGTACGAGCAAAACCCCGCGGAAT  
 CTTACCCCGCGCAACTGCAAAACTGACGGGTGGAATATTGTCAACGGCGGCGTATCGGGCGATAGCTTCGCGCAAGCCCTATACGGCGTCGCCCGGCTGTTTGACGACCAAAACCTAAGCT  
 TGTGATTGTGCGCATAGCGCGGCAAGCACTTCCTGCGCAAAATTCGCGAGGACGAGACCCGCGCCAAATATCGGAAACCATCATCGAAACCGCTGCAAAAGGAAACCATTCGCGCGTCTCGTCTG  
 GCGTCCCGACATCACATCGGCGCGTGTTCGCGCAATTGAGCGCATACCTCCGCTATGAGGAAATTGTTCGAGAAATACCGCATTCCTGTTTCGCGCGCGCTGGCGGAAATTTTGG  
 CCAATAATATCTGAAATCCGACCAATCCACGCCAACGGCAAAGGCTATCGGAAATTCGCCGAAAATTTGAATCAATTTTGAGAAAAATGGGTTTAGA

SEQ ID 732

SEQ ID 732  
LLLTACGKRSARTHAKIPEGSTVLALGDSLTPFGYGANPGESYPALQQLTGWNTVNGGVSQDTSQAQLSRLPALLARKPKLVTVGIGGNDFLRKVPFEEQTRANIAKILETVQKENIPAVLV  
GVPHITLGAIPGHLSHDPLIEDLSEEGYITPLFGGAWEILGNWNLSQDIHANGKGYRKPAENLQFLRKHGFR

SEQ ID 733

SEQ ID 733  
GAACGTTTGTGTAACCTCGACAAACGCCCGTTTCTTCGTATTCGTAAACACATCGTTGCTCCACGPTTTCGGCGTGCACAGCGTCAGGCGCGGGCGTATGCCCTTTGAAGATGCAATGCC  
CGGTGCCAAAGGCTCAAGGATGTGTCCGATTCTTTATCCCTGGCCCTTTCCCTTTAAAACTGCTGAAGAAGCCGGGTTTTCATATATGCCGTTTCGCCACGCGGAGGCGGAACGAGGAG  
ACAGGCCGCTGCGGCCCAATTCCTGCCCCGAGCAAGCGCAGGCGCTAACGTTGTAATTTGTCGCCACGGTCGCGGGGTTGCGCTCGCGGTAAAAACTCAAACCGCCCGCTCCAAATATTG  
CGCGCATTCCTGGTAAAAACACCGGAATCGGAAATTTGCAAAATGGTATTTGTGCGAAGCGCCGCGCGGTATCTTCAAAACGCCGCCACCTCCGCGGAAGACACGCGTTTGGCATCTCGGG  
GTTTTCGCCACCGCTTGAATTAAGGCGCTGCCCGCTGGGCTAAGAAATAAGCGCTTGTCCGCTAGGTGTCGGCGCTTCGTGGAACACTGCCAGCCGACATCTTTACGCGCGTGGCAAAACCGA



TGCCGCCGGAACACCTGCGGTGCATATCGTTGAATTTCTTATCCCGGATAAACCTGCCGGACACGTGCCGCCGCCGTCGTGTACACCGCTTTTTCAGCGACCATTTTTCCTCCGCG  
GCGAACCGGTATTCATGTCGCGTCCCGTCCACCTGTTTCGGGAAAGTCCAATTCGCGTACTGCTGCTGTTTCGGGGCTTGGTTGATATTTGTTGTCGCGGTAACTGAAACCGCGCTT  
ACCTTCCACGATCGCGTTCGCGCAATGCTTCGCGTACAGCTCGACCTGCTCCATAAGCTGCCGGCGGAGATCTCTGTTTTCAGGCGGTGCAACTGGTCTGCCGCGCGCTGTTCTGCC  
TGCTCTCAAAACATGCCGCCCAACGACATACGACGGCGGGCGGTGCGGTGGGGCGCAATCAATTCGCGTAATGGGAAACCGCTCTCTCACCTGCGCTCTGCTGCCCAAAAT  
CCTTGTGTCATAAATGTPGCAACATCTTATCTGCGCGCTGTTGTAAGTAAATCGGCAATACCGGATACCGCAATATGTTTGAGACCACTGCGGAATACATGGCAGCGGACAAC  
AATTCGGGATTTTTCAGCAGGGTTTCGCGCTCAACCTGCAAACTTTCTTTTTCGCGACCTGCCCGGTACCTTCTCCCTGTGATCGGTTTGACCTCCGCTTCATGAAGCTGAAC  
CGGACGGCTTCTCAATCCGGTTCGACGGGTGTTCTTCGCGGTATGCGCGCTTGCCAATAAAGCAGCAGCATCCATCTGTTTCTGTCAGGCATAAATGCTTCCCAAAAAATAAA  
ATAAAAAATACCAATATCAA

## SEQ ID 734

ERFVKLDRPVFLVFKHIVAPFAVRQRRQARRDAFEMQCPVKAQGCVRFFIPAPFFPKTAEAGFFIMPFRHAEQRQAAAAAPFLPPGKAQAVTVEIVATVGGVALAVKIQTARPIL  
ARIPVKHQRIGNLQNGIVGTARPARIQTPLRRRRLPSRGLPTVELKACAVGVRIISVAVGAAPVEHCQPDITPVGKTDAAGNTRHIVEFLI PRINPAGHVAARRRVPAVFPQRPFLR  
AEFVTDCAVHLFRBESPIAVLFRGLVDIVPAGNAETAIVLPRIFAQCLAVQLDLHLKLRRIQFCQAVELVCRRLVLPVFKQCRRTHTDGGRVGLGNGFPVMGNRLHLPALCLBQ  
PLCIKQHLILPRL\*VNRQNHADTGNIV\*DHCGIHETRQQFGIFQGFVNLQNSFFPHLPYLLPVDRLRPMKPELGTASQIRFARCFPGVCRACQ\*ROQHPSVSCRHKCLPRLIK  
IKNWHYQ

## SEQ ID 735

TTCGCTTCAAGGCCCTGCATGTACCTCATTCGCCACCCGTTTAAACACGGTTTTATCTGACAGCGCGCAATCCGCCCCCCCATTTCCGGAACAAGCGGTCCGACTCCCGCCCGCGCGG  
GAATGACGGCGGAAGAATCTATTTTCCCGA

## SEQ ID 738

LRFKALHVPCHPFFKHGFFYLGAQSAFFFAEQAVRTPARAGMTAERFYFSR

## SEQ ID 737

ATCGAGGCGCTTGAAGCGCAATCGATATATTTTCCACCGGAACGGACACCCCGCCCGCTTGCAAAACCTTAAAGACAAGCGCCCGGGTGTATCCGGCGCGCGTGGGAAATCACT  
TACCGCTTGATTTATTAATAAT

## SEQ ID 738

MQGLEAQSIYYFHRNGRPRPPCKPLKDKPGLIRAAVGNHLPDLFKI

## SEQ ID 739

GTGGCATCCGCTTCAACAATCAAAGGCAATATGTTTCAGAAAGTTGAAGTCACAAACGGGCTGTTACCGCCCAATGGCTTCAACCGCGGTAAACAAGAAATCAAAGGCAAAAACTCT  
CCCTGTGGCGCAGCGCTCAAGACGGTTCGGTAAATGGTTCGCGGACAGCCGGTAAAGCGGACAGCGCCCGCCCAAGACGACACCGTCAACCGGACGCCCAACGACGCGCA  
AATCGACACCAAGCACCTGCCGTCAACCTGCCCGGATAAATCACTGCCCTTTCAGCAAAACACCAACCGCGGATTTCAACACTTCCAAAAATCAGCGGTGCCGGGTATTACCTGAAT  
CAGCGGAAATGGCGGAAACCAACTTCTGCCGGCGTGGCATCTCCGACAAATCAAAGGCAATATGTTTCAGAAAGTTGAAGTCGCAAAAGCGCTGTTACCGCCCAATGGCTTCAA  
CCGCGTAAACAAAGAAATCCAAGGCAAAAACTCTCCCTGTGGGCAAGCGTCAAGACGGTTCGGTAAATGGTTCGCGGACAGCGGTACGCGCAACGACGCAAAAGCGGACGAGCT  
CAAAGCGGACGCCCAACGCGATGAAACCAAGCACCTGCCGTCAACCTGCCCGGATGAATCATCTGCCACC

## SEQ ID 740

VASASTIKGYVQKVEVTNGVVTQAQMASTGVNKEIKGKLSLWARRQDGSVKWFCGQPVKRDAAAKDDTFTADATGNDGKIDTKHLPSTCRDKSTAVCTKHAPLSNTSKRSVAGYYLN  
HGEWPEWNTSAGVSSDKIKGYVQKVEVAKGVVTAQMASTGVNKEIQGKLSLWAKRQDGSVKWFCGQPVTRNDKADDDKADANALETKHLPSYCRDRESSAT

## SEQ ID 741

TTGGCGAAGGTCAAAAATCAGCGCTCAGCGATTTACCTGAATCAGCGCATATGGCGGAAAGACAACACTTCTCGCGCGGTGGCAAAACCCACCGACATCAAAGGCAATATGTTGAAA  
CGGTTACGTCACAAACCGCGCTGTTACCGCCAAATGCTTTCAAGCGCGTAAACAAAGAAATCCAAGGCAAAAGACTCTCCCTGTGGGCAAGCGTGAAGCGGTTCGGTAAATGGT  
CTGCGGACAGCGGTTAAGCGCACGAGCCAAACGCGGACGCGCGCGGCAAGACACCAACCGCATCAACACCAAGCACCTGCCGTCAACCTGCCGCGACCGCTTCTGCTAGC

## SEQ ID 742

LABQKSAVTEYILNHIWPKDNTSAGVANPTDIKGYVESVITNGVVTAKMLSSGVNKEIQGKLSLWAKRAGSVKWFQGPVKRTEANADAAGKDTTNGINTKHLPSYCRDPFSAS

## SEQ ID 743

TTCGCTTCAAGGCCCTGCATGTACCTCATTCGCCACCCGTTTAAACACGGTTTTATCTGACAGCGCGCAATCCGCCCCCATTTGCCGAACAAGCGTCCGACTCCCGCCCGCGCGG  
GAATGACGGCGGAGCGGTTCTGTTGCTCCCGATAAATTC

## SEQ ID 744

LRFKALHVPCHPFFKHGFFYLGAQSAFFFAEQAVRTPARAGMTAERFLLPINS

## SEQ ID 745

ATGCAAGCGCTTGAAGCGCAATCGATATATTTTCCACCGGAACGGACACCCCGCCCGCTTGCAAAACCTTAAAGACAAGCGCCCGGGTGTATCCGGCGCGCGTGGGAAATCACT  
TACCGCTTGATTTATTAATAAT

## SEQ ID 746

MQGLEAQSIYYFHRNGRPRPPCKPLKDKPGLIRAAVGNHLPDLFKI

## SEQ ID 747

GTGCCGACAGACCGGATTCGCCCTGCGCGGAATGACGAAGCCATCTTTTGGCCGAAGGTCAAAAATCAGCGGTTACCGGGTATTACCTGAATAACCGCAATGCCCCGCGACAAAG  
GCGCTGCCGCGGTGGCATCCCCCGCACCGGACATCAAAGGCAATATGTTAAGGAAGTTAAAGTCGAAACCGCGTCTGTCACCGCCCAATGGCTTCAACCGCGGTAAACAAATGAATCAA  
AGGCAAAAACTCTCCCTGTGGGCAAGCGTCAAGACGGTTCGGTAAATGGTTCGCGGACAGCGGTTAAGCGGACGCGCGCGCAAAACCGCGCGGACGAGTCAAAGCGGACGCG  
AACACCGCATCAACACCAAGCACCTGCCGTCAACCTGCCCGGATAAATCATGATGCCAAA

## SEQ ID 748

VPTDPSRLRNGDEAILLABQKSAVTEYILNNGKWPADNGAAGVASPATDIKGYVKEVKVENGVTQAQMASTGVNKEIKGKLSLWAKRQDGSVKWFCGQPVKRDAGAKTGADDDKADG  
NNGINTKHLPSYCRDKHDAK

## SEQ ID 749

GTGTCGCGCTGTGTGTCAAAAATTTCCCGCGCATCAAAACAACCATTTGACCGACAATGGCGCTCTTTGTGCGCGTCCGCTCTTTTGGCGTATCCGATGCGTGGGACATATGGCT  
TTCCAACCGGCTTCAATGCCAACCGCCCTTCGAGCGCGTCTGCCGTGCCAGCGTCTGTTTTTCGCGTCCATTTCCATGCCGAAAGATTT

## SEQ ID 750

VCRLCVKTFPGASKQPFDRQCGFFAVRPFVSDACGRMAFFTGFNAKPPFERRPACQRLFFAVHFAERF

## SEQ ID 751

TTCGTTTATATCTCTCTTCAGGCGGCTGCTGTTTCGCGCATCGGCGATGGTGTGTCGTCGAGAAAGGTTTGGCGATGGCTTCCGCTTCCGTTGGTATTCCCTCTCGGCTTTC  
GTAATGACCGAGGCTTACCGGGCGGTATGGGCGAGCATATGCTGCTGAACGATTTGGCAGGAGAGCTGTTTGCACTGGCATTTATTCGCTGCTGATGAAGCGTTTTCCGGATCGCGCG  
TGGGGTTCGGCGCGGACAGTATGGATTTCAATTCGCGGTAATTCAGGTCGCGCGGTTTGAAGTCGTCGCGTAGCGGTACGCTTCGCGGTGCTGCTCAATATCGCGCCCGCT  
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CGGCATCACTTTATGTCGGTGGACGAGCTTCCGCGGCATTTGACGCTTACCCCGCAGACGATACGTTGCGACATCCGCGAGTTGGAGAGGGTGGACGCTGAAACGCCATCAGCGCGGCG  
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**SEQ ID 752**

LVYIVISFRRAAVCRIGRWCVDERFGDFRLRLVPLPGNDRGLRGMQGHAAERFQTRAVCTGIYSADEAFSGCGGRRRDQYGFHARNSGCRFGSRAGSGQLRRGGQYRRPV  
SDGGVPHAGLNAVKSASRCKEAEDETENPKAWRDFKPCPPASVYVGGRCRRIRGRYPADTLRHPRVGGGWQPETPSSRRIFGRKLAGGSARRPFPNPKRKRKPCADCGTHPRRFVAV  
RQYRYDHGSRGIRAGEAAQPADYQYPRRLRRFQYGLHGHHRPPFRYRGRDLRYQPVQSLRCDERHARRKRRFAPGLRLQGSQRHAGDDCQRARPPSRRGSQIIPQORA  
GQARRHYGV

**SEQ ID 753**

ATGCCGACGGCTTTTATAGCGGATTAAACAAAATCAGGACAAGCGCGGAGTTCATTCGCGTATTCGCATCATAGGCGGAAAAATCCGCGCTCCGCTATTCGCCGAAAAACGGGAATC

**SEQ ID 754**

MPDGLYGLFKIRTRRRSHCGIRIIGRKNPASVIPAAGI

**SEQ ID 755**

TTGCACGAAACACCACGCGCGGATTTCAAACTTCCAAAAATCAGCGTTCGCCGGTATTACCGGAATCAGCGCAATGGCCGGAAGACAACTTTCGCCGGCTGGCATCCCCCT  
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CGGTGAAACCGTTCGGTAAATGGTCTCGCGCAGCGCGTTAAGCCGCGACCAACAACGCGCAACGACGCGTCACCGACGACACCCAGCGCAACGCAACGCAAAATCGAAACC  
AAGCACCTGCCGTCAACCTGCCGCGATGAATCATCTGCCCTTTGCATAGAAACACCACTACGGCTTTCTATAAAATACCAAAACCGTCATTCACGAAAGCGGGAATCCAGAACGCA  
AATCTAAAGAAACCGTTTACCGGATAAGTTCCGCAAC

**SEQ ID 756**

LHETPRADFKHFQKISRCRVLPSRQAGRHFCRRGIPPSSDIKRYVQSVTVANGVVTAEKSDGVNKEIKGKLSLWGRRENGSVKWFQGPVKRDANNANDAVTDDTGTGNNEKLET  
KHLPTSCDESSAVCIETPTAFYKNTQVITPKAGIQNAKSKETVLPDKFPH

**SEQ ID 757**

GTGGCATCCGCTCCGACATCAAGGCAAAATATGTTGAAAGCGTTACGGTCGAAAAAGCGCTGCTTACCGCCAAATGCTTTCAAGCGCGGTAAACAAAGAAATCAAGGCAAAAACTCT  
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CAAAATCGACACCAACGACCTGCCGTCAACCTGCCGCGATAAATCACTCCGCTTTGCACGAAACACCAACGCGCGGATTCAAACTTCCAAAAATCAGCGCTGCCGGGTATTACCGG  
AATCAGCGCAAAATGGCCGGAAGACAACTTCTGCCGCGTGGCATCCCCCTCGCATCAAGGCAAAATATGTTCAAGCGTTACGGTCGCAAAACGCGCTGTTACCGCGGAA

**SEQ ID 758**

VASASDIKRYVESVTVKGVVTAKMLSSGVNKEIQGKLSLWAKREAGSVKWFQGPVKRNDANDVDDAGTDNGGKIDTKHLPSTCRDKSTAVCTKHAPIISNTSKSAVAGYTP  
NHGKWPEDNTSAGVASPPPTSKANFPKALRSQTASLPPK

**SEQ ID 759**

ATGTCGCGGCAAAACGAATTGCGGCGAGTGAAGCGCGTTCGCTTTGATCAATTGCGGCGCGCGCGCGCGCGTGGATGAAACGCGCTGCTTGCCTCCACTCAAAATACGGGCGAGATCGGG  
GGCGGGTTCGATGTTTTCAGCGGAGAACCGCGAGGGGCGGAATCCCTTGTGTAATGCACGATTACCCAATCTGATTGTTACGCGCGCATACCGGTGGGCGAGCGCGGAGGCTTTGGA  
TCGGTTGTTGAAATATGTTGGGGAACATTACGCTTTGTGAAAGCGGAGCGCAAAACCGCGTGGT

**SEQ ID 760**

MSGENELRQMKPGAVLINCGRGGPDENALLAALKYQIGGAGVDVLTTEPPRGNFLLNARLNLIVTPTAWASREALDRLFEILLANIHAFVKGBAQRVV

**SEQ ID 761**

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CGCGTATCGAAGGTATGATCTCTCGCGCGCACGCGAGCGCAAACTGAAGCTCTGATGCGGCGCTCAGCGCGCGGACAAAGTGGT

**SEQ ID 762**

LAKMPSRARFRLQTAFFRLICGIIIRLYPLFAKHNMTRKILVTSALPYANGSIHLGHMVEHIQTDVWVRPQKLRGHECTYCCADDTHGTVMIAQKQIAPEDMIAKVRKEHADFTGFF  
IGYDNYSTHSTENKQFSQDIYRALKANGKIESRVIEQLDPEKQMLPDRPVKGBCKPKHAQDQYGDNCEVCCTTYSPTLILNPSYSAVSGAKPELRESEHFFPKLGEADFLKAWTSGNN  
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AEGFLVFDGQKMSKRGFTTAKSYLBQGLNPEWMRYIIAALNGKIEDTDLNLQDFLSRVNSDLVGKYVNTAARASGFIARFPEGRPKDVGSGALLAKLAESDTLAEQYENREYARALR  
DIMALADIVNEYVDANKFWELAKQEGQDERLHEVCSELIINAFMLTAYLAPVLPQTAANAARFLNLDAITWKNTRTELGEHALNKVEHLMQVRVQKQVDDLEANKQSIQTASAPVEBGKY  
EKVABQAGFDDPMKIDMRVAKVLNCEAVEGSTKILKFLDLPFGFKRIIFSGIAASYNPFAELNRMVIAVANFAPRMAKPGVSEGMILSAATADGKLKLLDLDAGAQPDGVRG

**SEQ ID 763**

ATGTGCGGTATCGTCGGCGCATCCGCGCCATCACAACGCTCGTCGATTTTCGACCGGACGCGCTCAAAACGCTCGAATACCGGGTTATGACTCATCAGGCATTCGCTGTATTACAGCG  
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HCGTIVGAIRHNHVDFLTDLGLRLRYRGVSSGIAVSDGKIKRVRVRVQVLMEDAAREKSGSGIGIGHTRWATHGGVTEPNAPHISGMIHVHNGIIEPFSESRKRLBGLGYRFB  
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 SPASLEPGPHSHFQKRIHQPRATADAEVFLDGGPIFENPGKNAKSVFSESIRVKILACOTSYAAITAKYMLSEIAKIPADVELIASERYRYSIVADPDQVLITISQSGEFLDTHYAL  
 YAKSLGHRHSLSVCNVMSALPRESSLVLTRAGAEIGVASTKAPTQLVVLFLGLAVTLAKVRGVVSGEDEARYTEELRQLPGSVQHALLNEPQIAAQAQFVAKTISFLRGIGIHYPIAL  
 BGALKIKKEITYTHAEAYPAGELKHGFLALVDENMPVVVIAFPNDLILDKVKNAQJQVARGGELPVFADLGSFNATGVEHVIRAPREVGELSPVVHTVPVQLLAYHTALARGTDVDRPREL  
 AKSVTVB

SEQ ID 765

TTGAAAAAAGATGCGGACGGCTTCCTACCGCACTTCCGTTTCGATTATAAACCGCCTCCGGCGCGAAAAACAGCAAAATGCCGCTCTGAAGGCTTGGGCTTGCTCAAAAAAGGGAG  
GGATTTCCTCCCGCCTGACCGGGATGGGGCGTTCAGACGGCATTGCCTGCCGCCGGTTTATAGTTTTCGCAATCAATAT

SEG ID 766  
LKKKMR TASVPHLPFRIINRLPRRKTA KRLKAWACSKKGGISPPDRDGRSDGIACRRFIVFANQY

SEQ ID 767

TTGTATCAGTTTTTTTATGCGCGCTGTTCACAAACCTGCCGCCGATGCGCGCACAATCCGCTCTGAAGCCAGAATCGGGTTTCAGACGGCGGCAAAAAACGGCGGTTTTTCGCGCGGTTTCA  
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GCACCGATGATGCGGGCTCTCTTGTGCGCGTCCGTCCTTTTGGCGTATCCGATCGGTGCGGCACATATGGCTTTTCCAACCGGCTTCAATGCCAAACCGCCCTTCGAGCGCGCTCTCGCTGCC  
AGCGTCTGTTTTTCGCGGTCCATTTCCATGCCGAAGAATTTTGACCTGTGCAAAACATTTAAAGCGCGCAAAAGGC

SEQ ID 768  
LYOFFMFLPQTLPPDAATMPSEARIGFQTAANKNRRFSAGFIIMPRSPRGSGSDRFAGERGTGPCRCAACVSKHPPAHQNNHLTDNAASLSPSVLLPYPMRADINWFPQASMPNRRSSAVLFA  
SVCFPSISMSKDFDLCKTLKAAG

SEQ ID 769

ATGAGCAGCGTATGACGTTGTTTTCGGTATTTGGTACCGATGTTTTCGGGATTTTTATACCGTGTCCCAAGCCTTACCTGCCCGCTTCGGACAAGGTGCTGTGGTTTTGGTGATATGCCG  
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MSLMTPLFSLVIVPMFAGFFIRVPKPYLPASDKVLSVLVYAVILLIGVLSRVEDLGSRLGDMLATVNLVFCVTVGANLLALAVGLKSPWRIGGKGKGVSVGVSGSVRQLGCVLLGFVSGK  
LMCDIWMPSERAGHYCLMLNVLFLIGVQLKSSGVSRLQVLLNRRGTRLSVWFLLSSLGGLLPAASADGVSWTKGLAMASGPGWYLSGLVMTAYGAVGWGSMILLNDLARELPAFAFTPLL  
MKRPDPAAVGVGGATSDFTLPVIOGAGGLEVVPVAVSPGVVVNIAAPFLMVVFTLC

SEQ ID 771

ATGCGAAATGAAACAAATGCTTTTGGCCGTGCGCGTGGCGCGCGGTGTTGGCGGGCTGCGGCAAGGATGCCGGCGGTTACGAGGGTTATTGGCGCGAAAGTCGGACAAAAAGAGGGCGTGA  
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GCACAGGCATACCTFCGACGCGCGAAATGCGTTGCCGTCAAAACCAACGTATCAGCAGCGTCAGGCGCGCTACGCAAAFTGTAAACGGCGGTTTGAAGCCGAGTTTGACGAATTGAAAAAG  
AAATCAAATGCAACGGGCAACGCAACGCAATGTGTTGTTT

SEQ ID 772  
 MENTQMLLAVGVAAVLACGGKDAGGYEGYWRKESDKKKGVLAVKKKGNYFLNKINVPTGKEESLLLSEKDGLSINTGIGETPIKLSDDGKELYVERRYVKTDAAHKDKILAHQKKCCQT  
 AQAAYI.DARNALPSNOTYQOORAAETOLKRRFEAEFDELEKEIKCNGKPTLLP

SEQ ID 773  
TTGCGATACCGCAGGCACAAGCCGGCCGGTCGGACAAAACGCCTTCTTATTTGACGGATGGATTTCGCCCGAACGGAAATCCCCCTTGCAAAACGGACAGAATCGGACGGGTATTCAAACGCATCCGAACAAAAAAGCCGGACATTCCGCCCCGCCCTACCGGTATGGAAACCAACGGTCCGATTTCGGACGGCGGCATCCTCCCGTGTGCTACGCTAAACAACAATGTCCGGTTTGCGGTGGCAAT

SEQ ID 774  
LRYRRHKPKAGTKRLSYLFWISARTEIPLANGQNRGTGIQTHPNKKRRTPFPARTGNETTRPIRTAASSRLSYAKTMSVCRCI

SEQ ID 775

GGTGTTAAATCCCTCTCCCGGGCTACCGCAACGCCGCCGGAACCATCTTTTATTATTACTGACGACACATTGTGCCTATTGAAAAAACACCTGCTCGCGCTCCGCCCTGTACGGCATCG  
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GCAATCAAGGCGAGTTTGAAGGAAGCGCTTCCTCCCTTACCACAGCGCAACCAATCAACGGCGCGCTTGACGGCAAAGCCCATCTCGGTTACGCCGAAGACCCCGTCGAAC  
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## SEQ ID 776

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AIKGRFEGSRFLPYHTNQINGGALDGKAPILGYAEDPVELPFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIQRYMADKGYLKLGGTSMQGIKAYMRQNPQRLAEVLGQNPSTYIFRE  
LAGSGNEGFPVGLGTPLMGEYAGATDRHYITLGAFLFVATAHPVTRKALNRLDQGTGSAIKGAVRVDFWGYGDEAGLAGKQKTTGYVWQLPNGMKPEYRP

## SEQ ID 777

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GCCCTCGCTGCGGTAAAGCCCGCGTTACGCCCAAG

## SEQ ID 778

VQNIKSGKRLKIDTVTQSKTGFPCNAGADLPLTAABQPDRRPRLSVKPPFTPK

## SEQ ID 779

ATGATTTTCAGCTGTCCGGGCTTTATCCGAGCAGGTTCCGACCGTCCGTTCATCCGCTGAACCGGCAAGCGCTTTCTCAAAAAACCCATACCGCTGCACTTCATGCGGCTGTATG  
CGTAGGTTTTCACATTCAGACGCCATATGCGTCCCGAAGCAGTTTGGTGTCCAGTCCGTTCATGATTATATAAACCACTGGGTGCGGATAAACCTTTGTTTATC

## SEQ ID 780

MISACPGFIRSRFRSVPSEPAGRISQKTFYRCNFMRLYGVGFALQTAVASRSSIVSQSVHDYINNGADKPLFI

## SEQ ID 781

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AGCGGGGTTTGGCTGCGCGCTGATTGGCGCGTGTATTATCAGGCGGATGCGCTGAATCTGGCGAAGTTTTCGTTGGACGGGGCGTTCTGATTATCGTTGCCCGCGCTCTG  
CTTGGCGGCTCGCTGCGTGGCTGCA

## SEQ ID 782

MPKVMFGVVLASLMCLGIGYGIHSATGEIPRKQGEFVVGII GLVAVAMLTCVVLNMRKAARSMMKRLRDSVQAALNRSGQGNALVGMFLAVAREGLSVFFPACRIQTEPDVADAGRRG  
SGGFCRRDRVLDGRDAPESGEVFPDGGVSDYRCRRSACRLAACAA

## SEQ ID 783

GTGGCAGCGGTCAAGGATGGGCTTGGTGGTATGGCGTTTCTTGGCGTGGCGCGCAAGGTTTGGAGAGCGTTTTCCTGCTTGGCGTATTAACAGAGCCCGACGTTGGCAGATGC  
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TGCGCGCGCTCTGCTTGGCGGCTCGCTGCGTGGCTGCGATGAGGACGCGATTGGAAGCGGCTTCAGGACATTGTTGTCGACCCATCAAAATATTGACAGAGACAGTCCGTTGGGTGTG  
CTGCTCGCGGATTTTTCGCTATACCGACCATCCGCGCAGGGCGGGGCTTGGTTCGCTGCTGATCTTATCCCGTATGATTGGTTCGCGCGCAGCAGGCGCTGTAACCTT  
TAACCGCTAAGAGGAATTGAAA

## SEQ ID 784

VAAVKDGPWSVWRFLPWRKVVRAFPFLAVFKQSPWQMPAGAVAGVLAADVIGALYQGGMRNLAKFFPRWTGAFLIIVAAGLLAGSLRALHEAGTWNALQDIVFDPKYLHEDSFLGV  
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## SEQ ID 785

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CGCAAGCATTCAGCGCTCTTATTAACGCGCTTCCGGAAGACCTTGCACCACTTCGCGGCACTACGCGCTTGAAA

## SEQ ID 786

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PRGLVVADSGFKDTANEDLEKLFPQLADYKAVVQGEVKELAAKTFTFEAVKAGDIEKAKSLFAATRVHYERIEPIAELFSELDPFIDACEDDFKDGAKDAGTFPHRIEHALWVEKDV  
SGVKETAARKIMTDVEALQKEIDALAFPPGKVVGGASELIEAAGSKI SGEEDRYSHITLSDPFQANADGSKKIVDLFRPLIEAKNKALLEKTDTNFKQVNETLAKYRTKDGFEYDKLSEAD  
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## SEQ ID 787

TTGACTCATGGCGTTTCCTTCAATATCCGTGACAGGCGTGGGCATCCCTGCACGCGCTTTTCCATTAAACGATAGCGGCGGTCTGAAAGCCCGCCCTGCAACATATGGCGGATATAGCG  
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TACCGGTTTGT

## SEQ ID 788

LTHGVSNIRAGWASLHAFVPLTDSGGLKARPATYGGYSLTKIRTRRAAGSTNGTEPVRVPLGRLEZFPFLSRGGATRTGFC

## SEQ ID 789

ATGAGTCAAACCAACCGCACACCGCAACAGCAATCTGTTCAAAACCGCCCTTGCCTGCGCGCAATCGCGCAATCGAGGTTATTTCCGCGCAAAAAACAGGCGAAACCGCGG  
AACGCACCGCCGAAGCAACACTCGCCCAAGGCTATCCCTGCTACGGCGCAATCAGGCGGATTCGTACCGCGCGCGGCGGCTTTCCATTATGTGCGCTTCGACGTAAACCGCGCA  
AAGTCCCAAGCAGCTGGAAGAACTGTTCGCCACACTGACCGCGCGCATCGAGTTTCTCAACCAAGCGCGGAGAAATACCAAGACCGCGGACGACAAACCTCCGTCAGCGCGCAGCGCATTTTG  
GCTAAAGGCTTCAACCCCGCAGGATTCAGCGTTACCGTGGGGTGGCGCAGCGCTGTTTTCGACGGCGGTTTCGACTCAAAGACAAAAACGTTTCAATTTCAGGAAATGCGCGACTTCC  
GCAACGATAGCTGCAAAAAAGCTGCTGCGACGCGGATTTGAGCTGCAAAATCTGCGCTTCAACCCCGAAACCTGCCAAACCGCCCTGCGCGACATCATCAACACACCGCCCAACCGC  
CGTCATCCGCTGAGTATCGACGGGTGGCAGCTAAATCGAAACCGCGCGATGCGCGCGCAACCTGTTGGCTTCGAGACGCGCGCGGCAACCCCAAGGTTTCGATCCCAAAAC



GCCTGCGAGGTTTATGACGCGGCGTGGCCGCCAACAGCCTCGACGAACCGGAGTGGGCGAAAAACGGCAGCTATCAGGCAGTCCGCCCTATCCCGCGCTTTGTCGAGTTTGGGACAGGA  
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CAAGACAGCCATATGCGCTTGGCGAATCCGCGCGATCCCGAATTCTCTAAAAACACTGCCTTCTCCGCGCGCCTACAGCTATTCTCGCGGACCGCCTCAAGGGACAGCTTGATGTC  
GGCTGGTGTTCGTGCTATCAGCAAACTTCGCGCAGCGTTTCATCTTCGCGCAAAACCTCTCAACGCGGAACCGCTGGAGAATAATCATCAGCCCTTCGGCGCGCGCTATTCTTCG  
TCTTCGCGCGGCTGGAAAAAGAGCGGATFTCTGGGACAGAGGCGTTCGCGCGTA

**SEQ ID 790**

MSNQPAQPPKRNLFKTLALVGAIGAIGGYFGGKGQGETAERTAESQHSQPAYPCYGEHQAGIVTTPRQAPSINCAFDVTAQSAQOLENLFRTLTARIEFLTQGGEYQDGGDKLPASGSL  
GKAFNPDGLTFTVGVGSSLFDRPGLKDKKTVHLQEMRPPNDKLOKSWCDGLSLQICAFPTPETQQTALRDIKHTAQTAIVRWSIDGWQPKSEPGAMARNLGRDGTGNPKVSDPKT  
ADEVLWTGVAANSLEDEPMKXNGSYQAVRLIRRFVEFWDRTPLOQBTDTFGRKYSGAPMDGKKEADQPDFAKDPEGDTIPKDSHMLANPRDPEFLKKHCLFRRAYSYSRGPASSGQLDV  
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SEQ ID 791

TTGTGCCAAGAATCCGCCCTTTTCCACGCGCGGCACGACGAAGAAATAGCGCGCGCGGAGGGGCTGATGTATTCTTCCAGCGGTCGCCGTGAGGAGGTTTTCACGAAGATGAAACCG  
TCCGCAAGATTTCCTGATAGCAGACGAACACAGCCCGACATCAAGCTGTCCGCT

**SEQ ID 792**

LSQESAFSHAGQDREIAAEGADVFFORFAVEEVLHEDETVGKICLLADEHQPDIKLSA

**SEQ ID 793**

GTGGCGGATGCCAACGGCGGGCGGTGCAAAACGGCGACACCGTCATCTCATCAAAAGACTCAAGGTAAGGCGAGCTCGATGACGATCAACAAGGTACGAAGGTCAAAGGCATACGCG  
TGCAGGAAGGCGATCAACAATCGCGTCGCAAAATCGACGGCAGCGCGATGAATTTAAAATCCGAATTCGTCAAAAAAGCC

SEQ ID 794

VRDANGAALONGDTVLINKDLKVKGSSMTTKOGTKVKGIRLOEGDHNI GCKIDGSAHNKSEFVKEA

SEQ ID 795

ATGGAATATTTCGCAACCTGAAGAAGCATCGACCCGTACGCAACATACAGCGCTGCCAACCTGATGGCGGGCTGCCGCTGTATTCTGCTGATTTTGGTCTGCTCAATGTTGTTTTCCGC  
TTCGGCTCATCCCTTGGCTTGGCTGTGCTGCAAGTTTCATGTTTGGGGCGCGCTTTCCTTATCGCTGCCCTTGTGGCGCTGCTTGTCCGACCTGCTGCAATCTGGCGGTTG  
TCCGCCATTATCCCGTCTTTGTGCCACCTTGCCCGAATCATCCGATGCTAAAAATTCGCC

**SEQ ID 796**

MEYCEPEEASDPYATYRRANLHAGLPLFVVILVLLNVVFPPLPAHPLANLVPAGFEVLGGGFPLSLPLVALLVPTCCILARCPPLSRLCHPCPNHPSKNSA

## SEQ ID 797

AAACAACCACTTTGACGACAATGCGGCTTCCTTTGTCGCGCTCCGCTCCTTTTGCCGTATCGATGGTGGGACATATGGCCTTTCCAACCGGCTTCAATGCCAAACCGCCCTTCGAGCGC  
GTCTGCTGCCAGCTCTGTGTTTTGCGCGTCCATTCATGCGGAAAGATTTTGACCTGTGCAA

## SEQ ID 798

KOPFDROCGFFVAVRPFVSDACGHMAFPTGFNAKPPFERRPACORLFFAVHFAERF\*PVO

SEQ ID 799

GTGCCGTCTGAAGCCGGTTTCAGGTTTCAGACGGCATCCCAAAACAAACATCCGATAAGGACGGCAAACCATGTCATTACCCCTTGCCCGCAATGCGCCTCCGAATACACCTA

SEQ ID 800

VPSEAGFRFOTASONKHPIRTANHVTTPLPAMRLRIHL

SEQ ID 801

ATGCTCGCTCTGAAACCGCTTCAGACGGCATGGCACAGGAAAAAGCTATGCGCGAAACACTTTAAACACCGTCATCTCTGCCGCGCGCAAGGACACGCGCATGTATTCOCACAAATGCCCAAAG  
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CAAAACCGCATGCGCTCTGGGTGCAAAACAAACGCAACAGCTCGGCACCGGCCACGCGGTCAAAACCGCCCTGCCCACTTGCCTTCGAAAGCGCGCACGCTGGTGTGTATACGGCGACGCTTCT  
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CGCTAACCCGCCATTCTCGAAGAAAAAGCAAGCTAGCTGCACCCAAAAAACCATCTGGCTGATTAACACAGGCATCTCTGCTCTCGGCAACGCCAAATCGGAACTGGAACCTTTC  
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SEQ ID 802

MPSETASDGMQAENAMPONTLNTVLILAAGXGRMYSQMPKVLHCIGGKPMVERVIDTAAALNPONICVVGHGKQVLDTVKRDVAVVEQTQBLGTGHAKTALPHLASEBGRTLVLYGDVP  
LIDVETLETLLAAGNEVGILLFDVPADPAGLGRIIRDGSGSVTAIVEEKDASMTQKTIRENTGTILVLPNAKENLWLSLSNNNAQGEYITDLIAKAVADGIKVRPVVRASHLAAGVFN  
KRQLAELERIPQTQBAQELLKAGVTLRDPARFDLRGLRKHGQDVVIDVNVVIGEVELGDNVEIGANCVIKNAKIGANSKIAPFSHLEGCEVGENRIGPYARLRPQAKLADNVHVGNFVE  
TKNAATGKGTKANHLFYIGDAEVSQSKTFEGAGTITANYDGVHKHKTIVGDEVIRGSCNVLVAPVTLGNKVTGAGSTITRNTEDNKALARAROPTVDPGHRPEKIDQ

SEQ ID 803

ATGCGTAAACACTTCCTTATCTGACCGTCTCCGCCGCCCTTTGTCTGGGCTGCGCGTGGGAAACTTATCAAGACGGCAACGGCAAAACGGCGCTCCGTCAAAATAATCCCGCGGCACGC  
CCGTTTATTACCAAGACGGCAGCTACTCGAAAAATATGAACTACAACCAATACCGTCCGAAACGCCGCCCGCTGCTGCCGACCAAAACGGCAACAACGCCGACGAAGAGCATCGCCACA  
CTGGCAAAAACCAAAGTTTCAAAACCGA

SEQ ID 804

MRKTFLLILTVSAALLSGCAWETYODGNGKTAVROKYPAGTPVYYODGSYSKNMNYNOYRPERRAVLPDOTGNNADEEHROHWOKPKFONR

SEQ ID 805

ATGCAAGAAAAACCGACCGTGTGGCTGTTGCACCTCGACAACACGCTGCACGATCGCGACCGAGGCATCTTCCACCTCATCAACCGCGCTATGACGGCGCTATATGGCACGCGCCCTCAAACTCTCCGAATCCGCGCGCTCCGACCTGCGTCAAGCATATTGGCACCGTTACGGCGCAACGCTCGCGGGAGTCAAAATCCACCATCCCGAAATCGACATTTGGGAATTTTTACGCGAAAGCCATCCGATCGATGCAATCTCTGACGAGCTGACACGGCATGGCGGATACGGAAAAACCCCTATGCCGTCTGAACGGGGCGCAAGGCGGTTTTTTCACACGGCGCGTCTGTTTTACGTCCGTGCCGTTGCCGGCGCACTCGGTTTGGAAAACTGTTTTCGACGCACTGTTCGGCACGGATAGTTTCCGACTGCTGTACAAACCCAATTCGCAAGCGTATCTCAATGTCGCGCGCTTGTGGACGTCACCGCGAATCTGCAATATAGTGGTCAGCACGAGCGCGACAACCTTCTACGGCAAAAGCATTTGGGCATGAAACCGTCCGGTTCGGTGGCAAAATCCCGACGAACCGCCCTTTATCGATGCGCTCCGTAAGCGATATGGCGCAACTGGCAGCATTCGAGAAATCTTTCAGAACCGCGCGCAAAATCATTCACATACCGCGACCCCGCGAAAATACGAAGAAGATGCTATTCGGTGAATAAATCTTCCCTATCT

## SEQ ID 806

MQENPTVWFLDONTLHDADAGI FHLINRAMTRYMARLKLSESAADLRQDYWHRYGATLAGLQIHPIDIAFLAESHPI DAILTRLHGMADTENTLRLNWRKAVFSWSPSYVRAV  
AGALGLENCFDALPGTDFGLLKYKPNQAYLNVCRLLDVPFBCTIMVDDSDNLHQAALGMKTVRPGAKSHAPPPIDASVSDMAQLARYAETLSERRQNHYNTRTPRKYRMLCVKPSLS

## SEQ ID 807

ATGAACCGAAAAATTTGGCTGCTGCCGCTGCTGGCGTTTCGGCATACTGCGAGGCGCAGACGGAAGTCAGGCTGGCGGTGCAATAAGTCGTTACGCTGCCCAAGGGGTGATTGGCGCT  
TCGAGCGGGCAACAGATGCGAAAGTGTGCGATTATTCAGGCGGGCGGCGGAACGAAATGCTCAACAACTGATTGAGCCGAGCAACCCGATTGCGCGAGCGGTGATCGGTTTGGACAA  
CGCAATATTCGCGAAGCGCGGGAAATGGGCATTTTGGCGGCGGCGCAACCCGAAATCGCCCCGTCGGGTGCGGCTGCTTTCGCTTTGGCGGTGATTACGGCTATGTGCTCCGTCAT  
TACGACAAAAAATGGTTGAAGGCAAAAGCTGCCCTGCCGCAACCTCGCAGGATTGACCCGCGCGAATATAAAACCTATTGGTGTGCGGCTCCCGCCACATCTTCCCGCGCT  
TGGGCTTCTGATGGCAACATCGCGGTCTGGGCGAAGAAGCGCGTTTAAATGGTGGGACAGATGCGGCGAAGCGGTGAAGGTCGCGCAAGGTGGAGCGAGGCTATTACACCGA  
CTTTTCGACACACGCGCGCGGTATCCGCTGGTGGTGGTTATGCCCGCAGCCCTCGCGCGGAAGTATATTTTCCAAAGGCAATACAGCGAGCGCGGACGGGCAACCTGTTTTTAA  
GGCGCGGTATTCGCTCAGGTGCAAGGCGCGCGGTCTTGAAGGCGCGGAACAGCGCGAAGCTGGCGGCAAACTGGTGCAATGGCTGCAAGTCTGGAAGTGCAGAGCGGTTCGGCTG  
AAATGTGGGTTTACCCCGCGCTCAAAAACACGCGCTGCCCGAGCTGTTCCGCTTCGCCCAAGCCCGCGCACATACCCGCCCGCGCAGCGGATTTGATGCGAACCAGCGCGGATG  
GGTTCCCGCTGGATCAGGACGGTTTGA

## SEQ ID 808

MRRKIWLPLLAWSAYLQAQTEVRLAVHKSFLPKGLIARFERANDAKVSIQAGGANEMLNKILSRANPLADAVYLDNANIGKAREMGLAAQSPESAPVAVGLPSALAVDYGYSVH  
YDKWFEKGLPLPQTQLTRPEYKNLLVVPSPATSSPLGLFMANIGGLGEGAFKWAQMRQNGVVKAGWSEAYYDFSHNGAYPLVVGYAASPAAEVTPSKGYSEPTGNLFLK  
GGVPRQVEGAVALKGAQPKLAALVQWLQSLLEVQAVPSEWVYPAVKNTRLPDVFRPAQAPATTAPAQRDIDANQRCWVSEWIKTVLK

## SEQ ID 809

ATGGACTTCAAACAATTTGATTTTACACCTGATCAGTGTTCGGTGGGGCATCTGGTGAAAAGGCGTGGCGTTCGGGTGAACCTTGCCTCCGCGCTGCTTATTTCTTGGTGG  
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GATTATTCGCGCATTTGGGACGGTGGGGCTTCCACACATCCGTAACCCCTTAAATCGCGCGCGCGGTTTGGCGGTGGCGTGTCTTAAAGACACGCTGCTCAATTTTCCCGCGCG  
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AAGTCGTGCTGCCCAACAGCGTGGTATGGGCAACAGCATGTCACCGTTCAGCTGCGCTTTGCGCGCGCAAGTATAGTCGCGCTGCGATTACACTGCGATTGAAAGTGGCGAA  
AGAGCGCGTGTGAAAGCGCGCGCGCAACCCCTTGAGCGTTCAAAGCGAAGCGCGCGCGCGCTACATCACCCTTGGCGGACAAATGCAATTCATTTGGCTTGG  
GCAACGAAAGCAGACCGCTGGACGCTGCAATGCGACTTGAACGAAACAGTGGTGGAAACCTCCGCAAGTCAATATCAACATCCCGTCCCGCAACGCGGACATACATCATCAATCT  
GCAACGAAAGCAGACCGCTGGACGCTGCAATGCGACTTGAACGAAACAGTGGTGGAAACCTCCGCAAGTCAATATCAACATCCCGTCCCGCAACGCGGACATACATCATCAATCT

## SEQ ID 810

MDFKQDFLHLISVSGHGLAEKAWAFGLNLAAALLIPLVGMKAKRIIVAVMRAAMTRAQVADTLISFLCNVANTGLILVIAALGRLGVSTTSYFALIGGAGLAVALSLKDLNPAAG  
ALILFRPFKVGDFIRVGFPGYVREIKMVQTSRLTIDNEEVLNPSVVMGNSIVNRSLPLCAQVITGVVDYKDLKVAEVLKAAAEHPLSVQNERQPAAYITAGDWAETITLWAM  
ANEADRWTLQCDLNEQVVENLRKVNINIPFPORDIHLINS

## SEQ ID 811

ATGGACGCGTTGCACACCATCGCCGAAACCTGACGAAAAACGTCAAACCGTAAGCTGTGCCGAATCTGCAACGCGCGGAATGCTTGGCGCGCATTCACAGCGTTGACGCGCTGCG  
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GCGCGCGCGAAAGCGGTGCTGAGCGGATACCGCGTGGTATTTCGGGCTGCGCGCGCGCGCGCGCGCGGCAAGCAACCGCTGCGCAGCGTTGGTTGCGGTTTGGCTTTCGCGG  
GGAAGTTGCGAAGCAATGCGCGTTTTCAGCGCAACCGCAATCCGTCGCGCGCGCGCGCTGCGCTTGGCGGTGCGCGCGCGGTGGAACCGCGCGGATGCTGCT

## SEQ ID 812

MDALHTIARNLTKRRTQVSCAESCTGGMLAAAPTSGAGSSQWDFQSFVTSNKAKEYRLGVLPETLLEHGAVSRTQVYEMARGAKAVAQADYAVGISGLAGPGGEGSKPVGTVMWGFAPFG  
GSCBAMRRPDGNRESVRAQAVAFALERLAGLVZMGDDAV

## SEQ ID 813

TGCCCCGCCCTTCGGGCGCGCAGGGTTGCGATCGTTTGGCGGGCGCGCACGCGCGCTGCAAGGTGTGCCGCTGTGTGTCAAAACATTTCCCGCGCATCAAAACACCATTTGACCGA  
CAATGCGCGCTTCTTGTGCGCGTCCGCTTTTGGCGTATCCGATGCGTGGCGACATATGGCTTTTCAACCGGCTTCAATGCAAAACCGCTTCGAGCGCGCTGCTGCTGCCAGGCTC  
TGTTTTTGGCGTCAATTTCCATGCGCAAGATTGTTGACCTGTGCAAAACATTAAGCGCGCAAAAGGCTGAAGATTGACACCGTTACGCAAAAGCAAAAGCGGTTTTCGCGCAATGCGCG  
CGCGGATTGCGACTGACGCTGCCGAGCAGCGCGACCGCGCGCTGCTGTGCTGAAGCGCGCGCTTACGCCCAAGTAGGTAACTGCGCTGCGGTGCGAGTAAACTGCAAT

## SEQ ID 814

CPALRGGRVIRIGLRGARGRAGVFPVCQNISRRITTI\*PTMRLLCRRPFCRIRCVRTYGLSNRLQCQTALRAPSCLPASVFRPFPCKRILTCAKH\*KRQKAE\*HRYAKQNGFLPECR  
RGFATDRCAARPPPLAVGKAAYVAVGKRLRLRLQVKLH

## SEQ ID 815

TTGAATGCGCGGAGCGGATAAGCCGCTGAACCTTCAGGCGGTTTTTAAATGGCGAACCTGATGCCGTCTGAAATATGGATGCGGGTATCTGCAATTTTCAGACGGCAATTTTAAAGCGCA  
CATATCATGCGCAATAAAGAGGGTAGGGGA

## SEQ ID 816

LWAGADKPPPEPSGGFLMANLMPSEIMWRVSAIFRRQFLSRTHYAAIKBEGG

## SEQ ID 817

ATGCCGCTGAAACCTGCAACGTTTCAGACGGCATTTTATTCGGCGGGGATTTGTTCAGACAGCATCGCGCGCTTTTCAACGAGCCGCGCAACCGTTCCAAACGCAAGCGGACCGCC  
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CGATGCGCGGAAATACGACGCGTAATCCGCTGAGCCAGCGCTTCGCGCGCGCGCGCATCTCATAGACGTTTGGCGGTGACCGCGCGGTTCGAGCAGGGTTTCGGCAACACGCG  
CAAGCGGTATTTCTTGGCTTTGTGCTGTATGTACAAAACCTGCTGCAACCATTCGCAACTGCTGCAACGCTTGTGAATGCGCGCGGCAAGCATTCGCGCGTGCAGGATTCGCGCACG  
CTTACGCTTTGACGTTTTTTCGTCAGTTTTCGCGCGTGTGTGCAACGCGCTCATTTCCACCCCGCTTTCAGACGCGGTTTAAAGAT

## SEQ ID 818

MPSETCNVSDGIFYPAGICSDSIAAVFNQPGQPFQREGDRLRADGFAVAVKTAHCFATSAARKGKPEPNRADGFAPAAARAGDAGNTDGVIRLSHGFRARHLIDGLAADRAVFBQGFQHA  
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## SEQ ID 819

ATGCAAAACCGTCCACAGGAAACATCAAAATGAAACCGCTACTTCTTTTCCCTTTGCGCAAGTTCGGCTGCGCTGCTTGGCGTGGGCGCTTGTTCGCCCAAAATGCTGATGCGCGGA  
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TTTGTCCGAATTTGGGACAGGCGGAGAAATGGGCGCAAGATGCAAAATTCAGCTCCGCCAACCTGATTACCGTGCCTTCCCGCGCTTTTTCACGAGAAAAAGACGGCGAGTTTCAAAA  
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SEQ ID 820

NQTVTHGNIKMKHRTFFSLCAGPGCLLALGACSPKIVDAGTATVPHTLSTLKTADNRNPASVYLKKDKPTLTKFMAWCPCLCLSELGQAEKWAQDAKFSSANLITVASPGFLHEKKDGEFOK  
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 TENPSYEDVSYRHTGAETVKVITYDADKLSLDDILQYFVRVVDPTSLNKQNGDTGTQYKRSVYITYDPAEKA VIAAALKREQQYQYQLPLVVENEPLKNFYDAEEYTHQDYILKPNPGYCHIDI  
 RKADEPLGKTKAAPQKGFDATAYKPKSDAELKRTLTBEQQYVATQNSATYAFASHEYDHLFKPGIYVDVWSGEPLSSADQYDGGCWPSPFTRPIDAKSVTEHDDFSFNMRRTVEVRSRAA  
 DSHLGHVDPDGRDKGLRLRYNGASALRGLPILEOMDAKYGALQKGVKVK

**SEQ ID 821**

ATGCGGAAACCTTACGGCCGGGATTTTCAGACAACTTGGCGGCGAAATACGTACAAATACGCCCTATTTCAGTTTCTAAAATTAAAAGGAAAATTCATGTTTCAGCTTCTTCGGTCGCAAGAAAAAACAGGAAACCGCGGCTTCGAGGAGGCCCAAGTTCAGGAAACCGCAGGAAAAGTAGAATC

SEQ ID 822

MPKFGPDFOFTLPRKIRYNTFYKFLKLGKFNVOILLPSOEXTGNAGSRGGPSSGNRSKSR

SEQ ID 823

ATGCCGCTGTAAGCAGGGGAAGCGCGTGA AAAAAGCGGTGGAACGCGTTGAATCCGCAAAAGAAGCTGTGCCGAAACCGTCGGCGAGGCGTGTGGGCAAGTTC AAGAAGCCGTTGGCAGCAA  
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CGAAGAGCTGGA AAGCCGTGCTGATTACCGCGGATATGGGCATGGAGGCCACCGAATACTGTGATGAAAGACGTCGCGCGGCCGCTCAGCTCTCAAAGGGCTGAAAGACCGGCAACGAATTCGGC  
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AAGTCAAAAGCCCTTTCAGCAGCCATTGGGGCTGACCGGGGCTATCGTTTACCAAATCTGACGGCAGCGGCAAGGCGGCATCTCTCGCCGCGCTTGTCTCCGACGCGCCCGCTCCGCTA  
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SEQ ID 824

MPSEAGAEAAEKAVERVESAKEVAEATVGEAVGQVQEAVATTEEHKLGMWAARLKQGLAKSRDKMAKSLAGVFGGQIGEDLYEELETVLITGDMCEATEFYLMKDVRGVSRLKGLKDGNEL  
GALKKALYDLIKPLEKPLVLPETKEPFFVIMLAGINGAGKTTISIGLAKYFQAQKSVLLAAGDTFRAAREQLQAWGRRNNVTVISQTTGDSAACVCFDAVQAQKARGIDIVLADTAGRLPT  
QIHIMEEIKKVKRWLOKAPGAPHEITVVLDAFIGONAVNOVKAFDDALGITGLITVKLDGTAKGGIILAAASDRPPEVRYIGVGEGIDDLRPEDARAPVDAIID

SEQ ID 825

ATGCCGCTCCGAAACCGCAGACCGAACCGTCATTTCCACGGAAGTGGGAATCTAGGACGCGGGGTTTGGGCAACCGTTTATCCGATAAGATTTCCTGTGGCAGAGGTCCGGATTTCGCGCTCGCGGGAATGACGAATTTTCGAGATTGCGGTGTTGTGCGGACGGGTTTCGAGATTGCGGTATTGTGCGGAATGACGGTTCGGGTATTTCCTCCGCGCCGCGCCCGCGCTGTAAACGGCGGGCGATTAAAAATGCCGTC

SEQ ID 826

MPSENGRPNRHSHGSGNLGRGVHATVLSDKFPCGOVRISACAGMTNFEIAVLSDGFRDCGIVGNDGSGISPRPPRACKRRRAIKNAV

SEQ ID 827

ATGCCGTC TGAACCTTCAGACGGCAATTTTAAATCGCCGCGCGTTTACAGGCGCGGGCGGGCGGGGAAATACCGGAACCGTCATTTCCGACAATACCGCAATCTCGAAACCCGTCGAC  
AACACCGCAATCTCGAAATTCGTCATTCGCCGCGAGGCGGAAATTCGGACCTGTTCGCAACGAAACTTATCGGA

SEQ ID 828

MPSEPSDGIENRPPFTGAGRARGNTRFTVI PDNTAI SKPVROHRNLEIRHSRAGGNPDLSARKLIG

SEQ ID 829

GTG CAGGCGGAGTTTACGCTACGCCGCCGAACGCATTACCCACGATTATCCGGAACCAACCGCTCCAGGCAAAAACAAAATAAGCACGGTAAGCGATTATTTAGAAAAATCCGTAACGATT  
CCATCCACCCCAGGGTGTCGGTCGGCTACGACTTCGGCGCGTGGAGGATAGCGCGAGATTATGCCCGTTACAGAAAGTGGAAACGACAAATAATATTCCTCGACATAAAAGAGTTGGAAAA  
CAAGATACAGAAATAAGAGAGACCTGAAGACGGAATAACAGAAAAACGGCAGCTTCCACGCCGTTTCTTCTCTCGGCTTATCAGCGGTTTACAGCTTTCAAACCTCAAGACAAAATTCAAACCC  
TATATCGGTGCCGCGCTGCCCTACCGGACACGTCAGACACAGCATCGATTCTGACTAAAAAAAATAACAGGTACTCTTACCGGCTACCTTAGTGATGCTGACGCGAGCAGTTACGGTTTATCTCTG  
ACGGACATCCGCAAAAAACACCTTACAAAAAGCAACACGAGCCGCGCTTGGCGTTTCGGCGCGTACGGCGGCTGGGCATAGAGCTCGCGCGCGAGCTGACCTTGAGCGCGGCTACCG  
CTACCACTCAACTCGGAGCGCTTTGAAAACACCCGCTTTCAAACCCACGCGGCTCATTTGGGCATCGCTACGCTCTC

**SEQ ID 830**

WQADLAYAAERITHDYPEPTAGPKNKISTVSDYFRNIRTHSIHPRVSVGYDFGGWRIAADYARYRKWNDNKYSVDIKELENKNQNRDLKTENQENGSPHVAVSSLGLSAVYDFKLNDFKFX  
YIGARVAYGHVRHSISDSTKKITGLTATAYSPDADAAVTVYPDGHQPKNTYOKSNSRRRIGFGAMAGVGDVAPGLTLDAGYRYHNHGRLENTFRKFKTHBASLGMRYRF

SEQ ID 831

TTGCCCTTCACTTGCCGCTGCCTGCCGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGGTTTTTTGCGGGCTGGATTTCATTTTCGGCTCCTTAATTGG

SEQ ID 832

LPSLAACAAEEKRREEKRRREEKRVFCGLDSFSAPYSV

SEQ ID 833

TTGGCCTTCAAGGCCCTGTCATGTGCTCATGTGCCACCGCTTTTAAACACGGTTTTTATCTGCAGGCGCGCAATCCGCCCOCTCATTTGTGTAATCCGCCATATTGTATTGAACACACCGCCCG  
GAACCCGATATAAATCCGCCCTTCAACATCTAGTGAAATCTTTTTTTTAAACCGGT

SEQ ID R34

LRFKALHVPCHCHPEKTRGEYL.TGAOSAPSEVNPPYCIETPPGSTRYNPPENTSENT.FLTG

SEQ ID 835

ATGAACTTTGAAAACGACGACATTATTCATGCGCGGACACGCTCTCCCTGATCTCTCAAGAGCGGCACGATTTCGGAGCTGTTCGGCTGTTTACGCCCTGATTTTGGACGCATTAACGATC  
AGGTGCTGCTGCCGCGAAAAGCTGACCGGAATTCGCAACTTTGCCGTCAGATGTGTGTCTCGCAACACCCGTCCGGCGGCGCGCTGTGCTTTTGGCGCACGACAAGATTTGTGATTTTGC  
ACCTCAACAGGGGCGCGTTCGTCCACGCTCCGATTTGAAAGAAATCGAGGATGTGTCTCAATCCGCGCATCGAAATGGAGACGATGATTTTGAACATCTCGCGCGGCTGCCGGATTTGGA  
ACGCGCTCAAGCCGCTTATGCGATGATAAGGTGCGAAGAAGAGGCTCTCCGCGAGGGCGACGCGCTCGGCTGGAACCGCTGTCCAAATGCCTTCCACGTCGAACTGGCGCGCTGGTGG



GCAACGATGTCGTTCGACATTATGAACACGCTGTGSCGCGTCTTCCCTGATTGTGCGCGTGGGGGGGTGCATGCGGAGAAAAACACGCCATCAATACGCATACGCATTCCGAACA  
CCGCGAATCCTCGACCTCTGCTGCGGGGAGCGCCAACCGCGTGGTCAAAATCTGCGCGCGCATTTGGGCAACTGTATGAGCGGTTTGGAAAAAGACTTTGGAAGAT

**SEQ ID 836**

SEQ ID 836

MFNFNDLIHAPTSSLLIEERHDSLFVRYVALILDGITDQVLLPGKKLTESLCRQMVCSENIVRGALSLLAHDKIVDLQPNRGAFVHVFDLKEQDVFNARIEMTITLNLILAGLPDLR  
TRLKPIYAMIRCEEASGRGDVGVNRLSNAPFHELARLVGNDVLPDINMTLCARSSLI VAVAGVHREKKHAINVTHSEHRETLDLLLAGRRNRVVKILRRHLGNCMERLEKTLR

SEQ ID 837

SEQ ID 837  
ATGCAGGGCCTTGAAGCGCAATCGATATATTATTTCCACCGGAACGGACGACCCCGCCCGCTTGCAAACCTTTAAAGACAAGCCGCCCGGGTGTATCCGGGGGGCCGTGGGAATCACT  
TACCGTTGAPTTATTAAAAATT

**SEQ ID 838**

MOGLEAQSIYYFHRNGRPRPPCKPLKDKPPGLIRAAVGNHLPFDLFKI

SEQ ID 839

SEQ ID 839  
ATGCGCGGAAGACAACACTTCTGCGCGCGTGGCATCCCCCCTCCGACATCAAAGGCAAAATATGTTCAAAGCGTTACGGTCGCAAAACGGCGTCGTACCGCCGAAATGAAATCAGACGGCG  
TAAACAAGAAGANTCAAAGGCAAAAACCTCTCCCTGTGGGGCAGGGCGTCAAGACGGTTCCGGTAAATGGTTCTGCGGACACGGCGTTACCGCGCAACGACGCCAAAGCCGACGACGTCAAAGC  
CGACGCCGCCAACCGCATCTGAAACCAAGCACCTGCCGTCAACCTCCGCGGATGAACCAACTGCCAAA

**SEQ ID 840**

SEQ ID 840  
MAGRQHFCRRGIPPSDIKGKYVQSVTVANGVVTAEKSDGVNKEIKGKLSLWGRRQDGSVKMFCGQPVTRNDAKADDDVKAANALETKHLPSCTCRDEPTAK

SEQ ID 841

SEQ ID 841  
ATGAATACCCCTCAAAAAGGCTTTACCCCTTATCGAGCTGATGATTGTGATCGCTATCGTCGGCATTTTGGCGGCAGTCGCCCTTCCCGCTACCAAGACTACACCGCCCGCGCAAGTTT  
CGAAGACCATCTTTTGGCGCAAGGTCAAAAATCAGCGGTATACCGGGTATTACCTGAATCAGGCATATGCGCGGAAGACAACACTTCTGCCGCGGTGGCATCCCCCTCGACATCAA  
GGCAAATATGTTCAAAGCGTTACGGTCGCAACCGCGTCGTTACCGCGGAAA

SEQ ID 842

SEQ ID 842  
MNTLQKGFTILMIVIAIVGILAAVALPAYQDYTTARAQVSEAILLAGQKRSVATGYTLNHGINPEDNTSAGVASPPPTSKANMFKAIRSQTASLPK

SEQ ID 843

SEQ ID 843  
ATGCGTTTATCTCTATATAAATGTTTTTATTTTGTATTTCCTTTAGGTGGGTGTGGTTTGCAGAGTAGGGGCGGCAGTGTGCAAAATGTTCAGTT

SEQ ID 844

MRLSLYNCFYFVPSFRWVFAEVGGGSVENCQF

SEQ ID 845

SEQ ID 845  
GTGGGAATGACGGGATTTAATGATGCCGCGGCAACGAAAAATCGAAACCAAGCACTGCCGTCAAOCTGCGCGCAAGCTTCATCTGCCGGTGCATAGAAACACCAACGGCGGATTTC  
AATGCTTTCCAAGAAAAAGGAGCTTTTAAAAAATAGAAAAATCCCAACCAACCCATTC

SEQ ID 846

SEQ ID 846  
VGGTGFNDAAAGNEKIETKHLPTSTCRDASSAGCIETPRADFKCFPRKRSFLNKRKFTPTPTLF

SEQ ID 847

SEQ ID 847

TTGTCCTTTTAAGGGTTTGCAAGCGGGCGGGCTCGTCCGTTCCGAAGCCATCCCTTTTGGCCGAAGGTCAAAAATCAGCCGTTACCCGGGTATTGCCGAATCACGGCATATGCCGGAAAAAC

TTGTCATATCCCGCAAAGCGGGAATCTAGGTCGTGTCGGCACGAAACTTATCGGG

SEQ ID 848

SEQ ID 848  
LSFKGLQGGRRPFRSHPFGRRSKLSRYVLPESRHMAGKLRHSRESGNLGLSARKLIG

SEQ ID 849

SEQ ID 849  
TTGGCCGAAGTCAAAAATCAGCCGTACCGGSTATTGCCCGAATCAGGCATATGGCCGAAACATTCGTATTCCCGCAAGCGGGAATC

SEQ ID 850

LAEGOKSAVTGYCPNHGIWPNFVIPAKAGI

SEQ ID 851

SEQ ID 851

GTGCCGACAGACCCGATTCCCGCCTGCGCGGGAAATGACGAAGCCATCCTTTTGGCCGAAGGCCAAAAATCAGCCGTTGCGCGGATATGCCCGAATCAGGCAATGGCCCGCAACAAAG  
GTGATGCCGGCGTGGCAFCCTTCGCGCGAAATCAAAGGCAAAATATGTTAAAGCGTTACGGTCGCAACGGCGTGTACCCGCGGAAATGGCTTCAAGCGCGCTAAACAAAGAAATCAAAG  
CAAAAGACTCTCCTCTGTGGGCCAGGCGTCAAGACGGTTTCGTTAAATGGTTCTTCGCGACGCGCGGTTACCGCGCAACGACGCGCGCGACACGACGACGTCGCGCAAGACGACGCGCGCGG  
CGCGCGTGGCAACCAAGCACTCTGCTCAACCTGCCGCGATGAACCAACTGCCACC

SEQ ID 852

SEQ ID 852  
VPTDPSRLRGND EAILLAGCGKSAVAGYCPNHGKWPANNGDAGVASSAEIRKGKVKSVTVVANGVVTAEKASSGVNKEIKGKRLSLNARRQDGSVKWFCGQPVTRNDADNDQVAKDDAAG  
NAIETKHLPSCTDEPTAT

SEQ ID 853

SEQ ID #53

ATGAACTGTCCGAACGTGTCAACCCCAACGAATTTGCCGCGCGGCATTGTAGTTTCGGCGACGAAGCGCGGTGTGCTTGCCTGTGTCGGCGAGAAGACGATGGACGAATTTGTTCGGCAACA  
CCTTGGCCGAAGACATCCGATGCCGTCCGAACCTGATTTCGCCGAAGCCCTGACCGAGCGGACGATTTGGCAAAATTTGAAAGGCATCCGCTCTAAAACAGTGATCAACAAGTCTATAT  
CGGTTTGGGTATTATCCCGACCCGCTGCGCGCAACGTGATTTTGGCACAACCTTTGTGAAACCCCGGGCTGGTACACCGCTTACACCGCTATCAGCGCGAGATTGCCCAAGTGGTGTGGAA  
GCGTGTGTGAACCTCCAGCAGGTGTGCATGATTTCGACCGGTTCACCGTTCCTGTGGCAGCGCGCTCTTTGTGTGACGAAGCGACCGCGCCGCGCAAGCGATGGCGATGGCGCACCGCGTGGGCA  
AAGTGAATTCGACGCTTTCTTGTGGATGGCGCGCTGTATCCGCAAACTTTGGACGTGATGAAAAACCGCGCCAAATATTTTCGCTTCGAGCTGTGTGGTTCAGCGATTTTGTGCCAACCGCA  
TGAAGCGCAATATCTCGGCGCGCTGTTCCAATACGTCCGTAAGACGCGGACGTGCAAGACTTGCAGGACGTTATCGGCGCTGTAAAGCCAAAGGACAATCTGGCTGTGCTGTGCTGTCGCGGAC  
ATCATGAGCTTGGTTTGTCTGAAGTCTCCGCGTGAAATGGCGCGGATATGCTTTGGGCAACACCCAACTTTTCGGCGTACCGATGGGCTTGGCTTGTGCTTCCGCGCGCTTATTTGGGT  
TTAAGACGAGATTCAACGCTCCGCGCGCGCGCATCATCGGCGTATCAAGAACGCACTCGGCGCAACCTTGCCTTGGCATGGCTTGTGTCCACCGCGCAACACACATCCGCGCGA  
AGCGACATCTCAATATTTGTACCGCAGCGCATTCGTGGCGAATTTGGCGGCATGTGCGGCGTATATACGCGCCCAAGGCGTAAACGCGATCGCCAACCGCAATTCACACTGGCTTC  
GTCTTTGCCGACCGCTGGTTTTCAGACGCGCTCAAGCTGGCTTCAGAGTCTTCTTCGATACCGTTACCGTGCATTTCCGCGACCAAGAGAAGACGACCAAGTGTTCGCGCTGCTTTGG  
AATTCGGGTATCAACCTCGCGCAGCGCTCAACATACTCAAGTTGCGGTGCATTCATGAACGTCGGTATACGAAGATTTCGCGGATTGTACCGCGGTTTACCGGCAAGGATACGTTTAC  
CTCGAGACCGCGCATTTGGCTATGAACCGCGCATGATTTCCGCTCGGAGCTGCACCATGAAGCTCAATGCGCATTCGCGAAATTTTCGGCATTTGCTTCCAGCCCAACTCCGGCGCACAG  
CTTACGCTCCCGAAGCGCAACCGCGGCTACCGGCAATTTGCTTGTGATATGAAACACAGCTGAAAGCCATCACCGGCTTGAAGCGGATTTCTTCCAGCCCAACTCCGGCGCACAG  
CGAATACAGCGGTATGCTGCCATCCGCGTTATCAGGAAGCCCAAGCGAAGCACACGCAACATCTGCTGATTCGCCAAATCCGCCACGCGCACCAACCCGCCACCGCGCATGCTC  
GGTTTGAAGTGTGTCGTGTCGATACCGGACGACGACGCGCAAGCTCAATATTGACGATTGAAAGCCAAAGCGCAACACACCGGATGCTTGTGCGCATCATGATTACCTATCTCGTCCA  
CACACGCTTTCGAAAGAAGCGATCCGCGACATCTCGCGGATCATTCACGAAAACGGCGGACAGGTTTACATGGACGGCGCAAACTCAATGCCAAATCGGCATCATGACCGCGCGCA  
AGCTCGGCGGCGAGCTGTGTGCATGAACCTGCACAAAACCTTGTGATCCCTCAGCGCGCGCGCGCGCGGATGGTCCGATTGGCTTGAAGGCCAATCTCGCGCGCTTTCGCGCGG  
CATACCTGACCGACACCCACGCGCAAGTCCGCGGCAAACTTCGTTGCCGCGGACGCTTCGGTTCGATCCATCTTCGCGATTTACTTGGATGACCTGACATGATGGGCAACAG

GCATGGAACAGGCAACACGCTGGGCACTGCTCAACGCCAACTATGTCGCTAAACGCTTGAGCGAAGACTATCCGATTCTGTATACAGGCAAAACGCCCGCATCGCGCACGAATGCATCGT  
CGATTTCGCTCGCTCAAGCGCGAAAGCGGCATACCGGAAACCGCATCGCCAAACCGCTGATGGACTACCGCTTCCAGCGCGCGACGGTTTCTTCCCTGTTGCGCGCACGCTGATGATC  
GAACCGACCGAGAGCGAAAGCGAAAGCGGAACCTGACCGCTTTCATCGCGCGCTGAAATCCATTCCGCGCGAAGTGCAGAAAGTCATCGACGCGGAATGGCGGAAAGACGACAAACCCACTGG  
TCAACGCGCGCGACACCGCGCGAGATATAACGCGGAATGGCGCATCCGTACTCTCGCGAAGAACCGCTTCCCGCTGCCCTTCTGCGCGAACACAAGTTCGCGCCCTTCGTCACCG  
CGTGGACGACGTGTACGCGGACCGCAACCTCGTGTGACGCTGCCCGCATGGAATAATTATGAAGAC

## SEQ ID 854

MKISELPNPNPAAHRLSPGDEAALLAAVGEKSMDEFVGNLTPQSIRMPSELDPALTEADALAKLKGIAKSNVINKSYIGLYPTTRVPNVILENVLENPGWYATTPYQAEIAOGRLE  
ALLNFQVQCIDLTFPVAGASLLDEATAAAEAMAMAHVRGVKVSERFPVDARVYPQTLDMKTRAKYFGFELVVSDFQAQDEGEYFGALFYVVGKDGVDQLQDVIIGRLKAKGTIVAAAD  
IMSLVLKSPAELEGADIALGWTQRFVPMGPGSPHAAYFAFKDEFKRSAPGRIIGVSKDASGKPALRMALSTRQHIRREKATSNICTAQALLANLAGNYAVYHGPVKRIANRIHTLAS  
VFADALVSDGLKVVHVFDTVTVDGSKKADQVFAALESYGNLRSVNNQVAAAPHETSVYEDLADLYRAFTGKDTFTFADDVKGRINAELRLQDDILQHPVYNSYHTHEMLRYLKK  
LEDRLAMNRSIMSLGCTMKLNATAEMLPITWTFESDIHPYAFEAQTAGYRELLADMENSLKAITGPDALSFQPNLSGAQGEYSGLMAIRRYQEAQGEHRNITCLIPKSAHGTNPATAHL  
GLKVVVDPEDEHGNVNDIDLKAKAQHRDALSAIMITYPSTHGVEEGIRDICRIHENGQVYNDGANLNAQIGIMQPAFVGADVLHMLHKTFCIPHGGGGPGMGPIGLKAHLAPFARG  
ETLTDTHSASAGQTSVAAAAPGSASILPITWMLTMMGKQMBQATRWALLNANYAKRLSEDPILYTGKNGRIAEHCIVDLRLKASGISTETDLAKRLMDYGFHAPTVPFVAGTLHI  
EPTSESKAELDRFLAALXISIRREVQKVIDGENPKDNLPLVNAPHTAADITGEWHPYSRREAVPLPLFVREHKFWPFVNRVDDVYGDRLNLCSCPHENYED

## SEQ ID 855

GGGACGCAATATATAAGGAGTGAGTACCTGTTCTCTTATTAAGAATTAATCTTTTGAGGCATTTCTGTTGAAGTTTATTAACACATCTTCAGAAATCCAACTGCTTTATATCTCT  
TCCCTAACCCGTTTTTATTTCTTCCCAAGCTCGGGCTGTTGTTGTATAAATCCTGTAAATGCTTTTAACTGCCTGCTTTAAATCAGTTCGGTAATATCTGTAAATATATCTTAA  
CAACAGGCATATATACGACGGCGAGGATGCGCTATTTAGTGTATTTACCCGTAATATTGATTTCGCATACAGGCTTCAGATGATTTTATGTCGGTTTACCGCTGGAGAAATATGGAA  
AACACCGTTTGCGCGCTGTCTGAAAATGAAAATCGCGAGTATCGCCACATTTGTAGGACGAGTATCCGAACCGCGCTGATAACTGAAAGCACCAGCAATCAAAAGACAC

## SEQ ID 856

GTQYIRSEYLYFFYRINLLRHFLKFKIKHIFRNSKLLYYLFPMPFFIFFPSLGSFV\*IL\*LLFNCLL\*ISSVIIICNIFLNRHIDGKDAIVVFRNIDFVIQGF\*FLIGFTAGRIHE  
NFTVRLV\*K\*KIGSIANICRTSIRTGLITESTEAIRKH

## SEQ ID 857

AACGGTTGCGCGAATATATTGTGTAACCGTGCAATTGCATATCGTAAATAAACGTAAATAAAAATAACAATATAAATCAGCATGTTGCAACTTTGTTTTTATTTTGTGTTGACGGGCAA  
CATATCAT

## SEQ ID 858

NGCANIFV\*PCICIS\*INVKNNNINQHVAFLFFILC\*RAYTH

## SEQ ID 859

TTGACGCAAAATATCTTATCTTTGTCGCGTGACAGTGGGCGAGGTTGGCGGTCATTTTCTTATCTCTGAAAGTGTTTAAAAACGG

## SEQ ID 860

LQNLFILCRADGAGLGHFSLPLKVFKKR

## SEQ ID 861

GTGCTTCATCACCTTAGGGAATCGTTCCCTTTGAGCGGGGGCGGCAACGCCGTACCGGTTTTTGTTAATCCGCCATATCGTCAAGATGCGGTTTGTGTTGCAACCCCTTAAAGGAA  
AAACCATGAAAAAATGTTGTATTGTTCTGTATGCTGTCTCTCGCGCTTCTCTTTCGCGCGGTAAACATCAATCGCGCTTCGACAGGAGCTGGAGCGCTGCGGGCATAGGCC  
GGCGAAGCGCAAGGCATTCGCGAATACCGCGCGCAAAACGGCGCTTCAAGTCTGTGGACGATTGATCAAGGTGAAGGCGATCGGTCCGGCGTGTGCGGAAGCTGAAAGACAGGCT  
TCCGTCGCGCGCGCCACCAAAAGGCCCGGCCAAACCGGTGCTGCGGTAAAAAA

## SEQ ID 862

VLRHRESFPLSRGGATPYRFLIRHIVARCGLLPATLKGRTNKKMFVLFCLMFLSCAFSLAAVNINAASQLEALPGIGPAKAKIAEYRAQNGAFKSVDDLIKVGIGPAVLAKLDQA  
SVGAPAPKPAKPVLPAYKR

## SEQ ID 863

GTGGAACCGATACATTGGCAAACTATTGAAAAACATAGCCTGTTTTTCCGGTTTTATCGTATTATTCGAAACTTACCCCATGATAAGGAAGCGGTTTATGCTGCAAGAACTTTGG  
CGAANTCCATCGCGCTTACCGAGTCCGGCTGCATTCGGGCGAAGCGCTCGCGCTGACCTCGCACCCCGCGCTGAAACAGCGGATTTCCTTCGCGCGCACCGATTGGACGGCGAGAT  
GGCGGAACAAATCAAGCTGAACCTTATTGTATCAACGATACCGCGCTTATCCACCATCGTTACCGACAAGGCTGCGCGTCCGGCACCATCGAACACATCATGTCCGCACTGTCCGCC  
TACGGCATCGACATCCGCTGATTGAGTTGAACGCGCCGCAATCCCGATTATGACGCGCTCCAGCTGCGCTTTATTACCTCTGCAAGATCGCGGCTTGTAGACCAAAAGGCGCAAA  
AGCGTTTTTTGAAAACTCAACCCGCTGAAATCAAAGAAGCGGCAATGGGTCCGATTATACCGCTATGACGTTTTAAGGTAACGCTGACCATCGAATTCGACCATCTGTTTTCAA  
CCGACGCGCGCTTACGTTTGAATTGATTTCGCGCGCAATCTTACATCGCGCAATTCGCGCGCGCGCGCATTTTCGCTTTATGACAGAAAGTGAATGATGCGCGCCCAATCTCGGC  
TTAGCGCGCAATTTGAACAACGCCATCTGTGATGGCGACACGGATGTCTGAAATCTGAAGGCTTGCCTATCCGATGAGTTTGTGCGCCACAAAATCTCGACGCCATCGCGGATTGT  
ATATCGTCGGACATCCGATTGTGCGCGGTTTGAAGGCTACAAATCGGACACCGCTTCAACACGCCCTTTTTCGCGCAGTTTTCGAGACGAAACGGCTTACGAATGGGTGGAATTTGC  
CGACAGCGATGATTTCGCGGACGCAATTCACGAGCTGAACATCAGAAATTCGCGA

## SEQ ID 864

VETDTLANITIEKHSLEFRFYRIIPKLPPLIRKRFMLQRTLAKSIGVPGVGLHSGERVALTLHPAPENSIGISPRFTDLGEGEIQIKLNPYLINDTRLSSFTIVTDKGLRVOTIEHIMSALSA  
YGINALIELNAPEIPIMDGSSLPFIYLLQDAGVVDQKAQKRFLKILKPVKEAGKWVRFPTFDGFKVLTLEFDFHVPFNRSPPTFEIDFAGKSYIGELIARARTPGFMHEVEMMRAHNLG  
LGGNLNNAIVIGDITVLNPEGLRYPDEFVRHKILDALIGDLYIVGHPIVGAFFGYKSGHAVNNALLRAVLADETAYEWVEPADSDDLDPAFHELMIRNG

## SEQ ID 865

GTGCGGAACTTATCGGGAAGAAAGGTTCTTGAGATTTTACGTCCTCGATTCCCGCTTTCGCGGGAATGACGGGATGTATAGTGAATTAATTTAAACCAGTACGGCGTTGCCCTCGCCTT  
GCCGTACTGTCCGCGCTTCGCGCTTGTCC

## SEQ ID 866

VRKLIKKRGLRFPVLDSPRGNDGMYSELNINQYGVASPCRTVRGPAALS

## SEQ ID 867

TTGCGCTTCAAGGCCCTGCATGTCCTCATTTGCCACCGTTTAAACACGGTTTTATCTGACAGCGCGCAACCCGCCCTTCATTTGCCGAACAGCGGTCGGACTCCCGCCCGCGCGG  
GAATC

## SEQ ID 868

LRPKALHVPHPKFKHGYLITGAQPAFPAFQAVRTPARAGI

## SEQ ID 869

ATGACGGGCTTTGAAGCGCAATCGATATATTATTTCCACCGGAACGGACGACCCCGCGCGCTTGCAAAACCTTAAAGACAAGCCCGCGCGGTTGATCCGGGCGCGCTGGGAATCACT  
TACCGCTGATTATTAAAAAT

## SEQ ID 870

NQGLEAQSIYYFHRNGRPRPPCKPLKDKPGLIRAAVGNHPLDLFTKI

## SEQ ID 871

GTGGCATCCGCTTCAACAATCAAAGGCAAAATATGTTTCAGAAAGTTGAAGTCGAAAAGCGTCGTTACCGCCCAATGGCTTCAACCGCGGTAAACAAAGAAATCCAAGACAAAACCTCT  
CCCTGTGGGCCAAGCGTCAAGACGGTTTCGGTAAATGGTTCTCGGACAGCGGTTACGCGCACCGGCCACAACGACGACACCGTTGCCGACGCCAACGCCATCGACACCAAGCACCT  
GCGTCAACCTGCCGCGATAAACATGATGCCAAA

## SEQ ID 872

VASASTIKGYVQKVEVAKGVVTAQMASTGVNKEIQDKKLSLWAKRQDGSVKWFCGQPVTRTGDNDTVDADANNAIDTKHLPSTCRDKHDAK

## SEQ ID 873

TTGGCCGAAGGTCAAATAACAGCGTTACCGAGTATTACCTGAATCACGGCATATGGCCGAAAACAACGACAAGGCCGCGTGGCATCTTCTTCATCAATCAAAGGCAAAATATGTTAAGG  
AAGTTAAAGTCGAAAACGGCGTCTGTCACCGCCCAATGAATCAAGCAACGTAAACAAAGAAATCAAAGACAAAGACTCTCCCTGTGGGCCAAGCGTGAAAACGGTTCCGTTAAATGGTT  
CTCGGACAGCGGTTAAGCGCGCCAAACGTTGCCGCGCCAAACGACGACGAGCTTACCGACGACAAAACAACACGGCATCGACACCAAGCACCTGCCGTCAACCTGCCGCGATAAATCA  
TCTGCGGTTTGCACGAAACACCGCGCGGATTTCAAACACTTCCAAAATACAGCGGTTACCGAGTATTGCCCGAATCACGGCGAATGGCCGAAAGACAAACGACAAGGCCGCGTGGCAT  
CCCCCCCCCTCAACATCAAAGGCAAAATATGTTGAAGCGTTACCGTCAACAACGGCGTCTGTTACCGCCACAATGCTTTCAAGCGCGGTAAACAAATGAAATCAAAGGCAAAAACCTCTCCCT  
GTGGGCCAAGCGTCAAGCGGTTCCGTTAAATGGTTCTCGGACAGCGGTTACGCGCCAAAGCCGACGACGCGTACCGCCGACGCCAACACGCCATCGACACCAAGCACCTGCCG  
TCAACCTGCCGTGATACGTCATCTGCCAAA

## SEQ ID 874

LAEGQKSAVTETYLNHGIWPNNDKAGVASSSSIKGYVKEVKEVGVVTTATMSSNVNKEIKDKRLSLWAKRENGSVKWFQGPVKRANVAAANDDDVTDKNNNGIDTKHLPSTCRDKS  
SAVCTKHAPIISMTSKSAVTEYCPNHEGWPKNNDKAGVASPPSNIKGYVESVTVNGVVATMLSSGVNNEIKKRLSLWAKRQAGSVKWFQGPVQRAKADDAVADANNAIDTKHLP  
STCRDTSSAK

## SEQ ID 875

TTGCTGCTTTCAGTGTGATGAGAAATTTCTCTTGTCAAGTGTAAAGTTATAATGATTATATACTATATACACTACATCGCAATGAAAAATCGGAAAAACAAAAACCCCTCCGCG  
TCATTCGCGGAAAGCGGGAATC

## SEQ ID 876

LLAPSVMRNFFLSSVVKIMLIYYITLHRNEKSKTKNPSAVIPAKAGI

## SEQ ID 877

TTGACCTTCGCGCAAAAGGATGGCTTCGTCAATTCGCGCAGCGCGGAATCCGGGTCTGTGCTACGGAACCTTATCGGGTAAACCGGTTCTTTAGATTTTGGCTTCCGGATTCCCACTT  
TCGCGGAATGACGGGATTAAGTTTCAAAATTTATTC

## SEQ ID 878

LTFQKDGFIPIPAQAGIIVCRYGNLSGKTVSLDFAFRIPTFAGMTGLKQMLP

## SEQ ID 879

TTGTGGGAATCTGTGGGAATGATGAAATTTTGAGTTTATAGGAATTTATCGGGAGCAACAGAAACCGCTCCGCGCTCATTTCCGCGCAGGCGGGAATCCCGACCGATCGGCGCAGAAACTT  
ATCGGGTAAACCGGTTCTT

## SEQ ID 880

LWESCGNDELLSFRNLGATETAPPSFPRRESRPIGAETTRVKRFL

## SEQ ID 881

ATGAATCATCGTTGCCGGGTATTGCCCTGAATCAGCGCAATGGCCGGAAGACAACACTTCTGCCGCGTGGCATCCCCCACCAGCATCAAAGGCAAAATATGTTAAAGCGTTACGGTGC  
CAAAAGCGCTCGTACCAGCGGAAATGGCTTCAACCGCGCTAAACATGAAATCAAAGGCAAAAACCTCTCCCTGTGGGCCAAGCGTCAAGACGGTTCCGTTAAATGGTTCTGCGGACAGCC  
GGTTAAGCGCGCGCAACAACCGCAACATTACCGCGCAACCGGCAACCGCATCGAAACCAAGCACTGCCGTCAACCTGCCGCGATGAATCATCTGCCGTTTGCATAGAAACACCACTT  
ACGGCTTTCTATAAAAAATACCCAAACCGTTCATCCACGAAAGCGGGAATCCAGAACGCAAAATCTAAAGAAACCGTTTACCCGATAAGTTTCTGCGCGATCGGTGGGGATTCCCGCT  
GCGCGGAATGACGCGGAGCGGTTTCTGTGCTCCCGATAAATTC

## SEQ ID 882

MNHRCLVLPESRRMAGRQHFCRRGIPTDIIKGYVKSVTVAAGVVTAEMASTGVNNEIKKRLSLWAKRQDGSVKWFCGQPVKRADNNGNITADNGNAIETKHLPSSTCRDESSAVCIETFP  
TAPYKMTQVIPTKAGIQNAKSKETVLPDKFLRRSVGIPACAGMTAERFLPLLPINS

## SEQ ID 883

GTGATTACAGGCAATACCGGCAACGATGATTATCGCGGCGAGTTGACGGCAGGTGCTTGGTGTGATTTTGGTCCGCGGTGTCTCTTTGGCGACGTCGTGGTCCGCGCTTTGGCGT  
TGGCTTCGTTGCGTTAAACCGGCTGTCGCGCAGAACCTTTTACCGAACCGTTTTCACGCTTGGCCACAGGAGAGTTTTCCTGCTTGGATTTCTTTGTTTACGCGGTTGAAGCATTTTC  
GCGGTAACGACGCTTTTTCGACCGGTAAACGCTTTTAAACATATTGCTTTGATGTCGGAGGCGGATGCCACGCGGCTTGTCTGTGTTTCCGCGCATTCGCG

## SEQ ID 884

VIQAIIPGNDSSRQVDRCLVSLVPAVSSLATSSVPALALASVRLTGPCQNEHTEPFSRLAHRESFLFWISLFTFVZASVTTPTATVTLTYLPLNSEADATPALSLSFCHSP

## SEQ ID 885

GTGGCATCCGCTCCGACATCAAAGGCAAAATATGTTAAAGCGTTACGGTGC AAAAGGCGTCTTACCGCCGAAATGGCTTCAACCGCGGTAAACAAAGAAATCCAGGCAAAAACCTCT  
CCCTGTGGGCCAAGCGTGAAAACGGTTCCGTTAAATGGTTCTGCGGACAGCGGTTAAGCGCACCGAAGCAACGCCAAGCGCGCACCGACGACGTGCCAAAGACGACACCGCGGCAC  
CAAAATCGACACCAAGCACCTGCCGTCAACCTGCCGCGATGAATCATCTGTTGCCGGTATTGCC

## SEQ ID 886

VASASDIKGYVKSVTVAAGVVTAEMASTGVNKEIQGKRLSLWAKRENGSVKWFQGPVKRTEANAKAGTDDVAKDDTAGTKIDTKHLPSTCRDESSLGIA

## SEQ ID 887

TTGGCCGAAGGTCAAATAACAGCGTTACCGGGTATTGCCGGAATCACGGCATATGGCCGAAAACAACACTTCTGCCGCGTGGCATCTCCGCGCGGACATCAAAGGCAAAATATGTTT  
AGAAAGTTGAAGTCAACACCGCGTCTTACCGCCACAATGGCTTCAAGCAACGTAAACAAAGAAATCCAGGCAAAAGACTCTCCCTGTGGGCCAAGCGTGAAAACGGTTCCGTTAAATG  
GTTCTGCGGACAGCGGTTACGCGCGACGACAAGGCCAAGACGCGTCAAGCGGACGCGCACCAGCCGCAAAAATCGACACCAAGCACTGCCGTCAACCTGCCGCGATGAATCATCT  
TTGCCGGTATTACC

## SEQ ID 888

LAEGQKSAVTGTCYCPNHGIWPKDVTAGVASSAADIKGYVQKVEVNGVVTTATMASSNVNKEIQKRLSLWAKRENGSVKWFQGPVTRDDKADKDVADGTAGTKIDTKHLPSTCRDESS  
LPGIT

## SEQ ID 889

ATGCCGACGCTCTTTATAGCGGATTAAACAAAATCAGGACAAGCGCGGAAGTCAATTGCGGTATTGCGATCATAGCGCGAAAAATCCGGCTCCGTATTCCCGGAAAGCGGGAATCC  
GGAACGCAAAATCTAAAGAAACCGTTTCCCGATAAGTTTCCGTGCCGACAGACCCGATTCCCGCTGCCGCGGAA

## SEQ ID 890

MPDGLYSLTKIIRTRRRSHCGIRIIIGKNPASVIPAKAGIRNAKSKETVFPISFRADRPGFPPARE

## SEQ ID 891

GTGGTAAATCTTTGGCGCTTTGGCCAAACATAATCGAAGCCGAACAGTATTTTCGGCAGACATCTGAACGGCGCGCTCAATGGCCGATTCTTTCAATCATGCCCGATTACCTTGAATGG  
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AGCCCGCACCCCAACAGCAGCATTTCCAAAGGGCTGGGCGCGCTTGGCGCGCTTCTGCCCGGATCCCTCCATAAGCAGCTGTGCCGCTTCCGCGGTGCCGCAAAACACAT  
TCCGTCTATCCATT

## SEQ ID 892

VENLCRFADENRSRTVPFGRHLNGALNGRFPQIMPDIYLEDVDFGKHARRIVRPFRRNRRTAVSHPLTLFFGNHYHIDARTARHPQQQHPQAGPALGRAFCRRSLHNDVPAFRFRDRTX  
SVYTF

## SEQ ID 893

TCCGCTGATTTTATCAGCTTTCCCAAGCGTTTGCTGTACAATACCGCTTTTCGGAAGGCTGTGGCGATGATGTTTTCTTGTTCAA

## SEQ ID 894

SA\*FYHVSQAVCLYNTAFRKGVDVFLVQ

## SEQ ID 895

TTGTACGGCAGCCCGCTTTGCCATGCGCCCAACAGATGCGGATGGCGCGCAAAAAAGACCGCGCTTACAAAGGACAAGACCGGCCAAAGTAACGCAATATTTGACACGGCGCGCG  
GATTTTCCGATGCCCAACGCGTTTGTCCGGATGAACAGGATTCGACCGCGCGCTGTTCCGCGCTTATGCCCGCAGCTGAAAGGGCAATGGCGAAGCGCGGATAAGTGGGAAAGATA  
CCGCGCTTATCTTTGGTGTCCGACACGCGCAACCGCGGATGCTCCGCTGCTTTGTCAAAATACGGTGGCGCGGCTTTTTTTGAAGCGCGTTTCAGCAATGCTTACTGCCGCA  
TTGGCTCAAAATCGGTGATTATTTTCAGATAATGCGCGATTTCGCGTATGGGTGCTTACGGGGAACGGCGGAAAAATTTGGACATAAGTATTGCTCCCGCCTTATTCACCCGAGC  
CCAAACCGGATTGAGAAAGTGTGGCGAATATTAAAGCGTATCTGCGAACCGTTTGTCTGATTACGCCCGATTGACGATGCACTACTGCTTATTTGATTTAAT

## SEQ ID 896

LYGSRRLPCAQTDADGAKKTAAYKQDPKAVTHYLTRPAGFSDCQRVCDETFDRRLFRFYARSLKQGMARISGKRYRRLSLVSAQADNRPIAPVVCQNTVAGVFFEARFQCLLEA  
LAQKSVIISDNARFRMGALRGTAELGHKVLPPAPYSPEPNIEKVMANIKRYLRTVLSYARFDALLSYDFM

## SEQ ID 897

TTGTTCCGCAAAATGGGGGGCGGATGTGCGCCTGTAGATAAAACCGTGTTTAAACGGGTGGCAATGAGGTACATGACGGCGCTTGAAGCGCAATCGATATATTTATTTCCACCGGAAC  
GACGACCCCGCGCGCTTGCAAAACCTTAAAGACAAGCCCGCGGTTGATCGGGCGCGCGTGGGAAATCACTTACCGCTTGATTTATTTAAAT

## SEQ ID 898

LFGKGGGLRAQIKTVFKRVAMRYMGLAQSIYTPHNGRPPPCFLKDKPPGLIRAAVGNHPLDLFLKI

## SEQ ID 899

GTGGCATCCCCCGCCACAAAAATCAAGGCAAAATATGTTTCAGAAAGTGAAGTCGCAAAAGCGCTGCTTACCGCGCAATGAACCAAGCGCGTAAACAAAGAAATCAAGGCAAAAAAC  
TCTCCCTGTGGCGCAAGCGTGAAGACGCTTCGGTAAATGCTTCGCGACAGCGGTAAAGCGCAGCGCGGCCAAAGCGCAGCAGCTCAAGCCGACGCGCCCAACGCCATCGAAAC  
CAAGCACTGCCGTCAACCTGCCGCGATGAATCATCTGCCAC

## SEQ ID 900

VASPADKIKGKYVQKVEVAGVVTAEMKPSGVNKEIKKKLSLWAKREDSVWFQCGQPVKRDAGAKADVDVKAANALETKHLPSCTCRDESSAT

## SEQ ID 901

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CAAAAAATCAGCGCTTACCGGTTATGCGGAATCAGCGCAATGCGCGAAGACAACTTCTGCCCGCGTGGCATCCCCCGGCAATCAAGGCAAAATATGTTAAAGCGTTACGGTC  
GCAAAAGCGCTGCTTACCGCGCAAGTGAATCAAGCGCGTAAACAAATGAATCAAGGCAAAAACTCTCCCTGTGGCGCAAGCGTGAAGCGGTTGCGTAAATGCTTCTCGGACAGC  
CGGTACCGCAACGACGCCAAAGCGCAGCGCAAGACGACACCGTCACGCCATCGAAACCAAGCACTTCCGCTCAACCTGCCGCGATGAATCATCTGCCGTTGCTATAAAAACACCG  
CGCGATTTCAAACTTCAAAAAATCAGCGTTGCCGGTATGCCGAATCAGGCACATGGCGGAAAGACAACGG

## SEQ ID 902

HLSSGVNNEIKKKLSLWAKREDSVWFQCGQPVTRAKADADAGKDTNIDTKHLPSCTCRDESSAVCTKHAPISENTSKSAVTGYCPNHGKWPKNDSAGVASPAEIKGKYVKSIV  
ARGVTAQMPNSGVNNEIKKKLSLWAKREDSVWFQCGQPVTRAKADADAGKDTNIDTKHLPSCTCRDESSAGCIKTPRADPKHFQKISRCRVLPESRHAERQR

## SEQ ID 903

TTGAATAAATACATTTGACCGCGCGTAGGTTCGCCGCGGAATATTAACACCGCCCAAAAAATCAGCGTTGCCGGTATGCCGGAATCAGGCAATGGCGGAAACAACA  
CTTCTGCCGCGTGGCATCCCCCTCCGACATCAAGGCAATATGT

## SEQ ID 904

LNKIHHLGRLGLPAGILKHPKKSAGVAGYCPNHGKWPENNTSAGVASPPLRHQRQIC

## SEQ ID 905

TTGGCGGTGTTTAAATATTCGGCGGGCAACCTAACCGCGCTGCAAAATGATTTTATTTCAATAATCCCGCTTTCATGCAACAGCAAGCAAGCGG

## SEQ ID 906

LGGVLIFFRANLIGRANVFYSIIPAPMYTRASG

## SEQ ID 907

ATGAATCATGTTGCCGGGTATTCCTGAATCAGCGGAATGGCGGAAGACAACACTTCTGCCGCGTGGCATCCCCCACCGACATCAAGGCAAAATATGTTAAAGCGTTACGGTCG  
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GTTAAGCGCGACCGCGCGGCAAAACCGCGCGGACGCTCAAGCGCGCGCAAGACACCGGCAAAATCAACACCAAGCACTGCCGTCACCTGCCGCGGATAAATCATCTGCCGCT  
TGCAGCAACACCGCGCGGATTTCAACACTTCAAAAAATCAGCGTTGCCGGTATGCCGGAATCAGGCACATGGCGGAAACTTCTGTCATTCGCGGAAAGCGGGAATCCAGG  
TCTGTGCGCACGAAACTTATCGGTAAAAAGTTTCTCCGCTCTGAGTCTTGATTTCCACTTCTGTTGGAA

## SEQ ID 908

MNRCRVLPESRHMAGRQHPFRRIPTDILGKYVKSIVTAKGVVTAEMASGVNNEIKKKLSLWAKRQDSVWFQCGQPVKRDAGAKTGADVDKADGKDTDKINTKHLPSCTCRDKSSAV  
CTKHAHPISENTSKSAVAGYCPNHGKWPKNFVPAKAGIQVCRHGLSGKKVSPVLSFGPPLSW

## SEQ ID 909

TTGGCGGAGGTCAAAATCAGCGTTACCGGATTTACCTGAATCAOGGCAATGGCCCAAGACAACGGCTCTGCCGCGTGGCATCCGCTTCAAAAAATCAPAGGCAAAATATGTTAAGG  
AAGTTAAGTGAAGACCGCGTGTACCGCCCAATGGCTTCAAGCAACGTAAACAAAGAAATCAAGACAAAAACTCTCCCTGTGGCGCAAGCGTGAAGACGGTTTCGGTAAATGTT  
CTCGGACAGCGGTAAAGCGCACCGCAAGCCAAAGCGCGGACCGACGCTGCCAAAGACGACACCGCGGCAAAAAATCGACACCAAGCACTGCCGTCACCTGCCGCGAT  
GAATCATGTTGCCGGTATTCGCT

## SEQ ID 910

LAEQKSAVTEYYLHGEWPKDNGSAGVASASKIIGKYVKEVKVGVVTAQMASSNVNKEIKKKLSLWAKREDSVWFQCGQPVKRTANAKAGTDDVADKDTAGTKIDTKHLPSCTCRD  
ESSLPGLA

**SEQ ID 911**

TCCCCTGCATCCGGCGCGCTGATGTAGTCGGCAATCAAAATCCCGCTTTTCCCAAAAAAATCTCTGCATTTTGTTCGGAATACAGTTTGGCGACCAGAGTGGGCAGACCGCTGTGGACGATG  
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 TTTTGCTCCGTTTTCGCGTAAGGATTATTCGATTTGTATTATCCGCTGATTTTATCAAGTTTCCCAAGCGGTTGCTCTGACATAACGCTTTTCGGAAGGGTGTGGCGATGATGTTT  
 TCTTGGTTCAAGCTGTTTCAC

**SEQ ID 912**

SLHFPADVVGNIPLFPFKLLHFLPGIQFADQSGQTAVDDGGDFVFAVFFLHCRCLKIQTPAPQICCKAVADV\*IEFDGFENFASVLR\*GFIRFVYPPDFITPPKRFACITPLFGRVWAMMF  
SWFKLPH

**SEQ ID 913**

ATGCAAGCGGTTTTTAACGCTATTTTTCGGGAATGACACCATGCGAGTTACATCAAAATGGATAGACGGAATGTGTTTGTGCGGCACGGCGGAAGCGGGCAGCGTCGTTATGGAGGGAT  
CGGCGGCAGAAAGCGCGGCCAAGCGCGGGCCAGCCCTTTGGAAATGCTGCTGTTGGGGGTGCGGGCTGTTCGAGCATCGATGTGTTAATGATGTGCCGAAAAACAGCGTCAGAAAGTGAC  
TGACTGCCGTGCGACGGTTACGGCGAAACGGGCGGACGATGCGCCGCGCTGTTTACCGAAATCCATCCATTTCAAGGTAATCGGGCATGATTTGAAAGAAATCGGCCATTGAGCGCGCC  
GTTCAGATGCTGCCGAAAAATACTGTTCGGCTTCGATTATGTTGGGCAAGCGGCAAGATTACCCACAGTTTGGAAATGCCCGGGCGGAGAAA

**SEQ ID 914**

MQSGFNALPGNDTMTVTSKNWIDMGFCVGTAEGGHSVVMEGSSAABGAAKRGPSPLEMLLLGVAGCSSIDVVMIAERQKQKVTDICRATVTAKRADDAPEVVFTEIIRHFVILGHLKESAIERA  
VMSAEKYCSASTMLGKAAKITHSPETIAGAER

SEQ ID 915

ATGACGCTCCCTGATTACACACCCCTTTTCAGACGGCATAGAACTGACCGTCGAAATCAACCGCGCTGCCAAGAAAAACCTGATATATCCGCCCTATCGGCACACATACCGTCCGCATCAGCGTCC  
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GTTTCCACGGCAGGCAGCTTGCCTTACCGCCCATCAAGACACGCAATCTCTGCTGATGCCCTCTGAAATCCCGCTCCCCGAAGCGCGCCCGGAAAACAGCTTGGCTGCTGCGGGAGCTTT  
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AAACACAGGCAGCTCCCTCAACCGCGCGCTTGTTCGGCGCACCGCAATACGTTCTGGCGACTATGTCTGCATACAGCACTCTGCCACTCTGCCCATGCCCAATCCCGACCAAGCCCCGCTTTTGGGA  
ACTGACCTCCGCGCTTGCCTTACACGCCCGAAGCAAAACAGCGGATCAAAATCCACGGCAGGAGCTTTTTCGCCCTTGGGC

**SEQ ID 916**

SEQ ID NO: 1  
 LPTLHPTLSDGIELTVEINRRKKNLLIRPITGHTVRLSVPPCFVSALNRWLYENEAVLRRTLAKTPPHNTANRLPEHTVFWHGRLALTAHQDTQILLMPSEIETVEPEGAPEKQALLRDF  
 LPROAHSVLIPRIERHARATOLFPASSSLTSAKTFMGVCRKTTGIRLNRRLVGAEPTVADYVCITHELCHLHPDHSAPFWELTRRFAPYTFEAKQRIKINGRELFAIG

**SEQ ID 917**

ATGCTCATCATCGCAACCTGATTACTGCTGATACTCTGTTCCAGCCTGATTTTCCTCTTTCCTTTATGCTGCTCGCCTCGCCTTTCGCGGAAGGGGCGCACAAAGATGGCGGGGTCT  
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AACGCTCGCGCTCCAAGAGATTTTTCGCGCGCAGGTTTACGTTGCCAAGCGCGAGTGTGTTCAAAATCCCCCTTTTTCGGCTGGGGCTTGAAACTGTGTCAAAACCATAGGCATAGACCGCAAC  
AATCCGCGCGGAGGCCAACGAACAGCTCATAAAAACAGGGTTTGGCGCGCAAAAAACGAAGGTTATTGGATTACCAATTTTCCGCCGAAGGCAACCGCCCTTTCGCCGCGCAACCGGCAATACA  
AACTCGCGCGCGCGCATGGCGAAAAATGTTTGGATGGACATCGTCCCGCTCGCCCTCAACAGCGCGCAATTTTGGCGGAAAAATTCCTTTCTGAAATCTCGCGGGGAAATCAACCGTCAT  
CATCTGTCCGACCATCCGCGCAGCAAGCGCGCAGCGAAGCCGAAATTGATGGAAAAATGCGAACACCTCATTTGAAACGCAACAACCGCTTATTTCGCGCGCAGGCCCGCTTTCGCCCGCAAAATG  
CCGCTCGAAACCGCA

**SEQ ID 918**

MLIIRNLIVYMLILCSSLIFLFFPFLMLASFPFDGAHKMARVWVIGILNWSLKHIVGLKYRIIGAHEIPDRPSVICKAHQSGWETLALQKIPFPQVYVAKRELFKIPFGWGLKLVKTIGIDRN  
NRREANEDLIKQLGARKNEGYWITIFPEGTRIAPGKRKGKYLGGARMKMFEMDIVPVALNSGEFWPKNSFLKYPGEITVILCPTIPHASGSBAELMEKCEHLIETQQPLISGAGPFAAE  
PSETA

**SEQ ID 919**

GTGATGAAACATCATATTCTCGACCGCGACGGCGGTATCAACCGGGACCGCGACGACTTCGTCAAATCCGCCGACGAGTGGATACCTGTGCAAGGCAGCATGGATCGCGTGGCAATTCCTGA  
CGCAGGCAGGCTGCACCGCTTGCCCTGCGCCAAACCAATCCGGCATCGGCCGCAAAATATTTCACCGTTCAAGACTTCACGGAATGCATGCCAAAATGCACCGCCTCATCCGTGAGGCAGG  
CGGGGAAATCGACGGCATCTGGTTCTCCCGCATACCCGGCGCCGACGGCTGCAACTGCCCGAAGCCCAAACCGGCATGATTGAAGACATCTCTGCAACGCTTCAACGCCCAAGCTTCGGGAA  
ACTTGCTGCTGGCGGACAGCCTGCGCATTTGACAGGCAATCGATCGCTCGCGGAGAAACCCGGCTGGTTTCTGACGCAAAAGCGTAAACACGCTCTCCCAACGAGCGCAAGCAATTCG  
CGGACACACACAGCTTTTCGATATCCCTGCTCGATTTTCTCAACATACATCTCGGAGGAAACCGCGCACCGCGCAAGCCGAC

**SEQ ID 920**

VKLIILDRDGVINRRDDFVKSADENIPVEGSMDAVAFILQAGCTVAVATNOSGIGRKYFTVQDLTEMHAKMHLRIQAGGETIDGIWPCPHTGADGCNCRKPKPGMTEDILERFNAQASE  
TWLVGDSLELDLOAIDAVGGKPALVLTKGKKKTLQHGHELPCHTQVDFTLDDFSQYIMQENAAPOAD

**SEQ ID 921**

GTGTGTCGGGCAATTCGTGTCCGTGTTGGGAGAGCGTTTTTTTGGCTTTTCCGGTCAGAACCGCGCGGGTTTCCGCGCAGCGCATCGATTGCCTGCAAAATCGCGCAGGCTGTGCGCCGACC  
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TGCCTCGCTCAGGAATGCCACCGCATCTGCTGGCATTCACCATCTGCGCGCGGTGCGCGGCTGCGCGGTCGCGGTCCCGGTGCGATCAGCCGCTGCGCGGTGCGCGTATGATGAGT  
TTTATCATCAGGTTCTTGGGTTTGGCGGGTGTCCGGGATGGCATTTATACGAAATAATCGGTGGAATAATCGGTCGCGCTGTGCTGCATTAT

**SEQ ID 922**

SEQ ID 922

VSGQFVSVLGERFFAFSGQNGRQFSADGIDLCLOLAQAVADQPSFRSLGVEAFEDVFNHARFGLAAVAAVGAGMRAEPDAVDVFPACLTDEAVHFGMHFGEVLNGKIFAADAGLVGGDGNAA  
CTROPCHRTHAAPDRYPLVGGFDEVAVPVDDAVAVENDEFHEGSPGLGGFGDGTILKYRWKCAAL

SEQ ID 923

ATGCTGTGCCTATGCTTTCCTATTTTTGTGTGTAACGGCGCGGTGCTGCTGATGTGCAGGTGCACTACCGCTGGACGTATTTTTCGCGTGGCGCTGTTTGTCTTTTGGCGGGGGGA  
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CTTTTTCGTGATTGCCACTGGCGGAATTGGGAAACGCTGTTTCATTATAAGGAAGCGTTATCGGTATGGCGGGGCTGCTGCGCTTTGGCGGGATATCGCGTTTCGCGCTGGAGCGGTGG  
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TTATTTCGGCGATCATCAGGTACCGGTTTGAGGGCGTGTCGTCAGGAAGAAATGGGATTACGCTCAGCCGGATTATGTAAACGCAGTTTGCCTGCAGGAGCAATATTCGCGGCGGGATTTCGTA  
CAGCGCAGCATTTCCTCGACCTTGCCCTTCGACGGGCGTACTGATGGAGGCGGCTGGTTTGGGAAGCCAAAGACGGCTTCATCGCTGCCAATATGCGGATGCGCGGTTTCTGCGCGGAG  
GGTTGGAAGACTGCCGAACCGGGAGTTGGTCGGAAATTACCGCAACTATCTGTACGACGTTTGTGAAATTTGCCCGT

**SEQ ID 924**

NVAYAFFLFVFTAAVLLIVSRSHYKTYTFASALFVPLAGGLMLLTAQWQRALNPAVSFWVVLILFLRLKITHYKQPLLISDFLLIADWRNWETLFHYKEAVTGMAGLLALAGYAVFGWSGA  
DSLGMFWRWAGAVLFAAFAVSVRHFSKHPGAVKTYWLSLDDGRDVVFLNLPMSCRAVFPVVPVFGDGEAFARQMPSETRPYGMSSDEKPDIVVTLMESTLDPHCFDFAAAKIPDLKMFGRQ  
EDTVFSSPLRVHTFGGATKSEFAFLAGVPSDFGALASGVFVSVPHLITQGVFVRLREHGQYFCVALSPFFTKGYNNAKAYDHFQFNLMFQPDQLGYAPAHGNLNLHLSSEEMQYARHL  
EKRHPLDENVRQPMFVVLTKSEHQPYRTDINDVDLADPLNAKTSVSNALNDYQIRLADLDKAVSEFSDRYLHERGKFPVGYFGDGHVPPFEGVSVRKKWDYQPDYVTPQFAVRENTAGGFV  
QRQDFDLFAVGGVLMEEAGLEAKDQFPMRANMAHRLGCGGLEDPCPNRELGVGNRYLYDVLKIB

**SEQ ID 925**

ATGATGTTTTCCTGGGTCAAGCTGTTCACTGTGTTTTGTGCATTTTCGTGGTTTGCAGGGCTGTTTTACCTGCCAGGATTTTCGTCAAATATGCGCATGATTGATGCGCCCGCGGCAATC  
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CTGGGTTACGCTCAAACTGTGTTTGGGCTTGATGCTCTTGGCTTATCAGTTGTATTGCGCGCTGCTGCTGCCCGTTTTCAGGATTACAGCAATGCTTTTTACACCGCTGGTACCGCGTG  
TTCAACGAAATCCCGTGTGCTGATGGTTGCCGCGCTGTATCTGGTCTGTTCAAACCGTTT

**SEQ ID 926**

MMF S W F K L F H L F F V I S W F A G L F Y L P R I F V N M A M I D A P R G N P E Y V R L S G M A V R L Y R F S P L G F G A V F G A A I P P A A G R G S G S H V E V K L C L G L M L L A Y Q L Y C G V L L R R P Q D Y S N A F S H R M Y E V  
P N R I P V L L M V A A L Y L V V F K F F

SEQ ID 927

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**SEQ ID 928**

MPFETRRRLQAAALPQQATVFRHTAHYPTTSKTNPAPTGAGRNHKGTHMKLKIDIANNNFKHGGGTERKYTLDLVKGILNRQNTTTPAVYATKFOHGIPEYAMIEPHLVDQRRTLLKLSLFLPS  
SRLAQTRKNSAAKLIACHHADYADLLICGGTHGLYHLMHAQKNLLDLRLAIRNRNSNYATAKLIVASHMMRRRLVGLYGVPPERIQVAPPADTERFFPPQPRETAALRAKYGFADHETVF  
LFPSTGHTRKGLELLADFFQTEL PVKLAVAGSP LPRMKNVVG LGPCTDMPELYRAADFTTMSLYEPFGLVGVESALCGTRVVLSENMACTEVMNEBAGGFFSRQNPETLQAQAQAVS  
LKKGGHRLSDPMRALNYPNPSLSHHIDRLTDLASV

SEQ ID 929

[illegible]

SEQ ID 930

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 SLLRYFKGDAPKVAKSIWAGTLVALVITYIVLWQTAIQGNLPRNEPAPVIAAEGQVSULIETLSKFAQTGNMKIISLPSYMAIATSFLGVTGLFDYIADIFKWNDSMGGRTTAAATFLFP  
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SEQ ID 931

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GACCTTCCCGGGGGGGAACCGCACTCGTTTGGATGTGTAACGTGCATGGAATGATGGAGCAGTCCCGGATCCCGCGCCATCGTGGCTGCCCTGTGCCAAGCTGGTCAGGCCGACAGCA  
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TTTGCCTGGCTGGCGGCTTC

SEQ ID 932

LSGAVRVDGGKMSDKYINVDEGEIAKPSRLADKWDKSGEFTFLHDINPLRLDYIDGHADLRGKRVLDVCGGGGILAESMARRGAAPVKGIDMAEQSLEFARLHAALNNVADI EYECVRVE  
DLAGAEPHPSFOVVTCEHMEHVPDPAATVRACAKLVRPDSKVPFSTINKNPKSYLHLIVAAYLLKFPVKGTHTDWKKFISPALAEKCRQAGLDVADTKGMTYHVLSQLCDSTHWNM  
FACRPAP

SEQ ID 933

ATGCGCGCGTCTCTGAGCGGTACGATTGGGGGAAFTTGTTCCTCGACGGGCATTGCGCAGGGGATACCAACAGCAATTATTTTCTGACGACGACTTCGGGACGTTATGTGCTGAOCG  
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TTTGGCGGGCAAGCGCGCTGCCTGGTTGCCTGCCGTAAGAGTTTCGAGATACCGCGCTGCCGACGGCTGAGCAGTGTTCCTACACGGTGCGATGTTGGCGAAAAATGCACCTTGCOCGCGC  
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TGAAGGACAACTTCGGCAACCACTTCGCTTCGGGCATCATCCAGCCGACCTGTTAAAGACAATGTGTGCTTGACGGCGGTGAGGTATCGGGCTTCATCGATTCTATTATGCTGCGG  
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AGTGCCGGAGAAAAAGGCGTATTTCGACCCGCCAACCGCGCGCTGCATCGTTTGTGGGTGTCGCGCGCTGTGGATTTCATTTCGCGAGCGGGCGAGATGACGTTTATCAAGAAC  
CGAACGCGTTCGCGCACTGCTGTGAGTTTGGAT

## SEQ ID 934

MRGFLSGYDLGEFVSQGLAQGITNSNYFLITTSGRYVLTVEVLKQELPFFLELNRHLSMKGVAAAFVARKDRLDSVLAKGPACLVACLKGSIDTALPTAEQCFHTGAMLRHMLAAA  
DFPLEMZNPRYDAWTFEACARLLFVLSQDDAALLCEIDALKDNLGNHLEPSIITHADLFKDNVLLDGGQVSGFIDFYACRGNFMYDLAIVNDWARTADNKLDEALEKAFVGGYEGVRFL  
SAGEKAYFPTAQRAGCIRFWVSRLLDFHFPQAGEMFTIKDPNFRMLLSLD

## SEQ ID 935

ATGCCSTCCGAAACCCCTTCAGACGGCATTTCGTCAAACGCGGACGCACTCAATCCAACTCAACAGCAGGTTCGCGAACGCGTTCGGGCTTTTGATAAACGTCATCTCGCCCGCTGC  
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ACGCTTTTTCACGCGCTCATCAACTTATTGTCCGCGCTCTTGCCCAATCGTTGACCGCAATGCGCAAGTATACATAAAATGCCCCGCGCAGGCATATAAGAAATCGATGAAGCCCGA  
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GCTCCATCATTTCCATGACGTTTACCACATCGAACGAGTGGGTTCCGCCCGGCAAGTCTTCCACGCGGACACATTCGTATTGATATCGCGGACATTTGTCAAAAGCCCGGTGCGAGCG  
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## SEQ ID 936

MPSETLSDGISVKKRRTSHITQOQVQVAVRVVDPKRLHARLRKMKIQARHPKTDAGALGGREIRLFSGTQGAHALITADKRLFQRLIQLIVRRPCPIVDRNRQVIHKLAPAGIIEIDEAR  
YLTAVKQHTIVFKQVGVDDARRQMVAEIVLQRIDFGTQQRGIVLRDQGPARGFRPRIVTRVFHFRQREIGGGKVHFQHRGTMETLLSRQRGIRITPQAGNQAGRLARQNGIEPAVFARN  
RRGNRHALHTQMPVKLQKRQLFLPQHFKHQHTISRRRQKLIAGVNPRLNALQGNKFPQIVTAQEAHFIIGMTGIDRHINSLAQKRANPPSERRTAGKHIITHIRIAQGISLRQHMVS  
HTLRIRHIOARLTAHPQLGRDEFFPVVTRTFGDKLQIIPRRHMQVRFVFLDGGKHHAVRDPQLGTGTHDGGIGDVLHFFHARYHTIERVFRFPKVFHADTFVFDIGDIVQSRVQA  
GGFQRLLRHVDTDFKRRAPRHAFFREDAATAATYI

## SEQ ID 937

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AACCTGTTCCGCGCTCAACGCGGCTACCGCGACATTCGCGCGGAGCCGAAGCAAGCGCGCTTCATCCACCTCAGTCCGCGCAAGACATCAACCTCGACGATGATGTCCGCGCAAA  
GGGCACTACATGAAGCAGGCGGTGCTCGATTGCAACTGGAATCCTCGAGGAACCTGGGCGAAGCGGAATACGGGTCAAAATCGCAACCCCGGCGCGCGCAAGCGGTGGAAGCGGATA  
TTCTGAACGCGGTGCTCGGAAACCTGCTT

## SEQ ID 938

MTHTFVVTGVC CGKRTTAAPSLQKHLGCPYAEDEFTQANRDKMGAGIPLTDEDRYPWLGNIIRDWMTQQAQNGADHTIVTCSALRGYRDIIRGABGKAAPIHLSPPQDINLERMMSRK  
GHYMKAGVLDLSLELLEGEYGVKIANPPTPEAVEADILNVAENLL

## SEQ ID 939

TTGACGAGCACTTATGCGCATAGAAATCGAACGCGCTTTTGTGTTGAAACGCAAAATGGCGGCAATACGCGGATGAGCGCTGCTGCTGAAACAGGCGTACCTGTCTGTTGAAAAAG  
AACGCAACATCCGCATTCGCGATTGCGGAAACGCGCGTGGCTGACGCTGAAAGCTTATTTTCGAAATCAGCCGACGAGTTGGAATACGAAATCCCGCTTCCGATGCGGAAAGAT  
GATGAAACGATGTCCCGTTAAGATGAAACAGCGCTTATCCGCTGAGTGGGCGGCGAGCTGTTTGAAGTCGATGTTTTCCTTGGCGAAACCTGCGCTTGGTCTGCGGAAATC  
GAGTTGCCCGCGCAAAATGCGGATTTGACCGTCCGAGCTGGCTGGGCGCGGAATCACTTCAGACGATGATGTTTACCAATGCCATATTTAGCAAAACATCCGCTTCAAGCTGGAAGAAATG  
CCGTC

## SEQ ID 940

LTEHLMPIETERRFLIENDKWRQYADEPLLLKQYLSVEKERTIRIRIAGKRAWLTLKGYISLRSSEPEYEIPLADAEMMETMCPFKMKRRYPVWGGSLFVDDVPLGENSLVVAEI  
ELPAENADFDRPWLGRKITSDGMFTNAYLSKHPFSSMKNAV

## SEQ ID 941

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TATTCAGGCGCGCGGACGGAATAAGTTTTCGCGTGTGATTTTCAGACCGCGGGGAGTTTCGCGTCATTTCGCGCAACTGCCAGGCAAGCGTGAACAAATCCATAGCTTGGGGCT  
TTGCTCGGTTTGTCTCGCCCGCTTTGCGGTAGGTACGCTGCCGTGCGGCAATTTGGCTTCGCAATACAGTTTGGCTTCCGCTGCGTATGCTTTATAGTAGGACAGGTGACGGTATTTGCCG  
ACAACCGTACCGCGGATTTCGAAACGGAATTTGTA

## SEQ ID 942

MDRTAKNRLKTLRFGGLSVDLHRFELQRIGFAVVGIALCRNIVQRCBIEIRYIVAAHPHIFDDPGFHAAYAVFSRTRLQAADGIXFVAVGDFQTRGEPRVICRQLPGRBQIHSGLA  
LLGFALARFAVGVAAVGEFGFRIQFAPAVVFIIVGRVQGIADNRTAGFETDIV

## SEQ ID 943

ATGCGCTGTAAGAACCCATCTGTGCCGGGCTTCAGACGGCATATTGCTTCAAAGCAGGTTTCCGAGGCAACCCAGTTTCAAGATATCGGCTTCGACCGCTTCGGGCGTCCCGGGTTCGCG  
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GCGGACTGAGGTGATGAAGCGCGCTTTCCTTCGCGTCCGCGCAGAAATGTCGCGGTAGCCGCTTTGAGGGCGGAACAGGTTCAGATGTTGTTGCGCGCGCTTTTTCGCGCTGTTCGCT  
CATCCAGTCGCGGAGATTGCCAACACCGGATAGCGCTTTCATCGGTTCAGCGGAATACCCGCGCCCATCTTGTGCGGTTGCTTGGGTGTTGGAACCTGTCGCTTCGCAATAGGACAT  
TGACCGAGGTGTTTTCGACGGGACGCGCGCGGTGCTTTCGCGCAGCGCATACCGCGTAAACGCAAAATGCTGATGATTTACTATGCTTTCGCTGTCAGACGATGCGCAACAGC  
AGTGGGCAAGGCAAGCGCA

## SEQ ID 944

MPSETHPVGPRRRIHASKQVPRGNFVQNIQFDRFRAGVGDFPVFAQAQFLQDLRIEHPFHVVPFARHAFVVDVLRRTVEDEGFAFGSAQNVAAAFEGGTGYDGVVRAVLRLLR  
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## SEQ ID 945

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CGTCAACGACGTACTGGTCAAAAACCTCGCGGGCAGCGTCGCGGGCGTGGCGCTTCTGGTGGTCTGGGCGCAATGCTCGAGCGTTTGGTAGAAAACATCGCGGGCGCACAGTCGCTGGCG  
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GTC

SEQ ID 946

VLFSFHNLKQPNFVLLLRKALQMDGFTPTLSAQFLIGISAAAIIILILITVKKPRIRALLTLVIASLLTALATGLPTGSTVNDVLVKNPGGTLGGVALLVGLGAHLGRLVETSGQAQSLA  
DALIRMPGEKRAPFAPGVASLIFGPPIFFDAGLIVMLPIVFATARRMKQDVLPPALASVGAFSVMHVFLPEHPGPIAASFYGANIGQVLLILGLTAFITHTYFSGYHLGKVLGRAIRHVFPV  
ELISGGTQDSDPPEKPARAGTVVAVHILPHLLIFLNTGVSALESKLVSADETIVVQAKMIGSTPVALLISVLAALLVLGRKRGECSGTLEKTVDGALAPACSVILITGAGGHPGGVLRAS  
GIGKALADSMADLGIPIVLLGCFVLVALAIRAQGSATVALTAAALHAPAVAAAGFTDQLACTIVLATAAGSVGCSHFNDSGFLVGRLLIEMDVPPTLKTWTVNQTLIAFIGFALSAILPAI  
V

SEQ ID 947

TTGAAATATACGGTATGTGGGGCTTTTGGGTACAATCGCAACATCAGTGTTCAAAGTGGGGAAGCGCATGGATGGACGGTGTGGCGGGTACGGGGTCTTTTTCCTGCTGCCCTTCGGCT

SEQ ID 948

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SEQ ID 949

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CTGGTTA

**SEQ ID 950**

LNWAAYDGLAWRAVLSDAYMLKRLAWTVFQAATCVLVLPLGVFVAVWLARLAFPPGRALVLRLLMLFFVMPVTLVAGVGVLLAFPGADGLLWGRQDTPYLLLYGNVFFNLVPLVRAAYQGF  
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VGEYVLLAFSVAVLSVCCLPFLSAIVVKAWSAGESREVLMSESETQWAVNTRLRFSAAAVFAAAVLGVVYAAAAARLVLMRGLVFLFFMVSPVCSAGVLLLYPGWTAASLPILLANYALLAY  
PFVAKDVLSAWDALPPDYGRAAAGLGANGFQYACRITFPELLKPALRRGLTLAAATCYGEFAATLPLSRPEQTLTLITYLXLRAGEDNYARAVMLTLLLSAFVAVCFILLNGEGGRTE  
TL

SEQ ID 951

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CTATCTCTCTTACGGGCAATGACGCTGTTGTTGGACGGCAGTGTTCGACGACCATGGACTTATFCGGAAGGAATGGAAACATCA

SEQ ID 952

LRAPSCWCTTAKAENGRKRYNAPFSEDGKMSLSEILSYNQKPVESGEYEKYFTDKYPERGLAVLSCHDARIIGLLPDALGLKNGDAKLIKNAAGLVTHPWGSMVMSLLVAVFELAVRE  
DWTIAHDDCGMOGLNAEEFLGFVRESRIPEDRIETLEAYAGVLDGMLTGFNDVEDSVRETVDLIRNHPLMPRHIAVHGLVTHPVTGKLFVLDGVSVDGDLSEGHETS

SEQ ID 953

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GTGCGCGAAGAACCAATATCGCGCTCGCATTCGCGCAGGGCGACAGCTGCACAAACAACTCCGCGCGCAACTTCACGCGTGCTGGGTCATGCGCTTCAGACGCGCAGCGCTCCGCATCTTGTTCAG  
CCCCATGCAATATGTGTCGTCACGCGGAAATTCGCGCGCAACTCGATGTGCGCCGCGCTTTTCAGACGGGCATCCCGCTCGCGCGCCCGCTTATATCCGAAAAACAGGTTTGTATGAAAAA

**SEQ ID 954**

HKKIGLPGGTFDPIHNGHFHFIARFADEIGLDVAVFLPAGGPYHKDAASASAADRLAMVELATAEDARFAVSDCDIVRESATYTFDTVQIFRQFPFSAQL#H#LMSDSLSLKLHTWKKQQL  
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SEQ ID 955

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ATGGACGTTGGTTGATGCAGGAGAACCTCGTCGTCCACGTCATGCTCCCTGCCGTGGCGACTTCTACGACATTGACACCATCTGGGGCGGGCAGAAAACCGAGTTTCCACGCGCGAATGCAG  
AAGCCGTGGCACGCTGCAGAC

## SEQ ID 956

MNEQLQDLQKMGVAVNALEDIKARDISVLEFDQRTSLFARNIIASGDSTRQVKALANNVAVDLKEAGFEILSTEGDSGEWTLVDAGDLVVHVMLPAVRDFYDIDTWGGGKPSFHAGN  
KPMHAAD

## SEQ ID 957

AGCTGGAAAAATGCCGTCTGAAGCGGCTTCAGACGGCATTCGCTTGCCTTATCCCTTGAGGTAATGCACGAATGTATATGCAACGCCCTTGTCTGTACACGGCGTTCGGTCCGCTCTG  
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CCGGGAGGGGTTTTCAGGGGAGGGATTTCCACGTTTTCGCCCAATATGACGGGTTCGCCAAGGTATAGGCTTTGAAAAATGCGAAATCTTCGGGATGTGCCAAGGCATAGCAATTGC  
CCGCCCCGATGCGACAGGTTTCCGCGACGCGCAATATGCTTATTTGAGCATATTTCTCCACAA

## SEQ ID 958

SWKNV\*SGFRRLPCGYPLR\*CTNVTATPLLLTRRSVRSASLQCVRSISGKNASPTDKSTSVIRKSVANGIACPYICAPPIMTASSAPAHNANATSKLATVSPAAQ\*SACRIATMFLR  
PGRGLTGRDHSVFRPDMTGLPKV\*ALKNAKSSGMCQGIAPAPMHRFSAHAALMVLISIFSPQ

## SEQ ID 959

ATGGCATACTCTCGCGACTTAAGAAACAAAGCTTTAAACCATAGCGGATTAACAAAATCAGGACAAGCGCGCGCGCGCAGGCAATATGTTACGGAACCGATCCGCGCGCGCGCTCC  
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TCAAGAAACACGCTTTACTCGCGATTCGCTTAAAAACAAACAGGACGCG

## SEQ ID 960

MAYSADLRNALNHSGLTKIRTRRAAGSTNGTEPIRPAHLHRESFPLSRGGATPYRFLILIRYITDIAKTFAKPKQRLTCQETRTFCGFALKNKQAA

## SEQ ID 961

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GCTTTCCTGGCAGTTGGCGCAATGACGCGAACTCCCGCGGCTGTAATAACACCAACGCGGCAAACTTTATTCGCTCGCGCGCTGAATAAGCGGGTACGGGAAATACAGCATA  
GGCGCGTGAACCCGAAGTGTCAAATATCGGGTGGCGCGCGGACGATACGTAACGATTTCTTTCGACCGCTCCCTGAACAATATTCGCGCAAAATCGGCTATACGACGACGCGCA  
AAACCTATACGCTGAAGCTCAAATCGGTGCAGATCAACGACGAGCGCGCAACCG

## SEQ ID 962

MTFERSGNAYKIVSTIKVPLYNIRFESGGTVVGNLHPAYYDIRRGLYAEAKFADGSVITYGKAGESKTEQSPKAMDLPFLAWQLAANDAKLPGLKITNGKLYSVGLNKAGTGKYSI  
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## SEQ ID 963

GTGCCACGGCTTCTGCAATCCGCGGTGAAACCTCGGTTCTCGCGCGCCAGATGGTGTCAATGTCTAGAGTGGCGCACGGCAGGAGCATGACGTGGACGACGAGGTCTCTCTCATCA  
ACCAACGCTCATTTCGCGCTGTCTCTCTCGGTACTGAGGATTTCAAACCGGCTTCTTCAAATCGACGCGCAACGTTGTTGGCCAGTCTTGTACTTGGCGGTACTGTGCGCGCTGGCGA  
TAATCATTTCTGCAAAACAGCAAGTTTGTCTTTCGTTTCGGAACGGAATGCTTTGGCTTTGATGCTTCGAGGCGATTGACGCGCGCCCGGACCATTTTTCGAGGTCTTCGAGTTC  
TTGTTCTGTTATGTTTCTAACGGGATGTTTTCAGACGGCATTATAGCTCTCTCTTAC

## SEQ ID 964

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LFVHCFFNGMFSGLIASPY

## SEQ ID 965

TTGAACATTACCGCTTTCGCGAGTCGGCACCAAAATGCGCGTTCGGGTTGATGAGGCGCTCGCCGAATACGCCAAACGCTTCGGACGCGACGCGCGCTACGCATTCAAAGAAATCAAACCG  
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CTCGCTCAGACTGGCGGAACACCTCAAAGCTGGCGCGCAAAACGCGCAACAGCTGTCTGCTATCGCGCGCGCGGACGCGCATGACCGACCGCTCAAACAACAGCGCGCATGATGATG  
CGCTGTCCAGCTCACCTGCGCACGGCATGCTGCGCGCTTCTGACCGAGCAGCTCTACCGGCGGCTTCCATCTGCAACCATCTTATCATCGGGAA

## SEQ ID 966

LNI\*VLAVGTKMFRWDEAVAAYAKRFRDAAAYAFKEIKPEKRGAGVNAVQMAAEKRILEAIPQGAFLVVLDERGKAPTSVELAEHLKSWRONGEHVCFVIGGADGMDRLKQQAAMN  
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## SEQ ID 967

ATGGCAGCAATGGTATTCTCGCTCAAGCTCAACAAAGAAGCGGAAGGCATGAAATTTCCGCCGTGCCCAACGAATTTGGGCAACGCAATTTTGAAAACGTATCGCAAGAAGCATGGCGG  
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CGTGCAGGATACGTTCCGCA

## SEQ ID 968

MARMVFCVKLNKEABGMKFPPLFNLGKRIFFENVSQEAWAATRHQYMLINENRLSLADPRAREYLAQQMBQYFFGDGADAVQGYVPO

## SEQ ID 969

ATGCAACACGACGTTTACGACTACACCGCGCATACGCTTCTAAAAACACCGTCTGCGAGAAACCTACCGCTGCTCGGATTTTCATTCTATTCGCGACCGCGAGCGCGGCACTTGC  
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TGGGATTTCCCGCACTCGCGCTGACCATTTCCGCGCGTTTGTCTTGTTCAGTTCCTTAATAATTATGTGGCAGTACGCAACCGTCAACGCGCGCGGAGACAGTTACATCAGCGCGG  
ACTGACACTGTTTATCTCGCTTACAACTCTTCAGCAGCGCTGCTCAACATCTGCTGCTCTTAAACCGCGGACGAC

## SEQ ID 970

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AVFLTMSALARRTRLMNALGRFLTVGAVILMVAVVANLFLGIPALALFISAGVFLSSLIIMQVETVIDGGEDSYISAAITLFIISLYNIFSSLLNLSLNGDD

## SEQ ID 971

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## SEQ ID 972

VYSVTFSSRLHSRLCFYVFAVLYAQNKMPSENKCFQTAMFAMCFAYISRRLRTAGC

## SEQ ID 973

ATGTTACCGAATACACCGCGCGCGCGCTTTATCGCGCGAGTTTCGATCCGCGCAATTCGGGCACTCTGTGATGATACGCGAGCGCAATCTATGTTTACGAACTCATGTCGCCATCG  
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## SEQ ID 974

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FLMPPREIAEVSSIMIKLGVPEGMNMTVKRYVPAVYQKRIAHHNNNA

## SEQ ID 975

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TTAAT

## SEQ ID 976

LYIINGLKIHFIIGDILNKPLSPQGYIAFRASNFSNRGFH

## SEQ ID 977

TTGTTTTAATTGACTATAAAACAAATGGGTTAAACAGTATCCATACATCAGCTTTTTTATCATCTTACTTTTTTATTCATCCGATCGGCCAGACAGATTTCAAAGATGAAAAGCCTATTTC  
TATTCACACCAAT

## SEQ ID 978

LFLLIDYKINGLAQYPIYSPFIILLFIHPIGQTFDKDEKPIILFPI

## SEQ ID 979

GTGTTGCAGACGCAAAACCGGCCGCAACATCGTCTGCCGTATGCCGTCAAGTATCGGCACAATCCCTTGGGATACAAATCGGCCGCAATCCAGCTCGGCCGTAAAGAAATGAATCGTA  
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GGGTGAGAAATCCGCAATAAACCTGCCAAACCAAAATCGGGTGTATGCGTCAATTTTTTCATCATGCGCGTATCGAAGCGCAAGTCG

## SEQ ID 980

VFDSONPGMNTVCRIVKRYHNPRLRYNRAAIQLGRNEMRTAGNAATCFQSAFVRMKPGERGQDGRMDVHQPAFVMGAELRGQNPBKTCQNHQIGLICVDFPHHGRIBKS

## SEQ ID 981

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## SEQ ID 982

SLEVMEHCINAPAAATAFRPLCFSPMRFPVYFWEKCSFHRQIHPGYPIGR\*WHRLSVYLRAAHNDGFFRAGAQCQCHLQTCRFRACRAILRLPADDDVPSSGGFDGQGFPRFPFHND  
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## SEQ ID 983

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## SEQ ID 984

VCYLHSRVTYLLIMWSPKXYAVALGSSSTASGEYSYAGSYNSVASGNKSYAAGYASVASAGSVVIGDSRQVKPEADQGVAVGSKATVKNKARQVRVVGSEAKVNAERGIAIKKAKAGG  
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## SEQ ID 985

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## SEQ ID 986

MKI THCKLKEVQKEPLRSFVPEVTARSAADILGHIPDSAAIFYRKIRTVANRHLAALADGVFEGPAGPGSSYFGRRKRRRGRGAAGKAVVFGIPKRFRAYTVAAINDAEPTLFPVAVK  
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## SEQ ID 987

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**SEQ ID 989**

**SEQ ID 990**

**SEQ ID 991**

**SEQ ID 892**

**SEQ ID 993**

**SEQ ID 994**

**SEQ ID 995**

**SEQ ID 996**

**SEQ ID 997**

SEQ ID 998

SEQ ID 999

SEQID 999  
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[illegible]

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**SEQ ID 1012**

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**SEQ ID 1013**

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**SEQ ID 1014**

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**SEQ ID 1015**

SEQ ID 1015  
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**SEQ ID 1016**

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**SEQ ID 1017**

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CGGCGGCCCGCGCGGAGGACGATGCCAGAGGCGGTTTTTCTTCAGCTTCCAAGCGTTTGACGACGACGCGGTCGTG

**SEQ ID 1018**

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SEQ ID 1019

SEQ ID NO: 1019  
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 CTGAAGAAAAACCGGCTGTGCCCGATGTGGGGGGAATGGCGGATGGCGGCGCATGTATG

SEQ ID 1020

MAAKDVFQFENVRQKMGVNGVILANAVRVTLLPGPKGRNVVVDRAFGPGPHITKDGVTIVAKIELKDKFENMGAMQVKEVASKTNDVAGDGTITATVLAQSVIABGKHVYTAGHNPDTLKRGI  
KAVAALVEELKNIAKPCDTSKRELAQVGSISANSDEQVGAIAEAMEKVGKGVITVEDGKSLLENLJVEBGMQFDRGYLSPTFINDEAKQIAGLNDPVVILLFKKISINIRDLPLVLEQVAK  
ASRPLILIASDEVEGALATLVVNNIRGLIKTVAVAKPGPGDRRRAMLQDIATILGCGVVISSEVGLSLEKATLDDLQAKRIEIKGENTTVIDGFGDAAQIEARVAETROQIETATSDYDKE  
KIGERVAKLAGGVAVIKVGAATAVEAMEKKRDVEDALHATRAAEVGVVAGGCVALLRAAELENLTGNADQAGVQILVLAVESPLQITVANAGGESPVVVNVKVLBGKQNVYIAGNAGSGE  
YQDWITCMGVLDPAKVITRSALOHASAEIAGLMLITDCMIAREIPEEKPAVPDMGGMGGLMGGM

SEQ ID 1021

SEQ ID NO:1027

TTGTTGTCCTAGAGGTTTCAGACGGCAATTGCTTTACATCATGCCGCCCATACCGCCCATATCCCCCATATCGGGCACAGCCGGTTTTTCTTCAGGGATTTCGGCAATCATGCAAGTCGGTCGTC  
AGCATCAGACCGCGCATAGACGCGCGGTGTTGCAAGCGCGGAACGGGTACTTTTGGCAGGGTCGAGTACGCCCATTCGATCATGTGCGCGGTATTCGCCGAGGCGTTCGGTGTGAACCGTAGT  
TGCCCTTTGCCCTTCCAACACTTTGTTCACCACACGCTGGGTTCTCCGCCCTGCGTTGGCAACGAGTATGGCGCAGCGGAGATCAACCGCGCGCGCAATACGATTTGTACGCCCTGCGCTTTGGT  
GGCAATTGGCCGTGTGCGAGTTTTCCTAAAGCGGCACGGCGCGCAACAGGGCTACGCGCGCGCTCGCAACCGCTTCTTCAACCGGCTGCGCGGTGAGCGTGCAGCGCTTCTCCACGGG  
TCCTTTTCTCTCTTCAATTCGATTCGGTTCGGTCCGCCGCCGATTTGATCACTGCCACGCCCTCTGCCAGTTTGGCAACGCGCTCTTGCAAGTTTCTTTGTCGTGATTCGCTGGTTCGGCGGTT  
CGATTTGTTTGGCGGATTTTCGGCAACACGCGCTTCGATTTTGGGCTGCGCTGCCCGAAGCCGTCGATGACGGTAGTGTTTCTTTACCGATTTCGATGCGTTCGGCTTGACCCAAAGTCGTCCAA  
AGTCGCTTTTTCCTAAAGACAGGCCGACTTCTTCGGAATCACTACGCCCGCGGTGAGATGCGGATGCTTTCGACGATTCGCTTCGCGCGGTGCGCGAAGCGGGGGGCTTTGACGCGCAAG  
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CGCGCCCATATTTTCAAACTTGTCTTCAGTTTCGATTTCTTTGGCGACGGTTACGCCGTCTTTGTGATGTGCGGGCGCGGAAAGCGCGGTCAACACCAAGCTTCGCGGCTTTTGGGGCC  
AAGGTTACGCGCACGCGCGTTGCCAAAATATTCACGCCGTTTACCAATTTTGGCGGACTTTCGTCGCGAATGTACGCTCTTTGCTGCCATTTCAATTCCTCCAAAATCTTAAACCTGTC  
TGAATAAACCTGTTATACGCTGC

SEQ ID 1022

LLSFGFRHZZLHHAHTAHSPHIGHSRFFPRDFGNHVAVRQHQTGDRRGVLQRTGTYGPRVEYAHSDHVAVFAGACVTVVAFQHFVHHHAGFSACVGNDAQRRRLNGAQYDLVACVLY  
 GIAGVQVQSGTGACQOQYAAACNHAFFNGCAGSVQRVFHAVVFLFHPDFGRRAADFCHCHASCOFQGNALLQFFVVIAGRQGFDLIADGNTRFPLGCVBARVWDGVSVFFTFDFDAFLGATQVWQ  
 SRPFRQARDDFGNHYAAGQDGDVLQHRFAAABRAGGFDGNGPQDAADVHDQSRGQAFVTVFSDIQQAAGFPHLFBQHGQVADVADFFVEBQONKRIVQTGDLFFRVVQDKVRGQVAAVELL  
 TFNEVQLVQFPAFVNGHAFVADFHRFPGDNRLADFLVGVGNRDLGDFPGS IARPGDFVQLQFAGFVCSGNGFVDAAFPQITGRVHAGHNVHPAFGNDGLCQYGGSGSRVADYGVVGFGRDFVYHL  
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## SEQ ID 1023

TTGTTAATCCGCTATATTTCGCCCATCCCAAAACGAAGCGGAGGAATTTATCGGAAAAACAGCAACCTTCCGCGTCATTCGCGGAAAGCGGAATCTAGGTTCTGTCGGTTTC  
GGTATTTCGATAGATTCTCTCCCGCTTGGGGTCTGGATTCCCGCTCGCGGGAATGACCGGACTTTAGGTTCTGTTTGTGTTTCTGTTTTCGCGGAATGACGGGGAAGTTGGC  
GGTGTGTTCTTATGAGTGGTTTTTGTATTGGA

## SEQ ID 1024

LLIRYLSRHPKNEERQKFGKATATPPSPFRKRESRVRFLFPIDSCRVOGLDSRLRGNDRTLGFCFVSFVAGMTGKLAVVSYGVVFPV

## SEQ ID 1025

TTGAAAACGAAAAATTTTATCCAAATACAAAACCACTCCATAAGAAACAAACCGCAACTTCCCGCTCATTCGCGCAAAACAGAAAAACAAAAACAGAAAC

## SEQ ID 1026

LATKNFLSKYKNHSIRNRQLPRHSRKNRKYKTF

## SEQ ID 1027

TTGGATAAAAAATTTTGTGTTTCAAGCCTTACCCTTGCATCGCGTTAAATTTTACGATAAGCACATAGATTGTAAACAATCGGCACAAAGCCGTTGTTTTTCAGAGACA  
TTATCCCTGTGACAGCGTGTCTATATATGTTTGCCTATAACCGCTTGT

## SEQ ID 1028

LKKFFVFKPSPLAIGVKIPYDHRIDCKQSATSRFVPSDILPVRCPYICLPITAC

## SEQ ID 1029

TTGATAAAACAAATACCGCCATTTCATTCGGGCAAAACCGCACGAAACATCCGTTTTCCCGTTTCCAGACAATCCGGTACAGGACACCCCGCTGCGGATTCCCGCTGCACATCCGCAAA  
ATTCATACGCAAGGAAATGTTGAAAAACAAAGAAC

## SEQ ID 1030

LKTIPTAHSGRTARNIRFPVSTTIRYTPRCRFRHLIRQNFIRKENVENKKN

## SEQ ID 1031

TTGAAAATACCGGATTATCTCCAAGAAACTCCCTTGTGCGCCATACGCGCGCTGCGGCGCAAGATAACCTTGCCTAATTGACGAAATTTACGTTAACCTTACGTTTCCGCAACCA

## SEQ ID 1032

LKIPDYQENSPCAAIRRLPAQDNLCQFAEPTLIRFPHP

## SEQ ID 1033

TTGAACCCCGCACTTGGACATCTGTCTTCGGGGCGGTAGAATCAAACTTATTGGAAGTTCAATCCCTTCCAAAACAGGGCAACACAGATGACGCTTATGTCATCTCTGTG  
TGTGAAACATTCAACTCGGCTATAATCCCGTTTTCGCACTTTATCGACAGCGAAGATCCATCATGAACACCATTTTCAAAATCAGCGCACTGACCTTTCGCGCGCTTGGCACTTTC  
CGCTGCGGCAAAAGAAAGCGCCCGCATCTGCAATCCGAACCTGCGCGCTTTCGCGCGCAGGGGACACCTTTCATTCGCGCAGCAGATGACGAGGCAAGCTATGCAATGGGC  
GTGGACATCGGACGCTCCCTGAAACAAATGAAGAACAGGGCGCGGAAATCGATTGAAAGCTTTACCGATGCCATGACGCGAGTGTATGACGGCAAGAAATCAAAATGACCGAAGAGC  
AGGCCAGGAAGTGTATGAAATTCCTGACGAGCAGCAGGCTAAAGCCGTAGAAAAACACAAGGCGATGCGAAGGCCAACAAAGAAAAAGCGGAGGCTTCTGAAAGGAAATGCGGC  
CAAAGACGCGGTGAAGACCACTGCTTCGCGTCTGCAATCAAAACAGGGTGAAGGCAACAGCGACAAAGACGACATGTTACCGTGAATPACGAAGGCGCGCTGATTGAC  
GGTACCGTATTCGACAGCAGCAAGGCCAACGGCGCGCGGCACTTCCCTTTGAGCCAAAGTATTCCGGTTGAGCGAAGGCGTACCGCTTCTGAAGAGGCGCGCAAGGCAAGCTTCT  
ACATCCCGTCAACCTTGCCTACCGGCAACAGGCTGCGGCGGAAAAATCGGTCCGAACCGCACTTTGTTATTGACGTGAAGCTGCTCAAAATTCGCGCACCCGAAACCGGCGCGGCA  
GCAGCGGATCAAGTCGACATCAAAAGTAAAT

## SEQ ID 1034

LNPATWTSVLRRGRIKPYFGRFPNPPQNRATHRLTLVSSCVLRHSNSAIIPFRLYRQRRSINWTFIKISALITLSAALALSACGKKEAPASASEPAAASAAQGDTSISGTHQOQASYAG  
VDIGRSLKQNKQGAELDKLVFTDAMQAVYDGRKIKMTREQAQEVMMKFLQBJQAKAVEKHADAKANKEKEGAPLKENAKDGVKTASGLQYKIKQGGKQPKDDIVFVEYEGRLID  
GTVFDSKANGGPATPPLSQVLPWTEGVRLLEGGATFTYIPSNLAYREBQAGKIPNATLVFDVRLVKIGAPENAPAKQPDQVDIRKVN

## SEQ ID 1035

GTGTTGACGGGCAACATATCATCTGCGCGGAAAGTTACCGTATCGGCAACCGGACTGAAAAAGACAGCGTGTTCGCGGATGCGGTGCACATTGTTGATTGCGACT

## SEQ ID 1036

VLGNISSARKVTVSANATEKDSVFGDAHVHIVAT

## SEQ ID 1037

ATGACCGAAGCGACCTCCCGCGCGCTTTCTGAAAACCTGCACCGCGCGCGCGCGGCGCTGCTTACGGCTTGGCGGCACATCGCGCACATCCGTTCCGCGCCCTTCCCTCTTCCCAATCCG  
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GCTGACGGGCTTCCCGTTCGGACATATTCGCGACAAATCACTTTCCCTTGGCGCGCACACCGGAATCCGTATGAACGGAACGGCGGCTATTGCGTCCGCTTGAAGGCTACCCACA  
CTCGATGCGTCCGCGCTGACTTTGGATACCTGCTCCACCGCGGATTTGCTATCTTCCCGAAAGCGGTGTTGCGGATATTTGCGAA

## SEQ ID 1038

MYEPTSRRLFKTCTAAGAGLLQACGTSATSVPLPSSHVVVKARTVPLQTPRRSSDGNLLRVVASSGFAEDTNRVNTALTRLYNAGFTVTVQAGSRRPQRFAGTDAQRAADPQEVASG  
RVATPKVLMGLRGVGAARILPHIDFASLGARMREHGTLPFGSDVCAVLALLAKGNMSPAGPHAYSDPKPARGATMDAFIKGATQNLFTVDVPIYIQRADVETEGTLNGLNLVLAS  
LAGTFYMPDIDGILLFLEVGEQPYRIERMLNLYLSGILGKQRAIVFGDFRMEKIRLDYSSYDPSAVAKHLERPAKIPVITGFPFGHIAKITTPLGATRIRENGGYSVAFEGYPT  
LDASALTDLTLLPPDLPIFPESGVADISE

## SEQ ID 1039

ATGATAGTGTGTTCTTCCATCGGAAAGTAGGTCACGCAAAACCCCTTTCAGAAAACCCCGGATATCCGGGGTTTTCTTTCGCGGAAAAATGTCGGGGATGCGGGACGGCAT  
CTGTACGGTTCGGGTGCGGTTTCGGAGGAACGGCTTGAACTTTGGGATATTCAATT

## SEQ ID 1040

HIVVFFHAKVGHCTPPQKTPGYPGVFALPGKNVGGGTASVRCVPVFAERLETIGYSF

## SEQ ID 1041

ATGTTTGCCTATAACGCTGTGTTTTTAATAAATAATTCAGAGGTATCAAGTGTCTGATTCCAAAACGAAAGAACCGGCCACATTCGCAACGCGCGCGCTTTATGATTGCGGCATCG  
GGTCCGCGCTGCGCTTGGCAATATTTGGGTTTCCCTATATTGCTTTTGAACCGCGCGCGCGCTTCATCTGCGCTATCTGCTGCGCTTTCGACGCGCGGCAATCCCGCTGCTGCT  
GCTCGATTATGCCATCGGCAACCGTTACCGGGTCTGCGCGCTTGGCTTTCGCGCGCTCGGACCGTGGTTTCGAGCGGTCGCTGGTGGAAAGTGTATGACCAATATGCTCATCTGCATC  
TATTACGCACTGATTATCGGTTGGCGGCAAGCTATACTATTATTCGCTCAACCGCGCTGGGTTGCGGATTCGCAAGGTTTTTCTTTAAGGACTTCTGCAATGCGCGCGCGGAG



[illegible]

SEQ ID 1042

SEQ ID 1042

MFAYNGFLFNLNSRGINVSDSKTKERATPGTTRAFMIAAIGSAVGLGNIWFRFPYIAFENGGGGAFILPYLVALITAGIPLILLLDVYAGHRYRGSAPLAFRLGRWFEPVQWNVMTNIVICI  
YYAVLIGMAASYTYYSVNAAGADPGQFFFKDFLQMGAPALGLDFVGKVGAGPLAGVWVPTAAIDALGVQKGVARASSFFMPLILLVWFLINVLGICLSLTLPGAAGKLDAFLTPDPWSKLADSKV  
WVAAYGQIFFSLSICFGINVITYSSYLKKKTLGGTGLVVGFPANSSPELLAGIVFAALGFMQAAGGKAVNEVASGGIGLAFIAPPTTINQAPWGLMIGILFFGSLVFAGVPTSMISLILEVY  
AAIQDKLNI GRVNATLLVCLIPMGIVSTLLFGPATGLPVLVDMMQGVFNVTYGTIVAAGFVYVAALITIGRLPLRLRRHIALNASSRGGGLTACVQVPTVVMVLGYMLYDGTAGLLEKNYGYDPDG  
LNIIFWGMGSAALILGCLLSLILPWKGGQDFNVKDEHEHEQGGKE

**SEQ ID 1043**

ATGAGTACTTCCGCCATGTGTGATGATGGTTGCCCCATCGCGGTGATTTCGGGGCGGGCTGCTGCTTCCCTGTTAAGGCTGCCGGAAGAG

**SEQ ID 1044**

MTSAIVMMVAIAVIWGGLLSLLRLPER

SEQ ID 1045

ATGAAGCAGCCTCCGATTATCTCTCTGCTTACCGCTTGTGTCGCCGCCCTACTTTGCGCGGGTGCACGCCCTTCCCTCTGACCGGCCGCCGCTTCGCACCTGCGGAAAAGCGGCGCCA  
TCCAACCTCGCCCAACCCATACAGCGCGCGCTTCAGGACACCGGACGGCGCATTCAGCACCCGCGCTCAAAACGGGCGCGCTTTGAAAGCATCTGTA AAAACGGCGGTGTTGACCGCTT  
TGTGCATATTTCACATTCAAACGGCAAACCTGCATTGCGCACACCGCGGTTGAAAACGGCGTGGCGCAAGGCTATACGGAACAGGCATATTGCGGACGGCGATCTGTACCGGGACGGGCAT  
ATCGTCCGAGCGCAAACCTTTGGATGCGTGGGCAAGGTGGAACCGCAATGGCAGCG

**SEQ ID 1046**

SEQ ID 1046  
MKEAPITILLPASSAALLSAGCTALPSDRPPLRLTLPKSAPIQPANPYSRPPSGTGDGAFSTRASNGEVLKSIIVKNGVDFRFDIYHPNCKLHSHTPVVENGVAQGYTEQGILRTLILYRDGH  
IVRAQTLDSAGKVEREWQP

**SEQ ID 1047**

SEQ ID 1047

ATGACCCCTGTTTTCGCAACAAGTCCCCCTACCCCGCCCTTGCCGAAGAATTTCGGCAGCCGCTTTATGTGTACAGCCAATCCGCGCTGACCGGAGCATTGAAAACATATCAAAACCCGCTTTG  
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GATTTGGGTGCGTATGCCCGAGCGGTTCAAAAACATGATGGGGAACGCGCTCTGAAACTCATTTCTGAGCCAGGCCGCGACTTGGTGGTCAACGAGTGTCATTGCTGACGCGCTCGAAT  
TTGTCAAAACAGGTGAAGAGAAAACTTTGTGATGTCGATGCGCGCATGAACGATTTGATGCGCGCCGCGCTATACGATGCTCTATCCACCATCGAAGCGGTTGAAACCAAAAACATTGA  
GCCCTGACCGCCAAACATCGTGGCGCGGATTTGATGATGCGGCGCATCTCTCGCGAAAGACGCGACCATCGCTGCGAAGAAGGCGATTTGCTGCTTATCCGACGCGCGGCGCATACGCG  
GCTGATGGCTAGCAATTACAAACACGCGCAACCGTGC GCGGAGGTGTTGGTTGACGCGCGCGGATACAAACTCATCCGCGCGCGGAAACCTTGGAAACAGCAAAATGGCAACGCACTCG  
CTGCTTA

**SEQ ID 1048**

SEQ ID 1048

MTLFCFQVPPYPLAEFEGFTPLYVYSQSALTGAFENYQTAFAALNPLVCYAVKANGNLSIKHFASLGGSGFDIVSGGELARVLAAAGDAAKTIPSGVGKSEAEIEFALNAGVKCFNMESTPE  
IDRIQKIAARLGKTAHSVLRVNPVDVDAKTHEPYISGLKANKFPGIAYADALEAYRHAQQPNLKIGIDCHIGSQLTDLSPLVEACERILILVDALAAEGIVLEHLDLGGGVGIVYKDEGVP  
DLGAVARAVQKLMGTRRLKILILEPGRSLVGNAGALLTRVEFVKHGEEKNFVMVDAAMNDLMRPALYDAYHHIEAVETKNIPLTANIVGPICTGDFLGKDRITACEGDLILIRSAGAYG  
ASASNYNTRNRAAEVLVDGGGYKLIRRRRELBQQMANELACL

**SEQ ID 1049**

SEQ ID 1049  
ATGAAATACGGCGTATTTTTCGCGCGCAACGCGCCCTCTGCTTCCTCGCCCTGCGGTTACAAAGCGGGCTCTACCTGCCCAAAGAAGGCGATACGGCGGTTTCGGCGTGATCCAAACCG  
GTTTCGACGTTCAAGGCAACCGCAATCGCGCCCAACCGCAAAAA

**SEQ ID 1050**

SEQ ID 1030  
MKYGVFFAAATALLSACGYKGGLYLPKEGDTARFGVIOTGLQLOGKPQSAPPTQK

**SEQ ID 1051**

SEQ ID 1051

TTGTTTCGCAAAACAGGGTCATATTTTCGTTTTCATTTTGGGTTGGTGGGGCGGAATTCGGTTTGCCCTGAAGCTGCAAAACGGTTTGGATCACGCGGAACCGCGCGGTATCGCCTTCCTT  
GGGCAGGTTAGAGCCCGCCTTTGTAAACCGCAGGCGGAAAGCAGGAGGGCGGTTGCCCGCAAAAAATACCGCGTATTTCATCGGTAAACTTCCTTCATAAGCGCGGAATGTGGCAAGATTCTG  
GCATCTTAAACAAAAACACGCAAAAGCTA

**SEQ ID 1052**

SEQ ID 1052

LEPAKGHTFVFIFGLVGRITAVCLEANRFGSRRNAPYRLIWAGRGRLCNRRRKAGGRLPPQKIRRLSSVNFLEKRECGKIRHLKQKTRKLL

SEQ ID 1053

SEQ ID 1053

ATGATGCCGAAAGCGAGTTTATCCGCGCGAGCGAAGCATTATTGTAACACATCGAAGACCAAATCGACGAAACGGCTGGGATTTCGACTGCCGGTTTGCAGGAAACGTCCTGACCATCG  
AAGCCGGAGAGCGGCACGCAATATCGTCAACCGGCACACGCCCAACCAAGAAATTGTGGATTGCCGCAAAAAGCGGCGGTACCATTTCCGCGAACAACGCGCAATGGCTGGCAACGCG  
CGACAGCGCGGATTTTACGACGTTTTAAACGAAGCCCTGACGCGGGCTTCGGGCGAAGCGGTTGAGATTGCCGAATTG

SEQ ID 1054

SEQ ID 1054  
MEEFSEKTRASRAIPEHTEDQIDENEDFCRFAGNVLTIEAGDGTQITVNRHTPNDELWIAAKSGGYHFAEONGKWLATRDSRDFYDVLNEALSAAASGEAVEIAEL

SEQ ID 1055

SEQ ID 1055

GTGATGTCGATGGCAAAACCGCTTCGGCGGTAGGCGGTAAAGCGTTCGCGCGCGTCGGCGAGATCTTCCAGCGTGTGCGCGAGATTTCAAAAACGCGCGCGGGCAAGACCGAAGCGGTG  
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CGTCGGGAATAAACTCTCGGCCTCGTATTGTCAAAGCATTTTGTCCAATTCTGAAGCGCTCCGAACGAGTCGGACCAACCCAGTATCTGCGCGCGTCTCGGATAGCGCGCGCAATCAA  
CCGACAGGTAAAAAGGGGGATTGGTCAACATGGGTATAAAAGGTAACCTTTCGGCATATTGTT

**SEQ ID 1057**

**SEQ ID 1058**

**SEQ ID 1059**

**SEQ ID 1060**

**SEQ ID 1061**

SEQ ID 1062

**SEQ ID 1063**

SEQ ID 1064

**SEQ ID 1065**

SEQ ID 1066

SEQ ID 1067

**SEQ ID 1068**

**SEQ ID 1069**

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CGAAAGGCAAAATTTCCGCCATCAAATGTTTGAAGAAATACAAGGCGACGCCGCCCGGATGCCGGACGATTTTGCGCCCGCAGGCCGAAGCCCTGCCGGATTTGGTGCCTTGACGGGCTG  
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ACAAGGCTGGACCACTCGCGCGCTGGGAAGAAATGGCGGCCGCGAAACAGCGCGCTGGAATGGCTGGAAGCTCGATCGGTTGAACTGTGACGGTGAAGTGAAGACACGCTCCGGAATCAAAAGCAGGT  
CGCGGAAACCTGTCAAGCGCGCTGCCCAACTGCCCGCTGTGCTATGATTTGATTCACGATTAAGAACCCGATGTGGACTTGCACACCGAGCTTTCAGACGGCAGTTCAGACGGCAAGCCCTGCGCCGTACC  
GCGCGGAATGGGCGCAGCTTTCGGTTGATTTCAAACGCTGGGGCTTCGTAAGTCTGAAAGAACGCGAATCAAAACATGAATACCGGCTCGACCGATGATTGTTTCGCTAGCGACAGCA  
TGGCGAGCAGCGCGCTTTGAATCGGGAATACCGCTGTGAAAGACGAGCTGAAAGAGCCACCGCCCTGAAAGCTGGATTAATCAAGCCGTATCCACCGAAGCTCAGTTTTCGCCCTGTGTT  
GGACAACTAGCGAAGCGGACACAACTCCGCAATGATACGGAAGCCACGCTCATATAGATGCGATGAATGCCGAGCTGGTCCGGCATCAGCATTCGCTTCCAAAGCAGCGGAAGCGGTTTACATC  
CCCGTAGGCCACAGCTGACTCGTCGCGCGCGAACACGATTTTGCAGACGATATAGGCGCTGGAAGCCGCAATTTGGAAGAACCCGCCCTGGAAGAAATATCGGTCAAAACCTCAAATACG  
ACAACACGCTTTTGCCCACTACCGGCATCGCGTAAACACATATTCGCGCGGACGAGGACTGCTGCGCTTCTCATATCATCGAGAACCCATCTCGEACACGCGTTTGAAGCAATTTGTCGGACGCTG  
GCTCGGTTTGAAGAACCAATTACCTACGAATCGCTGTGCGGCAAGGCGCGAAGCAAAATCAGTTTTCGCGATGTGCCATCGGGCAGCGACCGAATACGCGCCCAAGATGCCGATTTTGGC  
CTGCGCCTCGAAGCGCGCTTGGCGCGCAATGGACGACAAACAACTTTGAAATGTATGAAAGAAATGGAGCTTCCCGTTCGCGCAGGTATGTTTGAATTGAATGCAACGCGCTGCAAAATCG  
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GGCGCTCGCCAGCAACACCCCAACCTGCAAAACATCCCCATTGCGACCGCGGAAGCGCGCGGTGCGCGCGCTTCACTGCAACCGCGCGGAGCGTCACTGTTCCGCCGACTATTC  
CCAAATCGAGCTCGCATATATGGCGCACCCTCCGGTGACAAAACCTCATTTCCAGCATTTCAAGCGCGGAGAGCTACACCGCGCACCGCGCGGAGTGTTCGGCAGTCCGCCGAA  
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GACCGCATCGGCAGCAAACTGGTCATGAGGTGACGAACTGGTCTGGAAGTCGTTGAAACCGAAGTGGATTGTCGCAAGAAAACCTGCCGAGATTATGGCGAAAGTGGACGGG  
GATTATTGGATGACCGCTGGTGGCTGAGGTGGCGTAGGGGAGAATTGGGAAGAGGCACAT

## SEQ ID 1070

MQQLTAPDGAFTGALYGVNLRLRSEYPHYCAVVFDAKGNFRHQMFPREYKATRPMPDDLRPAEALPDLVRLTGNFVLVIGQVEADDVIGTLAQGAHGLRVIVSTGDKMAQL  
VDERVTLVNMSGETLIDIEGVKAFGVRPDQIRDYALIGDKVDNVPVGVKCGPFAVKLEAYGSLQGVMEHAPEIKGVGENLQAALPQLPLSYDLVTIKFDVLDLHTELSDGIESIRET  
APKWAQLAVDFKRWGFRITWLKEAESNMNMGSTDDLPGSDSIGBQALNARIPEKRAEKATAPKLDYQAVTTEAQAALLDKLAKADTIGIDTETTSIDAMNAELVGISIAFQAGEAVIT  
PVGHSILTAPEQLDQVLRGLKPHLENPAKKIGQNLKYDQHVFPANYGIALNITAGDAMLASYIIESHLGHLELDELSGRWLGLTETTYESLGGKAKQISPADVAIGQATEYAAQDADFA  
LRLPARLRAQMDKQLEMKEYKELPVAQVLFMEHCNGVIDRAELARQSAELGAEIWKLEQEAATAAGCPFNLSFKQLQELFDKMGIPITKGLKTAAGGISTNEAVLEQLAPDYPLPKI  
ILQNRSLAKLSTYTDKLPKEMISPRDNRVHTTYAQAVALTGRLASNNPNLQNIPIRTAEGRRVRRAFTAPPGSVIVSADYSQIELRINAHLSGDKTLIAAFQSGEDVHRETAAEVFGTAPE  
NVSPQRRYARTINFLIYGMQYGLAKSLGIDNLSAKNFIDRYPARYPGVAETMQRTKEQAAAGQYVETLFGRRLLYLPDIRKNANARAGAERAIAINAPHQGTASDLIKRAMINVRNWS  
DGIGSKLVNQVHDELVELEVVETELDFVKEKLPQIMAKVDGGLLDVPLVAEVGVGENWEEAH

## SEQ ID 1071

TTGAGATGGCAGGCTTTGTGCGGATACAAGTATCCGACCTACGGCTTGCTATTGATTTCGAATCATTCGAATCGGCTATTTTACTTCCTTAAATTT

## SEQ ID 1072

LRWQAFVGYKYPTYGILLISNHSNRVYFLKP

## SEQ ID 1073

ATCGCGATATTTCCAGGGATGACAAAACGGGCGCAAAAAGCCCGATTGGAATAACCGAATCAGGCTTTTGTGATGTTCTGTTGATTTGTGCGCTAACTGCCAGCGGAGCGTCCGCG  
CCCGGTTTGGCAGGTCGGATTCTCGAATCCGACTGCTATTGAGATGGCAGGCTTTGTGCGGATACAAGTATCCGACCTACGGCTTGCTATTGATTTCGAATCATTCGAATCGGCTATTT  
ACTTCCT

## SEQ ID 1074

MRIFHGMKRAQKSPIGKSESGFVWFPCISICALTADRSVRARFGRSDSRIRLFPWAGFCRIQVSDLRILAIDFQSFESGILLP

## SEQ ID 1075

ATGATTTTGCATTATTTTGTGATGCGGATATTTACGGGATGACAAAACGGGCGCAAAAAGCCCGATTGGAATAACCGAATCAGGCTTTTGTGATGTTCTGTTGATTTGTGCGCTA  
ACTGCCGACCGGAGCGTCCGCCCGGTTTGGCAGGTCGGATTCTCGAATCCGACTGCTATT

## SEQ ID 1076

MILHYPCYADISRDKTGAKKPDWKIRIRLFCDLVLDLCANCRPERPRPVWQVGSNPTAI

## SEQ ID 1077

TTGAAAAAGATTTAATTGGAATGCGGGTATTTCCACACTTTCTCCATTATTTATCTCATTATAAAAAACATGAAAAAACCCCTGCTGCTACTCTCACTTGCAGCGGTGTCGCCGT  
TACCG

## SEQ ID 1078

LKKDLIGMRVFTLSPTIYPHYKNMKKNPCLHSHLQPCPPLR

## SEQ ID 1079

TTGCCAANTGCCGTCTGAAGCTTTTCAGACGGCATCATCTGTCAAATGCTCAAACATATGCGGAAAGTACCTTTTATACCATGTTGACCAAAATCCCGCTTTTACCTGTCGGTTGA  
TTGCGCGCGCTATCCGAGACCGCGGAGGATCTGCTGTTGTTGCGGACTGTTTCGAGCGGCTTCAGGAATGGACAAAATGCTTTGGCAATACGAGGCGGAGAGTTTATTCGCGACGAAAT  
TTGGGAAACGGAAGAAGCCATGCCGTCTGACACATCCGCTCTGCTTGCCTCGCAGCGCAATTCGCCCGGAATTCGCCAAGGATGCGCGCTTTGAACCTGTCGCGAGCGGTTTGGAAACAC  
GCTTCGCTTTCGCCCGCGCGCTTTTGGAAATCGTCGGCAACAGCGCTGGAAGATCTCGCGCAGCGCGCGCAACGCTTTACCGCTACCGCGGAGCGGTTTGGCATCGAACATCAGCGCA  
TGGAGGGCAAGGCA

## SEQ ID 1080

LPQCRLLKPRRHFPVKCSNNMPKVTFYTHVDQIPLFTCLRLIARAIIRDGGRILVWSDSFGRLQELDKMLMQYEAESPIFHEINWETREAMPSTSVLLACDGNLPRIPEGMAVLNLSDGFWNT  
ASVLPARVLEIVGNSLEDLADARERTAYRRSGFAIEHHGMEGKA

## SEQ ID 1081

ATGCAAAATCATGACAAAACCGCGCGAGGTTACACAAACGGATGAAATCAACCGATTTCAACACAGCCAATTTTAGCGCATTTTCAGCGTATCTTTATCGGAAAAATTCG

## SEQ ID 1082

MQNHDKTGARLHKRMKSTDITQPPFLAHFORLPMKIS

## SEQ ID 1083

GTGTTTCCCGACAAATACAAGTTGAGTTTGGGAAGAAAATATTTTCTGGCAAGAAAGTATGGTGTCTCAAATTCACAACCTCAGCGTTTGAAGAATTGTGAGACGACTTGTGTCAGA  
CCGAGCAAAATATCAATGACAAAATGTAGCTCCGCGTCACTGGAAGACATCCAACCATCTTGAACCTGAAACGTCCTATCAATATGTGATTTTCGCATATTTCAAACGGCGAACCGGT  
CAATATTTCACTCCTTAAAGAAATCAACAATATTTGCGCAAGGACGATTTCTTGGTACCGGTGATTTCCGTACCGGTTCCGTCCGGTAAACGCTATTTGACGCTTCCCGTATGCCCGG  
AATCCGGTGAAGGAATGAAGTGGCCCGCGTGTGCAAAATATCGGACTGCAAGCGGTTTCGACGACGAAACAGCCGTTCTGTTTCATGCTCTATTTGATCGCGCAGCAGGTTTGTGGG  
ACGGCAACAAACGGACGCAACCTATTTGCCAACCGGCTGATGATGGCGGGGGCTGCGGTATCTTGGAAATCTCCGAAATCGCAGATGCGCGGATTCATGAAGAAATATCCGCAATTTCA  
TCGACCGCGGACGATACCGATATTTCCAAGTTTGTGATCAAAATGTATATCGGCGATAGACTATTTCCGCGCGGACGAAGATATA

## SEQ ID 1084

VFPDKYKLSLEENIFLAKKVLVAQIHNLSRFENCQTTLLQTEQIINDKNVASASLEDIQTILNLKRAYQYVISHISNGEPVNISSLKRINNIVAKDDSLVFPVDFRTGTVGVTLIDGSRHAP  
NPKVEIEVARVLQNLGLQSGSTTETAVRFLYCMRQVFWDNKRTATLIFANGLMAGGCGILEISEMQMFRNEKLSAFYRTGDDTIDSKFVYQNCISGIDYFGADEDI

## SEQ ID 1085

TTGCTTCGCTTCCGCTACTATTTTACTGTCTGCGGCTTCGCCGCTTGTCTGATTAAATTTAATCCACTATAGATTTCGCCGACTCGCGCAACATGGGCTAAAAATCAATTTGACGG  
TTATCAGACGATGGAATAGGCACAAAGTGGCAGAAAAGGGGT

## SEQ ID 1086

LPRLAVFLLSAASPCCDLNLHRYFRPLAEHGLKINLTVIRRSRHKVAKGV

## SEQ ID 1087

ATGAAAAACACCGACAAACGGCAACCGAAACACACCGCAAGGCCCTAAACCGCGCGCATCCGCTTCTCGCGCGCTTACTTTAGCCATATGCTGTGCTGCGCATTTGCCCAAGCCG  
GGCGGGACACACTTATTTCCGCATCAACTACCAATACTATCGGACTTTGCCGAAAATAAGGCAAGTTTCAGTCGGGGCGAAGATATTGAGGTTTACACAAAAGGGGAGTTGGT  
CGGCAATCGATGACGAAAGCCCGATGATTGATTTTCTGTGTTATCGGTAAACCGGCTGCGCGCATTTGCGCGCGATCAATATATTGTAGCGTGGCAGATAACGCGGCTATAACAAT

[illegible]

**SEQ ID 1088**

[illegible]

**SEQ ID 1089**

ATGCCGCTCTGAAGTCGACGGTTTCGGCTTTCAGATGGCAATGCCGGCTTGTGTAAAAAGATATTCGACACCGCACGGCACAAAACCGTCCCCCGCATTCGCCCTCCGGTTCGTTTAAAC  
CCGAAAAACGGCGGGGTTCCGACCGAAAAAGAACGGGGATAAAG

**SEQ ID 1090**

MPSEVRRFGFOMALPACVKRYSDTARHKTLPRI PPPVGFYRRKRRGSDRKGTGIR

SEQ ID 1091

SEQ ID 1091

TTGGGAGGGCGCGGCTTCCGCTTCCGGGCGGCGCGCGGGATGTGGCTATATGTGCGGGTTCGGCGTATTTTGGCGCTTCGTTCGGAGATGGTCCAGGGAAGGGCGGGAAGGAAAAAAGGG  
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GGCTGTAAAAACCGACCGGAGCGGGAATGCGGGGCGAGGGTTTGTGCGCGTGCCTGTCGGAATATCGTTTACACAAGCCGGCAATGCCATCTGAAGCGGAACCGTCGGACTTCAGACGG  
CATTTGCTA

SEQ ID 1092

LGGRRFPFRFAARGMWLYVRFPGVFCRFCSEMVQGRAGRKRRGFLSTRSRNEWVHAKGIIILNTKSYHTFLLYPRSPFSVGTPPPSAVKTRRRRNAGQGFVPGVGLSPYTTSRQCHLKAEPDSFRR  
 HLL

SEQ ID 1093

SEQ ID 1093  
GCTGTCCTCCGCTACGCTAGCCGATATTCCTCGAGTCTAACGGCAAAGGGGAATACAAAGTCTTTACCGCTTATGTTAAAGGCAAAGCCACTGCCGGCAATTTGAAAGAAAAA

SEQ ID 1094

VSAVTVADI PRSNGKGEYKVFYAYVKGKATAGNLKREK

SEQ ID 1095

SEQ ID 1095  
ATGTCGGAATAAGTTCCACGATATGCGGCAGTCGCGACCGCGCCCGGACCGCGCGCGCTGGGGCTGATACGCATATCGGGGAAAAAAGCTGTGCCGATGGCGAGGCTTTGTGTGGGAAAA  
CGCCCGAGACCGCGCGGTGGCAACCTATGCTGATTTACGCGACGCGGACGCGACGCGCAATCGATAGCGGGCTGCTACTGTTTTTCGCGCGCGCGGCAAGTTTTACGGCGGAAGATGTCATCGA



GCTTCAGGGACACGGCGGGCCGGTAGTGATGGAGATGCTGCTGAACCCGCTGTTTGGAACTGGGCGCGGCGCTTGCCGAGCCGGGCGAGTTTACCAAAACGTGCGTTTTAAACGCAAAACCTG  
GACTTGGCACAAGCGCGAAGGCGTGGCGGATTGATGACACGATCCGGCCGTTTCGGCGCGCGCTGCGCGTTGCGCTCGCTCAAGGGCGATTTTTCGCGGCGGATACACGTTTGGTCGAAC  
CGTTGATTACCTTCGCGGATGCTGCGTGAAGCGGCGCTGGATTTCCTCCGAGGAAGACATCGATTTCCTGAAGCGGCGGACGCAACGCGCAAACTGGACGGCTTGGCGCCGCGCGGTGGATGA  
TGTGCTTGCCACGCGCAGCAGGGCGCGATTTCACGGAAGGCTCGAATGCTGATTTGGTGGTTCGCGCGGCGAATGTCGGCAAGTCCAGCGCTGTTGAACCGCGCTGGCGGGCGACGAAGTGGCG  
ATTGTTACCGATATTTCGCGGAACGACGCGGACGCGCTCAGGGAAACGATCCTGATTGACGGCGTGGCGGTGCATATTGTCGATACGGCAGGTTTCGCGGAGACGACGACGTTGGTCGAAC  
GCATCGGCATCGAACGCGAGCCGCAAGCCGATATCCGAAGCCGATGTCGCGCTGTTGTTGGTCGATCCGCGGAGGTTTGAATGAAAGACCGCGATGATTTCGATACGTTGCCGTGGA  
TTTGAAACGCATTGAAATCCACAGCAAAATCCGATTTCGACGCAACGCGCAGGCGGTTTCGTTACGGGCGCGGAACCGCTATCGCTGTTTCGCGGAAACCGGCGACGCGCTTGGACGCG  
CTGAAACGACGCTGTTTGTGCGAGGCGCGTGGCAGGCGCAAGCGACGAGGCGCTGTTTTCGCGGAGCGCGCACCTGATCAACGCACTCAAGCGCGCGCAGGAAGAATTGTCGCTGGCGCGCTT  
TGTGCGGCAACCATCAATCGAGCTGTTTGCAGAACCTTCGCGCTGGCTCAGTTCGCTGCGCGCAAAATACGGGGGAATTACGCGGACGACCTGCTGCGCGTGATTTCGAGGTT  
TTCGATCGGAATAA

**SEQ ID 1096**

SEQ ID 1096

MSDNVPTIAAVATAPGRGGVGVTIRISGNLLPMAQALCGKTPPEPRVATYADFTDADGQAIIDSGLLILFFAAPSPAFGTEDVIELCGHGPPVMEMLLNRCLELGALEAETGEFTKRAFTLNDKL  
DLAQAEQVADLIDASGRSAARLALRSKLGDFSRRIRHGLVEGLITLRLNVEALDLPFEEIDFLEAADARGKLDGLRRAVDDVLANAQQGAILREGIANVVLVGAPNVGKSSLLNALAGDEVA  
IYTDIAGCTTADAVRERLIDGVPHIVDTAGLRETDVVERIGIERSRKAVSEADVALVLDPREGLAEKTRMILDTLPSDLKRIETHSKSDLHAHAAGGFGTGASTVIALSARTQDGLDA  
LKRTLLCEAGWGESEGLFLARTRHVNALKAAQEKSLAALCGNHQIKLFAEHLRLAQVACGEITGEFTADDLLGVIPSRFCIGK

SEQ ID 1097

SEQ ID 1097  
ATGACGATATTTCAGTTTCTGTTTTGATTTTTTGTGTTTTACAGGAATGACGGGCTTTCAGTATTGAAAAAGTTGCCGTACCGGCCGA

SEQ ID 1098

HTIFOF SVFDFFVFTGMTGLSVLKKVAVPRR

SEQ ID 1099

SEQ ID 1099  
ATGACGAATTTTAGGTTTCTGTTTTTGGTTTTCGTCCCTGTGGGAATGATGAAATTTTAAGTTTTAGGAATTTATCGGAAAAACAGAAACCCGCTCCGCCGTCATTCCCGCGCAGCGCGG  
AATCCAGCCCCGTCGGTAGCGGAATCTATCGGATAAAACGGTTTCTT

SEQ ID 1100

MTNFRFLFLVPCPCGNDEILSFRNLSEKTETAPPSFPRRRESSPVGTETTYRIKRFL

**SEQ ID 1101**

SEQ ID 1101  
ATGATTGGGTTTCAGACGGCATTTTTTAAGGTGGCAGCGCGCCCCCTTTCAGGCTGTATCAAGACCCAATCCCGCAACTCTCCGTCATTCCCGCAACTCTCCGTCATTCCACGGGAAGT  
GGGAATCTAGAAACCGCAAAGCCACGAACTTATCCGAAACAAACAGCAACCTTAAAAATCGTCATTCCCAAGGAAAGTGGGAATCCAGTTCGTTGAGTTTCAGTTTATTTAAAAATAAATTTGA  
AACTTTAATCCCATCATCTCCCGCAAGACGGGAATCCGGAACG

SEQ ID 1102

SEQ ID 1102  
MTIVSTGIEYGR~~TAAP~~EOACTKPNPATLRHSRNSPSFPGKWESNAKPOELIRNNSNLKFVVIPTKVGIIQFVEFQLFKINFETLIPSPFRKRESGT

SEQ ID 1103

SEQ ID 1103  
ATGTGCCAATGCCCTCTGAAACCCGATGATTTTGGGTTTCAGACGGCATTTTTTACGGTCGCACCGCGCGCCCCCTTCAGGCTTGTACCAAGCCCAATCCGCAACTCTCCGTCATTCGGC  
AACTCTCCGTCATTCACGAGGAAGTGGGAATC

**SEQ ID 1104**

MCDCRIKPDGIFRRHFLRSHRRPLSGLYOASRNNSPSPFPOLSVIPREVG

**SEQ ID 1105**

SEQ ID 1105

ATGCCCATTCCTTCAAAACCGTATTGGCTGCCGCCGCATCGGCCAAGCGTTTCCGCGCTTTGGCGCAGACCCGCCGCCAGTCCGCCCAAACCGCTGAACGAAATCACGTTACCGGCA  
CGCAAAAACCTTCAAAAACCTCGCGGAAGAAAAATCCCGCGCAAAACCTTAGACAAGCTCTTTGGCCAAAGCAGCAACACGGCTTGGTGGCTACGACCCCGGCATTTCCGTCGTCGAAGCGG  
CAGGGCGGGTTCTAACGGCTTTACCATACGCGCGTGGACAAAGACCGCTCGCCATCAACGTTGACGGGCTGGCGCAGGCGGAAAGCGCGCTTCCGAAGCCTTCCAGAAATGTGTCCG  
GGTACGGGCACTTCAACGCCAACCGCAACACTTCGAGCGCGGAAAACTTTTCGGAAGTAACCATCACAAAGGCGCGGCACTCGCTCAAAATCCGGCAGCGCGCATTTGGCGGGCGAGTCA  
ATTACCAAAACAAATCCGCAAGCGCATATGTGTTCCGAAGACAAGCCCTACCAATTTGGGGATAAAGGCGCGCAGCGTTCGGCAAAAACAGCCAAAAATTCAGCAGCATATACCGCGCGCGTCA  
GCTCTTTGGTTTGGATGCCCTTATTGGTTTATACCCCGCGCTTCGGCAAGAAACCAAAACCCGCTCGACGAGGGCGATGTCCGAATTAATAAACGACGAGATATGCTTTTGACCGCGCCAAC  
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GAGCTACCGCCCGCGCACCGCGCTGCAATACAAAACGAATTTGGAACACAGGCCGCTGGGACAGCCTCAAGCTCGCTACGACAAAGCAGCGCATCGATATGAACACTTTGGACTTTGGGACATC  
CGAAAAATTACGATACAAACGGCATCAACGGCAGAGTTTACCATTCGTTCCGGCATATCCGCAAAAACACCGCGCAATGGAGTCCCGATTTTGA AAAACAACTCGACTTTTCCAAAGCG  
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GCTGATCGAAAAACCGGTGCAAAATATAAATTGGCTATTGGAACAATGTGTTTACCTTGGCGCGCAACGACGCTTCGCGCTGAATCGCGGCGCATCGTACGACGAAACGACGACGACGCGG  
AAAGAGTATCCGAAATACACCAACCGGCTTCGGGGCGAGATTCCTCATTTGGCTTCGGAACGCGCGCACGCGGGCTTCAGTACGCGCACAGGGTTTCGACTGCGGGTTTACCAAGCATCTGC  
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AAACTGGGAATTTGGSCCTGCGGGGCGAGCGGCAAGCTGCGAGCTTCAAGCTTTTCGGCTTCAAAACCAAAATACCGGAGCTTTATCGAATTGACGTATATGGGCGCTTTTCGTACAGACGATAAA  
AACAAACCCAGATACGCCCCGCTTTCAGACGCGACGGCATTTGTGAGTTCGCGCTTTTGGCAAAACCAAAACCGCACCGCGCGCTTGGTGAAAGGCATAGAGTTTAAACGGCACTTTGAAC  
TCGACAGCATCGGGCTGCCAAAGGGCTGCACACCGGCTTCAACGTTCAGCTACATCAAGGGCAAGGCAACGCAAAACAAAGGCAAGAAACGCGCATCAACCGCTTTTCGGCTGGAGCG  
GGTTTACAGCCTGGGCTATGACGCGCTTCCAAACGCTGGGGCGTCAACGCTTACGCGCGCGCACCGCGCCGCGGCAAAAGGCTTACGCTTCGCGCGCGCGGTACACATTTACCAACAGCAGTACTACA  
TGGCCTTATGCCAAACACAGCAAGGCTATACGCTGTTCGACCTTTTCGCTTACCAATCGGCAACCTGCAACCTTACGCTTACCTTCGCGCGGCGAGGCTACAAATTTACCATTCGAAGC  
CTTGGAATGTTTACGCGAGCATCGCGAGTTTCGGCACGGTCAACCGCGTCAACAAACAAACCCACGCGCGCATCCAACGCTTTACCTTCGCGGGCGAGGCTACAAATTTACCATTCGAAGC  
GAAAGTTC

**SEQ ID 1106**

SEQ ID 1106

MPFPKPVLAALAAIAQAPFAPAADPAPQSAQTLNEITVTGTHKTQKLGEKIRRKTLDKLLANDEHGLVKYDPGISVVEGGRAGSNGFTIRGVDKRVALNDVGLAQAESRSEAPQELFG  
AYGNFNANRMTSEPEPSEVPTTKGADSLKSGSGALGGAANYQTKASADYVSEDKPYHLGIKGGSVGKNSQKPFSSITAAGRLPLGLDALLVYTRRFQKGTENRSTEGVEIKNDGTVFDPAN  
PSPSRYLITYKATGVARSQDPDQEWNVKSTLFLKLYNFNDRNRIGWIFEDSRTDRFTNELSNLWGTGTTSAATGQYRHRQOWSYRRRTGVEYKNELEHGFWDSLKLYDRQRIQDMNTWIOI  
PKNYDTNGINGEVYHSFPHRTQNTAQWADFEKQLDFSKAWAAQYGLGGGRGDNANSDSYPAKLYDPKILASNQAKITMLIENRSKYKFAYNWNLPHLGGNRFLMAGIKYDRKNSSA  
KDDPKYPTTARQQIPLHLSERAHAGFSYGTGDFWRPTKHLHLAKYSTGFRAPTSDETWLLFPHDPFLYKTNPELKAEBKAKWELGASGKGSFGLKSGFTTKTRFDIELATYMGVSSDDK  
NNPRYAPLSDGTALVSSPVVWQGNQRTAAWVKGIEPNFGTWNLDSLGLPGLKTLGNVSYIKGKATQNNKGETPINALSPWTAYVSLGADYKCRKWGVNAYARTAAKKPSDTVHSHDDLNKP  
WPYAKHSAKYLTFDLASAFLNLQNTLRAAAVITFKNGQYTWESLRSIREPGTVNRVNNKTHAGIQRTSPGRSYNFTIEAKF

SEQ ID 1107

SEQ ID 1107  
TGTTTAAGGCAAGCCACTGCCGGCAATTTGAAAGAAAATAACGCACACGTCCTTCGGTTTTCGGTTCAACGAAGCCACGATATCGGTTTTAAGGCAGAGTACGCCGAAGCAAAAACG  
ATGCAGACGCACAAAAGAGGGAATGCACAC

## SEQ ID 1108

C\*QSHCRQFERKITHVHRFSFNERHMRPKARYARSKNDADDERGNAH

## SEQ ID 1109

ATGAATGACTACACGCGAGCAGCTTCAAGGTAAGAAAGACTACCTTAAACCCCTTTTTCAGAGTTGGATGTTCTGAGTGGGAAGTGTACGAATCTCCGACAAACACTACCGCATGCGG  
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CAACTGCCGTGATCCCGAATGATGAGTGGATGAAGCGCGCGCAAGCGTTACAGCAACAGTTGGATATTTCCGTTATCCGCGGAGCAGGGGCGAGAAATGCTGGTACCATGATTTAC  
CAGAAAGGCTTGATGATGAGTGGATGAAGCGCGCGCAAGCGTTACAGCAACAGTTGGATATTTCCGTTATCCGCGGAGCAGGGGCGAGAAATGCTTAAACAGGACTATGTGACGG  
AAACCTCGCGCGTCCGCGACCGCGATTCCACTACCGCCAAATCGAAGGCGAGTTTACCAGCGCAATGCGCGTGTATGCGGAAATGCTCGAATGGCGGTGCGCGCGCGGAGGCTT  
GGGCGCGGACCTGCTCGAATGATTTGCGGCAACGCGCAATTCACCCGTGCGCGTGTCCGATATTTCCGACAGGTTTTCGCAACCGGAAATCTCCAAACCTCCGTAGTGGCGCGCAATGG  
AATATTGAGGCAACTGGATAGGCAACATCAAAATCGCCGCGCTGTCTGCTGAGGAGTTTACCAGAGCTATACCGGAAACGTTAGGTTTACAGCCTTAAGGAGAGCGGATTTGTTTGA  
CGGATTACGCACTTTTCCACTATTTTTCGTCGATCCCGCGTGCAGCATGATGAGGAACTTTGAAGCTGGTGTCCGAGTTTCGCAACATCATCTACATTTCTGCAATCCGGAACGCT  
CGCGCCAATTTGACACCTTTGACGGAACCCATACGCTCGGACGTCGCGCGCTTGTTCGACCAATTCGCGTTTACGCAACATATCGAAGCGCGCTACTGTTGAAAGAAATATCCCT

## SEQ ID 1110

MNDYTTQQLGKKDYKFLFAGLDVPEWEVYESPDKHYMRAREFRWHEGEMFYAMFEKQKASGASLIRCDRFDAAEAVNCLMPELLIAVAQAQSAELRNHWYAVEFLSTLSGELVRLITY  
HKRLDDEMNKAQAALQQLDLSVIGRSRQKIVLRQDYVTEFLRVGDRDPHYRQLEGSFTQPHAAVCRKMLEWACRAAEGLDLLELYCGNGMFTPLSRFTFRQVLATEISRTSVSAQNH  
NIEANWIGNIKLARLSAREFTPEATYTGKREFTRLKESGIVLTDYAFSTIPVDPFRAGIDERTLKLVSQFDNIITYISCNPETLRANLDTLTETHTVGRAALFDQFPFTHTESGVLLKKLL

## SEQ ID 1111

GTGGAATTTAGCAGAAACCCGAAATCTTCAGGAACAGCAGCAGGCGCGCAGTTATTTGCTGTGCGGACAAAGCACCAGCAGCAACACCGCGGCACATGCGCTCTCTCTGCTTTGG  
AAGAGGTCAGAAATTTTCGACACCAAAATCCCGACGGAACAGGTTTCAGGAGTCGCGCTGCTCCGCTCGCAAAAACCGACCGCGCGCTGAACAAAGCGCGCGCGAGCGCG  
CAATGGGCGCAAAATCAAGAAACGGTCAATGTTGAGCTTCACGCTTTGATGAGCGCAAGCAGCAGCGGTTGCGGAAGCTTTTGCCATCGCGTTCCGCAACGCTGCATATCTGTTGAC  
CGCTACAAAAGAGCGCAAGCGCGCAAAATTTCCAGCGCTGTTCCAGCGGACACAGAGCGCGCTCAAGAGCGCTGCGCGTTCGCGCAAGCTTCGCAATCTGTTGCGC  
CGCGGACTTATGGCAATGCGCGACCGCAACGAATGCAAGCGCTGAGTTTCCTGCGCGTACCGCCAAAGCGCAAGCGGAGAACTGGGCGCGCAGCGCAAAATCATCGAAAAGACTACATCAA  
AGAAACATGGGTTGCTTTGTTGCTGCGTTGCGAAAGCGAGCTGCAAGACCATATTTGGTTGAAGTACGCTATTTGCTGCGCGCGGACAAAGAGCGCGCTGTTGTTGTTGCGCAAA  
GGCATTAACCTTCGACACCGCGCGCATTTCCCTCAAACCGCGCTGAACATGAGCAAAATGAAGTTTGACATGTCGCGCGCGCAACCGTTCATGACACCTTTCTGCGCGCGCGTCAAACTGC  
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CGATGCGCAAGCGCTGATTTGTTGCGACGCGCTCACTTACGCGGAGCAGTTCAAACCAAGCGCTCATGATGTCGCGCAACCTGACCGCGCGCTGCATCTGCGCTTGGGCGCAGAT  
GTCAGCGCGCTGATGGCAATTAATCAGGATTTGATGACGCGCTGCTTCCGCTTCTTCAACAGCTGAGCAGCAAAAGCGTGGCACTGCGCTTCTTGAAGCTTCAAGAGCTGACGCTCAAT  
CGAATTTGCGGACATCCCAATATCGGACGCGCGCGCGCATATACCGCGCAACATCTCTGCTTATTACCGAAGCTTACCGTGGGCGCACCTTGACATGCGCGGTACGCG  
GTGGAATCCGAGCGGAAAGGTGCGACGCGCGCGCGTACCGCTGCTGATGAATATCTGCGGAATCTT

## SEQ ID 1112

VEFSTKTEILLQEQAGQLFVCAKAPENHTAAHALFSALEEGQNFSDTKIPTINGLQAVVVRLEKTDRAALNKAABAAKWAQNETVNVVHAFDEAQAQAAVAEAFALAFGNAAYRFD  
RYKKEAPKAPKQAVFHSAAEAAVEALRVAEQVYQSLCRDLGNAAPNECTPEFLARTAKAEKLGHAHAKIIEKDYIKENMGSPWVAKGSVEDPYLVLSYFGAADKEAPVVLVGH  
GITFDGTGILSLKPLNMDKFDKGAATVISTFCAAVKLQPLINLAIATCENMPSGAANKPGDVVSKMGLTIEVLNFDABGRILLCALTYAEQFKPAVIDVATLGTACTVALGHD  
VSGVMGNQDLIDSLAASYNVDDKAWQLPLFETYYDQLKSNFADIPNIGTFPAGTTAATFLSYFTTEGYPHALDLAGTAWKSGAEGKATGRPVPLMNYLRNL

## SEQ ID 1113

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GCAGACGCTCGCTTCGATGCGCGCGCGCGCAAAACACATCCGCGCATTTCCATTCCGCGAGCGGAGTAGAAAAAGACTATTTCCGCTATAAATCAAAAGAAATCATTCATCTTCAAAACACC  
CGGCGCGCGCGCAATACGCGCTTTCATCTACGCGGACCCATAACCGTCAGCTACTCTCCCGGATTTCAAAATTCGCGACCGCGCAGCGCGCTCGCGACGCGGACCGCGATC  
TTTATCTGCTGCGAGGACTCCGCGGCTACTTCGATGCGGAAATTAACAAACAGATTATAGAAATTCGCGCGCTGGATAGGCTCTAACGCGCAATTCGACCTCTTCCGCGCGCGCTTCC  
CGCTCGGCAAAACCGCGCTCTCTGCTCTCTACGCGCAGCAGCAGCGCGCAACCGCATTTGTCAAAGGGTAAATCACTTATCAGGTTTGGGCGATCCGCGTCAGAAACCGGCAATTTGT  
TACTTCTCTTATACGCGCGCGGAAAGCGGTTCTTATATGGGACACTTGCCAAATACCGCGCTCTCTTATACCGCGCAATTTCAACAGCAACACTGCGAGGCAAAATCTCGGC  
AACAGCGATTACGCGCGGATGTTGATATTCAAAACGCAACGATTACCGGTCGCGCTTTCCGCGGATGCCACGTCGCGCGGAAAGCGGCAATTTGAAGGCAAGTTTTCGCAAGT  
TCGCGCACCGCGCAGCAGCAAGTCAGCATAGCGGCAAAATCACCTTTGACGCGCAGCGCTCCCTCGATACCGTATTCGCGGTGTGAGTTATGAAAAAACTTGATGACACCACTCA  
AGATAACCAACCTTACTTAACAA

## SEQ ID 1114

VSIPTATPLPAGEVTLSDNGNIENINTAGAGSASDAPSRSRSLDAPQNTSGISIRQREVEKDYFGYKSKETSFIKTPGGAQVALSSYADPITVSYSPPDFKIPDRHAGQRLADGSRI  
FICCSDSGATSYAETIKQDYMKPGANIWPNGEIDLPAAGFPVKGTPPPAFSTGSSSTPEALSKGIITYVWGLIRVRNGQVFTSSYTPKSGSYGTLANTPVLSFTANFNSTLAGKILG  
NSDYGFVDVIGNATITGPTPSGDATSGGSGKLEKFKFKASTRSSSEVSIGKTIPTDGRSLDTPVGGVSEKLLDTSQDNHLATQ

## SEQ ID 1115

GTGCGGTTCCGCTACCCCCCGGCAAGCGCGCAAGGCGCGCGCAAGCGCGAGTAAGGCGAGGCTTTGTATTTCACTCGCATACTCAATCTTGATGATGAT

## SEQ ID 1116

VRFGYPPPAQAAAAASGSKRALYFIAYSILMHY

## SEQ ID 1117

GTGCTGCGTTGTGTCGCGCGTTTCTACCTTTGTTTATATAGCGGATTAAACAAAACCGGTACGCGGTTGCCCTGCGCTTCCGCTACTATCTGTACTGCTGCGGCTTCGTCGCTTGT  
CTGATTTTTGT

## SEQ ID 1118

VPAPVCRVSTFVYSLTKTGTALPRLAVLSVLSAASSPCPDFC

## SEQ ID 1119

TTGCCGTACTATCTGACTGTCTGCGGCTTCGTCGCTTGTCTGATTTTGTATTAATCCACTATATGATGCGCGCGTCCGCGCGCGGCGGCTTCGCGCGTTCTGCGCGCGCGGTCG

## SEQ ID 1120

LPYYLYCLRLRLVLFVNPFLYDAPRPPRVGLAFLPPPSGGVF

## SEQ ID 1121

GTGGCTCAAGCGCAGGACATTCATTCGCGGTTACGCTGCGGCTCCGTCGAAATAGCGCAATGCTTTGTAGTTGCGGTGGGCGTAAGACGCGGCAATCCGCTGTTCAAACCGCG  
GTCCGCGCCACTCTGCGCCCAACGATATGACGCGGTTGCGCGGTAGCGGCTTGTGACGCGCGCGCCACCGTTTCGCGTTTCGCGCAAAACCGCGCAAACTGCCAGCGCGCA  
ACAGGTTGCGGAGCGCGCAACCGCTTGCAGCGACATAAAGCGGCTCTGCCAACCGCTGTCGCTTCCGCGCGCGCTGTTTCGCGGTAGCGTTGCGGTAACGTTCCAGCGACAC  
CGAAAGCTGCGACCGCGGCTCAGCGGTAAGATGCGGCAACTGCACACCGCGCGCTGCGCGCAGCATATACGCGCAAGCGCGGCTGCGCAGCGGTTTCGTTTTTCGATCAAAGCG  
TCGCTACCGCAATTCGCGCTGATAAAGCGCAAAACCCCAACCGCTGCGCGCGCATTTTATCTGCCAGCCCAATAAGCGCTCCGCAAGCATCTCATTAAGCGGATTTGCGGCTGA

AATAATAGCTTGTGCCCCGACATTTGGCGGGAAACAGCAGATAATGGTTGTGCCGACGCGAGTCAGCTTTTCCGCCCCGGCCCTCATATCCAACCTGCCGACGGACAGGTCGGGTAACTGTCGATATCCGGCTGCCGCGCCCTGCAGGCAGTATTGGCGGCGGGCATTTGTGTGCGGTTTTGTGTCACAGAAGGGCTGATGCGGCCGGAATAATGCCAGCCGTCAGCCCCCTCGGTTTTTTCGGGAAACGCCCAACATTTTCCAAAAACCGGCGCGGCAATCCAATTTGCGGCTTCGCGAAATGCAGCCCTGCCGACTTCAGCCGGAAATCGTCAAACTCCGCGCGCCGCAATCCAACAAAACCCGCTGCTGCGCGCATATATCCCTGTGCAAGCGCCGATAGCGGCGCACCGCTCCGCGGGCTTCCCGCCAAATTTGCGCAGCAAGCCGCGGCTCGCGGTACAACACCGCATATATATCCGGCAGCTTGGCATACAAATCCGCCAACGAGCGATCAAAATCCGCTCGATTCGCGTTCGCGCGCTGCGCGCGCTGTCGCAACAGTGTTTCCAAACGTCAGCAGGAAATCCCGTCGATTACGCGGAACCCGCGTTTTCGCGCAGAAATCCCTTCCGGCGGATCCGCGGCAACCTTCGCGGCGCAAGCTGGGCGGACGACGAGCGCGCATATCCGATACACACTATCCTTCAATTTGCCCTTCTTAAAAAACACCGCCGACGCGGCGGCAGAACCGCGCAAGCCCCACGCGCGCGGACGCGGCGCATATATAGTGGAT

**SEQ ID 1122**

SEQ ID 1122  
 SQQSQSDIFPAVTLRLRRKCRNAPVVAVGVRGRGNPAVQRTARPAPLLRPTMDGVAAGVGIVDRAHRHFAFRHKPKLPAAEHGCRAAQPCQORHLKVLPTVVAFRPALFAVALVTFQEH  
 RKLRPAAQAVRMRQLHTRPVVRQHRRKPAVGRGRFPFRILKAVATRLRLKKQNPRLRPRIPTILPAQISPAESTIVSRFAEETIACAPDIGABQQTMMVVRQSRQLPFRGLIIQPCSPTRDRSG  
 AAYFAAAALQAVLRRGIVGVVHRRADAARKMPARQPLRFPFETPHIQNRRRQIQFCRLRKMPCRLQPEIVKLRRRQIQNPLVCRIIPVQPRFARHRLRRPSRQFRQPSRPAVHQHI  
 IIRQLGIQIRQSDQIRLIIAVERVAQNVFQQLRARQILPVDYARTAVCGRIIPFRHRSRPTLRSLTLAGQRRTIVPNVQAGGIRADRTEFTQGTQPAYPIHTILQFAPLKKHRTAAAE  
 TPQAFRAADAHHVID

**SEQ ID 1123**

ATGCTTTTAAAGCAAGCAAATTGAAGGATAGTGTATCGGGATATGCCGGCTGTGTCCGCGCTGTGTGTTGGGGTCGGTTCGGCGCGTATGCCGCCGGCTGCCCGACGTTCCGGACG  
ATGCCGGCTGCTTCGCGGCCAGCGTGCGGCTCGGAGGGTTGGCGGGAATGCCGCCGAAGGGGATCTGCCGCAACCGCGGTTCGCGCGTAATCGACGGGGATTCCTGCTGTGTCCG  
CCCCAGTTGTTGGAAACAGTTTTCGCGACGCGCTCAACGGCAATCAGCGGATTTGATCGCTTCGTTGCGCGATTTGTTATGCCAAGCTGCCGGATTTATGATCGCGTGTGTGTACGGCAGG  
GCGCGGGCTTTGCTGGGCAAAATTGCGGGGAAGCGCGCGGAGAGCGGTGGCGCGCTATCGGGCGTTGACAGGGATAATCGGCACAGCAGCGGGTTTGTCTGGATTTCGGCGCGCGCGAGT  
TTGACGATTTTCGGCTGAAGTCGGCAGGGCTGCATTTTCGGAGGGCGCAAAATTGGATTTCGCGCGCGCGGTTCGCGAAAATATGGGGCGCTTCGGGAGTTCGAGCGGCTGACAGGG  
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ACCGCTTCGCCACCGCGCGCTTCGCCGCTATATGCTGCGCAGCGGGCGGGTGTGCAATTGGCGCATTTCTTACCGCTGAGCCGCCGGTTCGCGAGTTTCGGTGTGCTGGAACGTTTACCGC  
CAACGCTACCGCGAACAAGCGCGGGCGGAACGCAACGACGGTTGGCAGGACGGGCTTTATGTGCTGTCGCTGGCAATGCGCTTTCGGCGCTTCGGCAGCTTCGCGAGTTTCGCG  
GGTTTGTGCCGAACCGCAAAACGGTGGGCGCGCGGCTCAACATGCTCCGCTACGCGCCGCAATGCTCGTTTCGGTGGCGAGGATGGGCGGGACGGCGGTTTGAACAGCGCGGAT  
TGCCGCGCTTTCAGCGCGACGCAATCAAAAGCAITTCGGCGATTTCGACGAGGCGCAGCGTTAACCGCGAATGGAATGTCTCGCTGGCTTTGAGCCACGACAAGTTGTATACAAGGC  
ATCGCTGCGCAGCTTGAACCTACCGCTTCGGTAAGACGGAAGCAATTGCGCGTATGCAGAAACGCGCAACAGCGAGGTGTTGTGTGCGCGGATTTGCGCGTTT

**SEQ ID 1124**

SEQ ID 1124

VFFKBEGLKFSVYVRVRLCAALCVWGAVGATYAGLPDVRDDAAALRAQRAAAEGWAGMPPEGDSAANGSRVIDGDFLLSRPQLLEHVLRLDALNGNQADILIASLADLYAKLPYTDVAVLYGR  
ARALLAKLAGRPAEAVARYRALHRDAAADERVLLDLAAAEFDDPLRKSLAGLHPAEAAKLLDPAVPLENVRGRFKTKTGLTGWHPFGGSGISPSVNKNNAANAPQYCIQGGGSRICSVTGPVRA  
AGLYDEAGAELKALADNHLYLLFRANVGTSYYPFRKSAYDAPGRAYLGMQYKNARQTVGVLPFYQAQLGSGSDGFDAKTKPPADRRALPYMLAHGACGVQLARSYRLSRRSQLSVLSERYR  
QRYREQGRAERNDGWQDGLYVSLARLGGSATVGVQWQARFAPVFKRETVGGAVNNAYRRNAVHIGWAQWGGTGGGLNSRLASAYAHNRNYGLIAAFSTEAQRNNVNSLALSHDKLSYKG  
IVPTLNYRFGKTESNVPTAKGRNNEVSFVADNRF

**SEQ ID 1125**

SEQ ID 1125  
ATGGCTGCCGGTGATGCCGGTTATACCTACACCCAAACGGGCGCGGAATCCACACGTTTCCGTGGCGGTTTGGAGCGTGTCCAAGTTAAACGTTATCTGGGAGAAAAATGCTCGCGCTACG  
CTCTGCCAAAAAGCGAAGCGCTTCACCTGCAAGCAGATGGTGAATCCGTCAAACCTTGGCGAAGGCTGGTTCTCGAAGCTA

**SEQ ID 1126**

SEQ ID 1126  
MDAIVAGVTYTORGGESTREFGGLERVQVKRYLGEKCGYACPKSERFTLOADGEIRONLGEQWFLKL

SEQ ID 1127

SEQ ID 1127

GTGCTAAATCCACGTTTATTCTCCTGATTAGACGGTTGTTCGGTAGTTTTCAGACGGCCTTTGCGCTCAAAGAACCCTCTGAAGACGGCTGGCAGCATTTGTACCCCATTTTTTGAAGCAAC  
GTCCTGAACCTTTGCGCGGACATCCGCCGCGCCGAACCGCTTACCGCCCCC

SEQ ID 1128

VLNSTFILLIETVVGSFOTAFRSKDRDKTAGTIVPHFLKHRLKPCADNPPAPNRLPPP

SEQ ID 1129

SEQ ID 1129

TTGCCCCGAAATGCGCATGCGCTTATTTCGCCCGCTGTGTCAGATGCGCGTCAGCGAGCGCGAAACTCTATCAAAATCATGTGGAAGACCGGTTTTTTCGCTCCCGAAGAACTCGATGCTTTAG  
ACGGCGCGCTGCAATCGGATGCGGAAAGGGCTGCAATTCGGTGTGTTTTCGAGACTACGAATTCGGTTTTCGCCGTGATGGGGATGGAATTCGAACCGCGCGGCAACATTCGCCCTGCACGTG  
GTTTTCGCGACTGCGCGGACACCGATGCGGAAGCTGGCTTGCCTGCACATTCAGACGGCGCTCCCGCGCGGCAATTTCCACGCGCGCAATCTCTCGGTATTCGAAACCGGATTAACCTGCACCGCATC  
CGCCAAATCCAGAACCATTCGCGCGCGCGGACACCTATCAAAATCAACTACCAACCCGCGCTGCACCTGCAAGCTTACGCGAACCCTGTCAGCTCTACGCGCGCTGCGCGACCGCGTCC  
CCTATGCGGTATTTGTCCTACCTGCCCCGATGAAGCGCGGCAATTCGCGGTGGACGCTGTGTTCTCGCCCGAACTCTTCTCAACATCGCTTCAGACGGCACCATCAGCAGCGAACCGATGAG  
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AAAATCGCCCAAACCGGTAAGTATGCGTACCGGACCGGTTTAAAGTATCGGTTTTCGCGACGCTTTCGCGAGATGACGACGACCATCTCGGCGCGAAGCGCTGCCGGACACCTCGTTCGCGG  
ACACCTTCGCGCGCGCTTTCGCTGCGAGCAATCCAGCAACCGCGCGCGCCAAAGAAATGAGTATGCAGATTATCGAATCGCTCGAAACCGAAGCGCGCGGCTTTATACGGGACGATCGGCTA  
TTTGAACCGCGTGTTCGCGCGCTTGGGGTTTGAAGCGCGTTCACGTCGTCATCCGCAACCGCTGTGCTCAAAACCGGTTTCAGACGGCATTTGTTTCAGGCATTCGGCGGACGAGATTCAAAC  
GCGCAAGCCCGAACGCGCAGGACAAGCGCGGGAACCGCGCATCCGTTTGAAGCCAAATCGCGGTATTCGGGGCGTGTACGGTGTGCGTTCGCGCATCGTTCATCGACAGCGACCCCGCGCGG  
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TCTGAAACCTCCGCGCAAGCGCTCAACCTGCCCCGCGCGGCTGCGGAAATCAAAATCAAAACAATACATTCGCGCATTTGCCCCGACCGCGCGCTTCGCGATCAAGCGCTGCTGCTTTCA  
GACGGCATCAGCGCTGTCCACGCGCTTTTAAACCGTGTACGCGACAAACAGCGCGCTTATTTTCGCGACCATCTGCCCGCAACAACTCGCTGCGCGCTTCAAAACCGACACACCGCG  
CCAATCTTCGACCAAGCGTGGCAAACCGCGGAAACGCAAGCGCGCTTCGACAGCGCTGTTCATTTCAAATTCGGACGCGCATCTACTCGAAGCGCGGACGAGCAACGCTGTTCGTCAAACATCGCGG  
ACAATGCGCTCAGCCCTCTTTAGATTTCAGACATTTTAAACGCGATAATGCGGCAAGCGGTGTTCGACGAACCGCAAAATATTTGCACACAANTCAAGTGATTGAACACACATCACACAA  
AAAACACTGCAAGGAGCGGAAGAAATCCGCGCTTCCAACGCTTTCGCGCGGTATTTGCGCGCGCTTCGCG

**SEQ ID 1130**

SEQ ID 1130

LPRIAMPYFALPDADVSRRAKLYQNHVESKFFRPEELDALDGLAQSGWQKGLHSVLPAFYTEFGLPLMGHESERGGNIALHWFADCAADTAEBSWLARHSDGLPAGISTPQSSVSETDYLORI  
RQIHEATRIGDTPYQINVTYTRHLHQAYGNFVSLYRRLRQPPVYAVLSHLPEAGQSAWTLICFSPFLNLINASDGTISTEPMKGTAPILGDGQDERRAAELQTPDKNRAENVHVIDLRLNDLG  
KLAQPGKVCYEPPEFKVSRFGSVWQMTSTIRAAQLPDTSFADTLRAAPFCGSIITGAPKKMSQMIISSELETFARGLYTGSIGYLMPCSGGLGFEAGAFNVITRLSLKPVSDGIVSGIGQDTSR  
AQARTAGQGGGEPHPFANPPYRGVYGVGSGIVDSDPAAEYRECGWKARFLNELRPDGFIFETLRAENRQCALLDRHLRLKRTSAQALNLPDPCENQITQYIATLDPGAPRITKALLAS  
DGISLSHAVLNRLDLQKRVILISPTLLPAQNYLRRFKTTHRAIFDQAWQTAETQKGLDQSLFNSDGLLGGERSNVFVKHKGQMLTPSLDLDILNGIMRQAVSDEPKYLLHTNQVLETHITQ  
RTLOGAEEIRLNSALNRGYPAAVLA



## SEQ ID 1131

ATGGCAATTCGGGCAAAATGTTTGTATACGCCCTTTTACACGGACAAAATGTAATTTTATGTAGAGAAAGCGGTGGCGAAAGTGTAAATTTG

## SEQ ID 1132

MAIRGKCFDYTPLLHQNVLICRESGGESVKL

## SEQ ID 1133

ATGGCAGACCGCCAGTTGCAACCGTTGAAAACGTAGAATTAGCGGAAAAGCAAGACCGATTCCAGGTATTTGAAAAAGCTGTTTGGAACACGAAGGCAAGGTTCTGCCGAAGATTCCG  
GCACGGTCCCGCTGCCGCAAACTACCCCTGCCGCAACGTATGCTCCGCGCCGCTACGAAGCCGCAAAAGCCAACTGCAAAATCGAAATGCTGAAAGTGCAAGCTGGGTCAAGGATTTC  
CGGCCAGCGCATCTGTCAGCTGTTTGAAGCCCGGATGCGGAGGTAAAGGCGGACCATCAAAACGCTTTATGGAACATTTAAACCCGCGCGCGCGCTGCTTTGGAGAAACCA  
ACCATACCGAAGCCGCGCAATGCTATTTCCAAACGCTACATCCAAAACCTGCGGACTGCGGCGGAAATGGTATTTCTTCGACCGCTCGTGTACAAACCGCGCGCGCTGGAACGGTGACGG  
GCTTCTGCGAACCAACGAATATATGCTCTTTATGTGCCAACCCCTGAGTTGGAACGTATGCTGTGCGCAGCGGCATCCACTGTTCAAATTCCTGGTCTCGGTATCCCGGGAAGAACA  
ACTGCGCGCTTCATCTCCCGCCGCAAGACGCCCTGAAACACTGGAACCTTTCCCGCTGGACATCCAGTCTGCGACCGCTGGGACGACTACACCGAAGCCAAAACCGCGATGTTCTTC  
CACACCCACACCGCGCAAGCGCTTGGGTATCATCCGTTGCGACGACAAAACCGCGCCGTTTGAACGTATCCGCTACTTCTGCAACCAAGTTGACTACCGGGTAAAGCGTGAAG  
CCATCGGCAAGTGGACGATAAATCGTTCTTGTCCCGATACCGGTTTACAAGAGAAAACCATCGATATCGGTATGAC

## SEQ ID 1134

NADRLQPPFENVELGEKQDQFQVFEKAVLEHKGSAEDSGTVPLPENYPCRKMLRAAYEAKEKALQIELLVQSWVKDSGQRIVSLFEGRDAAAGKGTIKRPMELNPRGARVVALEKP  
TTTERGQWTFGRYIQNLPTAGEMVFPDRSWYNRAGVERVTGFCPEFNEMLFMCAPELERMLVAGIHLKFWFSVSREBQLRRPISRRDDALKHKLSPVDIQSLERWDDYTEAKNAHFF  
HTHTGDAPWVIIRSDDKRARLNCIRYFLHQLDYPGKDKVKAIGKVDKIVLVPDTRYKERTIDIGHD

## SEQ ID 1135

TTGCGTAAATTCGCCAAGGCATACGCGGACGCGCGAGCTGACCGACCATCGTTGCCGAAGCGGCAAAACCAAGACTTGGCGCGCTGTGGAAGTGATGTTCACTGCCGACTATC  
TCGATTACCAAGCCGAATGGCGCGCGCTTACGAAGCGCAAACTCATCAAGCGCAGCCCGCGGCAAAACATTTATCGTTCAAACGTCGCTGGCGGTGATTGCCGGCATTTTGGCGCG  
GAACTTCCCTTCTTCTGATCGCCGCAAAATGGCGCGGATCTGCTTACGGGCAACACCATCGTCTGCAAAACCCAGCAGCGTAACCCCGATCACTGCCACATCTTCCCGCAAACTATC  
GATCGCGTCCGACTGCGCGCGCGCTGTTCAACCTGGTGGACGCTCGGCTGCGGAAATCGGCAACGCTTGTCCGCCATCCGCAAGTCGATATGTCAGCTGACCGGCTCGGTTGAAG  
CGGTCGCGAAGTGATGGAAGCGCTTCCGCCAACATCACCAAGTCTCGCTGGAACCTCGCGCGCAAGCCCGCCATCGTGTGAAAGACGCGGATTGGAATTTAGCGGTGAAATCCAT  
CTTGGCTTCCGCGCTGCGCAACACCGGTCAAATCTGCAACTGCGCGGAGCGGCTATGTTCCACAGCAGCGCTGAAAGACGCGTTCATTGAAAAATGACCGCGCGATGAAAGCGCGTCCG  
TACGGCAACCTTGCAGGCGGAAGCGGCGCGCGGAAATGGGCAACGCTGATTTGAAGACGCGCGCTGAAAGCGCTTGCAGAAAAAGTGAACGGCGCTCAAAACAGGTGCGAAATTTG  
TTTGGCGCGCAACCGCAGGACGCGGCTATTTCTTCTGAGCTTACCTGCTGACCGACACCGCAACAGTATGGAACATTTATGAAAGAAAGAACTTATGCGGCTCGTCTGCCGTTTC  
CGCTTTGCAACGCTGCAACGAGTCAACCGCTGCGCAACGACTGCGAATTCGCTGACGAGCTCGGTGTACACCAACCTGAAACGAGCTTCTACGTTACCGCGCGCTGCAATTC  
GGCGAAACCTACATCAACCGCGCAAACTTCAAGGCCATGCGAGGCTTCCACGCGGCTGGGAAAAATCCGGCATCGCGCGCGGACGCGCAACACGCTTGAAGAAATACCTGCAACCC  
AAGTCATTATCTGGAACCGACATC

## SEQ ID 1136

LRKIAQGIRGADELDTIVAEKGKTKDLARVEVMFTADYLDYQAEWARRYEGEIIQSDRPRENLSFKRPLGVLAGILPRNPFPLIARKMGPDVLTGNTIVVKPSSVPTINCHIFAEII  
DAVGLFAGVFNVDGPGABIGNLSAHPQVDMVSLTGSVZAGQVMEASANTKVSLELGGKAPATVLKDALDLAVKSLILASRVGNTGQICNAERYVHSSLDAPLEKHTAAMKGV  
YGNPAEABEAGAPFMGTLEERAVKVAEKVERAVRQGAQLVCGGKRTGGRYFFETLLTDITDMSMDIMKETPGLVLPVSADFLDQVIALANDCEFLTSSVYTTNLNEAFYVTRRLQF  
GEFYINRENFRAMQGFHAGWEKSGIGGADGKHLEBYLQTVIYLETDI

## SEQ ID 1137

ATGAAACAATTCGGCATGTATCATCAACGGACGCTTTGAAAACGATTTCAACGGCGAATGCGCGCAGCTATTGAACCCGCTCCACCGAAGAAACCATCGCCGCGCAACCCAAAGCGCGCAGGG  
CGGACGTTGACCGCGCGCGCGCGCGCAACCGGCTTGGAGCGCTTGCCTGCGGTGCAACCGCGCGCTATTTCGG

## SEQ ID 1138

MKQLAMYINRGFENDFNGEWRDVLNPSTEETIARBFKGRADVDRGARGATGLGASACGRTRRVFA

## SEQ ID 1139

TTGGTTTATTCCTCAAAATAAATTACCGTACAAGTTTCTTTACACGCGGATTTTGGGTTCAAGTCAAATACCGCTTACCGGTTTCTTTTT

## SEQ ID 1140

LVYSQINRYTSFTTRGFWSSQIRLTGFLF

## SEQ ID 1141

TTGTTTCATTTCGGGCGCTCCAGTTTGTAGTCCGATGATGTTTGGTTTATTCCTCAAAATAAATTACCGTACAAGTTTCTTTACACGCGGATTTTGGGTTTCAAGTCAAATACCGCTTACC  
GGTTTCTTTTTTATGTTTCGCGAGCGGCTGCTGCCGAAATATTGCTGAAATGCC

## SEQ ID 1142

LPHFGSSFWGCSPELFPNKLFPKLYLTRLGPKSNTAYRFSPLVSAGVLPKYCLNA

## SEQ ID 1143

GTGAGGCGCAGCTACCGTTTCGATCTTTGTTCAACGCAATTTCCATCCACGCGGTACGTTACCGGCACGCTGCGATTTTTCGACGACCGGCTCGCGCAACCTTATGTGCTGTTCTGTC  
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CAGACCGCATCGAGCGCGCGCGCGGCAACCGCGGAAGCAGACGCTATGCGCTGTAAGACTTCAGCGCACCCCTGAATGCGCGCTTCGACGCGCGGCGACACCAAGTCAACCGCTGAC  
AGCGCGCTGAACATCAGCGAAAGGACGCTGCAACCGCTATGCGCGACCATTTCCGCTTACCGCAAGCGAGTGGCTGCAACCAAAACAAATGACGACGCGCTCTATCTGTTGCAAAAC  
GGGCGCAAAACGTTGGCGCAACCGGCTATTGTCGGC

## SEQ ID 1144

VEGSYRFDTLNNGISIHGGVTARCFDSSRLAEFVSVFVLLLEGRLDFGINRRFRIDADGGKIVLIVAGBEVLPFSRYLYRGKTVKMTIKGMEQWLPREFYARFAPLLYREPVRINDLP  
PNLRGLAASCLQTVPKHGLBETLRREADVRLRLSLDLWDVSDGLEPAAGQTAEADAMPSEDFSRITLNAAPDGAHQVNRITAAALNISERTLQRRMRDHFGITASEWHLHKKMQHAYLLQW  
GGKRVGETATLCC

## SEQ ID 1145

ATGAGCGGGTGGCTGTCTATCTCCGCAACAAAACAGAAATAGCAATTCCTCCCAAGATGCCAACCTAAACTCCAAAGCGCGGTTCGTGACGACGCGTCTGAATGTGGGCAAAACACTGA  
CCGCGAGTCTCGCGGTAGAGTTTGACCCATATACCGCCACCGCGCAATCCGCAAGTTCGCGAATTTGTCTCGAACACTACCAAAACCAACAGACGCGGAAAGTTTAACGAG

## SEQ ID 1146

MSGVAVYLRNKNRIASQDANLNSKGRFVSSGLNVCKQLTGLGVDFPYRHRRAIRKSAEFVSNITTKTKTDEKPFNE

## SEQ ID 1147

TTGATAAATCATAAATCGCGTCAGGGGGCGGTAAAGCGGTTCCGCGCAGCGGATTGTCCGCGCAAGGTTTCAGACGCTGCTTCAAAAAATGGGTACAATCGTCCAGCGCTCTTCAG  
ACGGTCTTTTGAGCGAAAGCGGCTTGAAAACCTACCGACAACCGTCTCAATCAGGAGAA

## SEQ ID 1148

LINHKIAVRGAVSQAQDCPRKVS DGASKNGVQSQPSSDGLLSERPSENYRQPSQSGE

## SEQ ID 1149

ATGAGCCCATCCCCCTTTATCGAAATGAAGACGTCGCCCTTCGCGTATGGCGACGCCGCCGATTCGAACGACATCAATTTACAGCATTCGCGCAAGCAATTTTCCGCCGCGTATGGCGGTT  
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CGGCCGCGTATGGCGGTTATGTTCCACACGCGCGCGCTGTTTACCGATTTCGCGTATTCGACAAATATCGCTTTTCGATGCGCGCAACTGACGCAACTTCCGGAAGCGGTTATTGCGGAT  
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AAATTATGTTGACGCAACCGTTTACCGGCTCGACCGGATTCCTTGGCGGTGATTGCCCACTTGATCAGCGCGCTCAACAAGGCGCTTCGCTTCGACGACATTATGTAACGACGA  
CATTTGAAAAATCTTTGGAAATCGTCGATCAGGTAATTTCTTGGCGCACGCGGAAATATGTTCTCCGCGTCGCGCAGGAAATGCGGAACTGGATTTCGCTTGGTGCGCCAGTTTGTCTC  
GGCGGCTGGCAGACGCGCCGCTGGCATACCGCTATCCGCGCAACGCTGTTGACAGCAGGATTTCGTCGCG

## SEQ ID 1150

MSPSFPIEMKDVAFYAGDRPILNDINFSIPQGNFAAVMGGSGSKTTLMLRITGQIRPQSGQVLIBGRDLAGFSADELYEHRRMGVLFQHGALFTLSVFDNIAPFMRRLTQLPEAVIRD  
LVLLKLNVAVLRGVENLMPSELSGMSRRVALARTIALDFRIMLYDEPFTGLDPLISGLVLAHLISRVNKALRSTSMVTHDIEKSLIVDQVIFLAHGEIMPSPQEMRELDSPWVRQFV  
GGLADGPFVAYRPAQTSIQDQLLG

## SEQ ID 1151

GTGTATTTTAAGGCTTATCGGGAAGACGGGCAATTTTCAGACGGCATACGGACGGCAAGTGTGTGAAATGCCCTTGTGCGCGCGGATTTGTTCGTGCGGAAAAATGTTATCTTTCA  
AA

## SEQ ID 1152

VYFKAYREDGQPSDGIRTASVVKMPLSAADCLLWRKMLSPK

## SEQ ID 1153

ATGAATTTTATCCGTTCCGTCGCGGCGAAAAACCTCGGCCCTTATCAATCCTTCGCGAGTATCACGCTGTTTCTGCTGAACATTTTGGCGAAATCCGCGACGGCTTTCCGCCGTCGCGCC  
TGAGCGTGGCCCAAGTGATTTTTCGCGCGCTGCTGTCGCTGATGTTGTCGCTTCGCGGCTGTCGCTGATGTTTGGGTTTTCAGGGCTATACGAGTTGTCGAAATTCAAATC  
CGCCGATATTTTGGGCTATATGTCGCGCTTCTCTGTTGCGCGCAACTGGGTCGCTGTTGCGCGGATTCGTTTTCGCGCAGCAGCGCGCGCGTGGCATGACGAGGAAATCGGTTTGAATG  
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CAATTCGCGCGCTTCGCGCTGGCGGTAACGCTGATTCGCTGCATCAGGCGCTTCACGTCATCCGACTTCGGAAGGCAATTTTGGCGCGGACGACCGCGCAGCGTGGTTTTCGCGCGCTG  
ACGATTTTGGCGCTGATTTTATATGACCGCGTGGATGTTTACAGT

## SEQ ID 1154

HNFIKSVGAKTLGLIQSFGSITLFLNLILAKSCTAFARPRISVRQVYFAGVLSVLIVAVSGLFVGMVLGQYTLQSKPASADILGTHVAASLLRELGPVLAAILPASSAGGAMTSEIGLM  
KTTGQLEAMNVMAVNPVAVRVAAPRFAWGVFSMPLLASIFNVAGIFGAYLVGVSNLGLDSGIFWPQMNNITIHVDINGLIKSAAPGVAATLLAVHQFHCIPITSEGLIRASTRTVVSAL  
TILAVDFILFAMFTD

## SEQ ID 1155

GTGGATGTTTACAGATTGACAGACTCTCTGAAGACGAAACGCGGAACATCGGATATTCAGGAACCTTAAATGAAAAAGAACATATTGGAATTTTGGGTCGGACTGTTGCTCTTGATCGCGG  
CGCGCGCGGTTCGCTTCTCGCTTTCGCGCTGGCGCGCGCGCGCGCTTCGCGGTTTCGGACAAAATTTACCGGCTTATGCGCGATTTTCGCGGACATCGCGGCTTGAAGGTCAATGCCCC  
CGTCAAAATCCGACGCGTATTTGTCGCGCGCTCGCGCTATCGCGCTTGACCCGAAATCTTATCAGCGGAGGCTGCGCTTGATTTGGACGGCAAGTATCAGTTCAGAGTGACGTTTCC  
GCGCAATCTCTGACTTCGCGGACTTTTGGCGGACAGTACATCGCGCTGCAGCAGGCGCGGATACGGAACCTTTCGCGCGGACACCATCTCCGTAAACAGTTCGCAATGCTTCTG  
AAAACCTGATCGGTAATTCATGACAGCTTCGCGGAGAAAAACGCTGAGGCGCGCAATTCGGAAGCCGCAAA

## SEQ ID 1156

VDVYRLTDCIKTKRGTSDIQSTLMKKNILEFWVLGVFLIGAAVAFLAFRVAGGAAPGSDRTYAVYADPFGDIGGLKVNAPVKSAGVLVGRVGAIGLDPKSYQARVRLDLGKYQSSDVS  
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## SEQ ID 1157

ATGAAAAATCTCTTCATCAGCGCATTTGGGATCGGATTTTGGAGCATCGGCATGGCATTTGCGCTCCCGCGGACGCGAGTGGGACAAATCCGCCAAAACGCCACACAGGTTTGGACCA  
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CGCGCAAAAACAGCGTTCGCGCAAGAAATTTCAAAACCTGCTGATTCGCGACCTATTTCCGCGACGATGCTGAAATTCAAAAACCGGACCGTCAACGTAAGACAAATCCCATCGTCAATAG  
GGCGGCAAGGAAATCGCTCGTCCGTGCGGAAGTGGCATCCCGGTCAGAACCGCTCAATATGAGCTTTACCACTACCAAGCGCGGCAAAATACCGTACCTACAGCTGCCATCGCAAG  
GCACGAGCTCGGTACCGTGTACCGCAACCAATTCGCGGAAATCATCAAGCCAAAGGCAATCGACGGCTGATTGCCGAGTTGAAAGCAAAAACCGCGGCAAA

## SEQ ID 1158

MKKSSPISALGIGLISGMFAFSPADAVGQIRQNAQVLTILKSGDAASARPKAEYAVPYDFORMTALAVGNPWTASDAQKQALAKRFQTLIRTYSGTMLKFNATVNVKDNPIVHK  
GGKEIVRAEVGIPGQKPVNMDFTTYQSGGKYRTYNVAIEGTSLVTVYRNQFGEI IKARGIDGLIAELKAKNGGK

## SEQ ID 1159

TTGTTGCAAAAACCCATACC GCCCTCGGACGCTATGTTTGTGCGTTATTTGCCCGCTTTTGGCTTTCAACTCGGCANTCAGCCGCTGATGCCCTTTGGCTTTGATGATTTCGCCGAAT  
TGGTTGCGGTACACGGTAACAGGCTCGTGCTTCGATGGCGACGTTGTAGGTACGCTATTTGCCCGCGCTTTGGTAGGTGTTAAAGTCCATATTGACGGGCTTCTGACCGGGGATGCCGA  
CTTCGCGACGGACGAGATTTCCTTGGCGCCCTTATGACGATGGGATTTGCTTTGACGTTGACGCTGCGCTTTTGAATTTTCAGCATCTGCGCGGAATAGGTGCGGATCAGCAGGTTTG  
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CGTGCAGAAAGCGCGTTCGCGCTTTTGGAGATGGTCAAAACCTGTGTGGCGTTTTCGCGGATTTGTCGCACTTCGCTCGCGCGGGGAGGCAAAATGCCATGCCGATGCTCAAAATACCGATGC  
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ATAGCGCTCGCGATTTCAGCGGGCATTTGACCTTCAACCGCGGATGTCGCGGAAATCGGCAATAACCGCGCTAAGTTTGTCCGAAACCGCGGACGCGCGCGCGCGGACGCGGAAAGC  
GAGAAAGGCAACCGCGCGCGGATCAGACGACAGTCCGACCCAAAATTCCAATATGTTCTTTTCAT

## SEQ ID 1160

LFEXPIPPSDGMVCRFLFAAVFGFLGNQPVDAFGDFDAELVAVHGNQARAFDGVVGTVAALVGGKVHIDGLLTGADFGTDDFLAALIDDGIVFDVGRVFEFQHRAGIGADQGL  
KFGQRLFLRVGRGTFRVADRQCGHTLEIEIENRIGFGFMACRSVAAPEDGQNLGVLADLSHCVGRGGKCHADAQNTDAQCADEGGFHDVFPENGVCVLCFGFPRIAAALSVPLGEAGH  
EFTDQVFNHCRITGYGOGVAGSKVFRIAALLQPDVLPQAKRSQSLRGHNVTAELILAVQIKAHPRLIGFRVVKPSADAPDQYACGFDGGLDLQYADVAEIGVINGVSVRTAEERAAHARS  
EKGNRRRADQDEQSDPFQYVLFH

**SEQ ID 1161**

ATGCAATCAGAACTCAAAAACGGCACTGCACATCGCGGGGGACATCACCGTCAAAACCCGTGACCGGGGACGCATTGGGGCTTTCCGGCAACAATGCCGCTGAAAGAAACATTGGCG  
TCGATTTCCGAGGTGTCAAAACGTGCCGATTCCGCCTGCATGTGCTGCTGCGAAGTGCTGCGCGGCTGCAAAGGCAGCGTCAGGCTGACCGGCATTCCCGAATCCGTGCGCGCGCTGTC  
CGAACTGTACGAAATCAAAGACTGGCTGAAATCA

**SEQ ID 1162**

MHTELKNGTLHIGGDITVKTLTGDAFGRFROOCLKETLAVDFGGVKRADSA CMSLLLEVLRGCKGSVRLTGIPESVRALS ELYEIKDWLKS

SEQ ID 1163

ATGCGAGGCAACACCTTTCGGACAATCTTACCGTGACCACCTTCGGCGAAGGCCAGCGCGGGTTCGGGCTGCATCATCGAGGGCTGCCGCGCGGGCTTGGAAATTAAGCGAAGCGGATA  
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CGCCCTCTTAATCGCAACACCGACAGCGCAGCAAGAAGCTACGGCAACATCGCCACCGCTTCGCGCCCGGCACACGCCGACTATACCTTATTTGGCAGAAATACGGTACGCGCGACTACCGG  
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CGCAAGACATTCGCGTCAATATCGCCATCAAACCCACAGCTCCATCGCCACGCGCGCAGCAAGCATGCATCTACGCGCAACCCCGTCGAATCTCGCACCCCGCGGCAGGCACGATCCCTG  
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TCGGACAAAG

SEQ ID 1164

MAGNTFQIQITVTYTFGESHGAGLCIIDGCPGLESEADIQFDLDRRKPGTSHRVTTQRREADQVEILSGVFEGKTTGTPTIALLIRNTDQSRQSDYGNLATAFRPGHADYTYMHKYGTEDYR  
GGGRSSARETAARVAAGAAVAKWLKEKFGTEITAYVTQVGEKKIRFEGSEHISQNPFFAANQSQIAELBHYHDGVRKSLDSVGAKLHIAANVPVGLGEPVFDRLDAELIAYAMEGINAVEG  
VEIAGAFDSVTQRGSEHGDELTPQGFLESHSGGILGGISTQDQICVNIAIKPTSSIIATPRRSIDITHGNPVELATGRHRDPCVGLRTAPIAEAMLAIVLIDHALHRAQNADVAADTPDISR  
SDK

**SEQ ID 1165**

ATGCTTTTATCAAGAAACCTCATCAAGAACTCTCTTTTACCGCGCTCGCATTTTCGTCGCTCTCTTGGCGGTGTGGTGTCCACGACGAGCGATCAAOCTGCTTTGGCCGGCAGCTGAOC  
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 CGACAGCGAAATGTCGCTGTGGCTATCTCTCGGATGTCGGCTTGAACAGTGGATACGCCCCGTATGCACTGTCAGTTTGCCTGTCCGTTTGCCATCTCTGATTGCCGTATGCGAGCTTTGGGTGATA  
 CCGTGGCGAGAGCTGCGCAGCGCGGAATATGCCGAATTTTGAAGCAGAAACGAGGAATTTGCTTTTGGTGGAAAGCCGCGAGTTCATTAATCTTGGGCAAGCGCAACGCCGAGGGTTTATTTCG  
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 TCGCCGTGCGCTTTTCTTATTTCAACCGCGCAGCGGACATACCTCAATATCTTGATTGTCATCGGTTGTGTTTAAATTTACCAAAAGCGGCTGACCTGCTTTTGAAGCCGTGGAAGA  
 CGGCAAAATCCATTTTGGCTCGGACTGCTGCTATGCAATCATGTTTCGTCATCGCAATCGTACTTCTGCGCGTCTCGCAGTATGCCACGCCGCCCTTCTGGCAGGCGTGTGGCAAA  
 AGTCTGACATTTGAAAGCGGAAAA

**SEQ ID 1166**

MYQRNLIKLSFTAVGIFVLLAVLSTQAINLLGRAADGRVAIDAVLALVGFVWIGTPLLILLVLPFISTLTVLTRYHRDSEMSVNLSCGLALKQHIRPVHQFAPVFPFALLIAMQULAVI  
PWRLRSRETAETILKQKQLSLVEAGEFNNLKGKNGRVYFVETPDTESGIMKNLFLREQDKNGDNIIFAKCGNFSLANDNKRTLELRHGYYRSGTGRADYNQVSQFQNLIIISTTPKLIID  
PWSHRRITSTAQILGSSNPQHQAELMWRISLTVSVLLICLLAVPLSYFNPRSGHTYNILIAIGLFLIYQNGITLLFEAVEDGKIHFNLGILLPMRIIMFVIAIVLLRVRSMPSPQFFWQAVGK  
SLTLKGGK

**SEQ ID 1167**

TTGTTTCACACAAACCGAAAATGCCGTCTTAAAAACCAATTTTCAGACGGCATTGTGCCCTTAAAAACACGTTTTTTTCAAGCGCGACCATACCAAACACCCACAGGTTGCTTCCACCTTGG  
TACAACCTTTGCTCCATCAA

SEQ ID 1168

LFHTNRKCR LKTNFOTAFVP+NTFFOARFYOTPTGCLPPFVQPLLHQ

SEQ ID 1169

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SEQ ID 1170

SECRET//NOFORN  
 MKKTYAYILLIIGFASAPAFATRPADPPEYGYNRAVSFKFNDQADRYIFAPAAARGYRKVTPPKPVAGVSNFFNNLRDVSFSGSNILRLDIKRASEDLVRVGINTTFGLGLLIDYAGAGGVDP  
 NKIFLGLDTPASGHWKNSNYFVLPVLGPSTVRDALGTGITSVYPKNI VFHTPAGRWGTTAAAAVSTRBGLLDLTDLSLDEAIDKYSYTRDLYMKVRARQTGATPAEGTEDRIDIDIDELVE  
 SAETGAARPAVHDSVSETOAEAEAGEAETOPGTOP

SEQ ID 1171

ATGCCCTGTGAAATCCGTGTCGCGACGGCATTCCTTCCTCGGAACGGACAGTCGCACTACAGATTGGCCGTATAATCCCTTTTTCGCGCATACCGCGCGACAGCAAGGAAAAACCA  
TGTAAGGATCAACCGCAGCGTATTGTCCTCATCTCTTAGAACCTTTTGGAACTGGCTGCAAAACCTTCGCGGGCAACCACTCGACGGACTGACCTCGAAGACATCCAAGCGATGC  
CAATTCTCTACCTTGTCCGCCCGTGC GAAACGCCGCAGCAGATATGGGACGAAATCGAAGCCGTTTCGAAGACATTTTCGCCGCCGAATTCGCCGACTGGTGCAGAACGCAACCGAGTGG  
CTTGCACTCATGTGCGACATTTTCAACGAATGGTTTCGACATCCAGCTTTCTACCGTCATCACCAGCTTCGAACACGAACCGCTTCGCCGCCGAAGCTTCCAACCCATCACTGAACT

SEQ ID 1172

SEQ ID 1172  
 NPSENPCSDGIPPRNGQSDTTWAIIPFLIRIPRDSKGKTYEVNRSVFLVIPLEPFWNLQTLPGNHLOGLTLEDIQADANSYLVRPCETADEVNDEIARFEDIFAAELADWCEDEREH  
 PALDADITPNEWFDIOLSTVITDLEHEPLARAPOPINLN

SEQ ID 1173

SEQ ID 1173

ATGAAGCTGACCGTCCGCAATTACCATTCTCGACGGCTACGGTCTATGTCAACAATGCAAGCTACCTCGAATTTCTCGAGGAAGCGCGCTGGGGGTTTTGTGAAAAACGGCGACTGATGCAAG  
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GCTGACCCAGACGATTACACTTGCCAAAACGGCAAAACCGCCGCGAGAAGCCGACATCACTTGTATGCCCGTCCACGCCGCCACACAACGCACCGTCAGCCTGCCGCCACCTTGTCCCGCGCA  
CTGGAAGCCTTGTCCGAA

## SEQ ID 1174

MKLTVRNHLDG YGHVNNARYLEFLZEARWAFPEKRGMLHLAGLILIVARIDIRYSRPAVEGDVLQPSCLKTPGMRRIVLQTTITPLNGKTAAREADITLMPVHAATQRTVSLPATLARA  
LEALSE

## SEQ ID 1175

ATGAAAAAATACTACCGCCGCCCGCGTCCGACTGATCGGCATCCCTCCCTGCCACCGTCTCATCCCCGACAGTAAAAACCGCCGCCCTTCTCCCTGCCCGACCTGCACGGAACCGG  
TTTCCACGCCGACCTGCAGGCAAGTACCCTGATTAATTTTGGTTTCCCTCTGTCCGGGTTGTGTAGCGAAATGCCAAAGTACCAAAACGGCAACGACTACAAAAATAAGA  
TTTCCAGTCTCGCGTTGCCAGCCCATCGATCCGATAGAAAGCGTCCGCCAATACGTCAAAGACTACGGACTGCCGTTTACCGTCATTTATGATCGCGCAAAAGCGTCCGACAGGCA  
TTCCGCAACAGGTTTATCCGACTTCCGTCCTTATCGGCAAAAAGCGGAATCTCTCAAACTTATGTCCGCGAACCGGATTTCCGCAAACTCTACCAAGAAATCGATACCGCGCTGCCGC  
AA

## SEQ ID 1176

MKKILTAAVALIGILLATVLIIPDSKTAPAFSLPDLHGKTVSNADLQGVFLINFWPSPCGCVSEMPKVTKTANDYKNKDFQVLAVAQPIDPIESVRQYVKDYGLPFTVITYDADKAVGQA  
PGTQVYPTSVLIGKKGELIKTYVGEPDFGKLYQRIIDTALAQ

## SEQ ID 1177

TTGCCACGCGCGGTATCGATTCTTGGTAGAGTTTGCCGAATCGGGTTCCGCCGACATAAGTTTGGAGATTTCGCCTTTTTGGCCGATAAGGACGGAAGTCGATAAACCTGTGTCCG  
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AATCTTTATTTTGTAGTCTGTTGCCGTTTGGTGACTTTGGGCATTTCCCTCACACAACCCGGACAGGAGGAAACCAAAATTAATCAGGGTGACTTTGCCCTTCGAGGTCCGCTTGA  
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## SEQ ID 1178

LRQRGIDFLVEFARIGPADISFEDFAFPADKDSRINLCABCLSDGFVRIINDGKRQSVVFDVLADAFYRIDGLNGEDLEIFVIVVCRFGDPGHPAHTTTRGGKPKINQGFALQVGVG  
NGFSVQVGGGEGRGFTVGDDEGGKEDADQCDGGGEYFPHSDKASSARARVAGRLTVRCVAANTGIRVMSAAAVLPFGSVIVVSTMRMPGVFRRHENCNTSPSTAGRILYRMSRATI  
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## SEQ ID 1179

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## SEQ ID 1180

MPSEAKTETMFLFFQIIRPDITFRHSTFRQILFHHRRIACRQVRGRNVFCNHRACADRAASDGYARHHPAPRPDIVLQRNRTDFRVALKAFVFTVKLVVGRIBQAFRPHHIFADHQ  
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## SEQ ID 1181

ATGGAATCAAAATCTTTTTCTCTGCTGCTGCGTTTGGCGGTTTCGGTGTTCGCCCGCTCATATATGCCGCGCATCGGCATCGTCCGACAGCGGTGCGCGGTTTTTGGCGCGCGCGGTT  
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CAAAATGTGATGATGGGGCCGAATGCCCTGCTCTATTCGACCAACCAAGTTTGACCGTGAAAAACAACCGCTTTGAGGGCTACACGGAATCCGCTCCGATTACGTTGGAGGACGATGTC  
TGGCGGGCGCGCAGGGTGATTTGTGATGCGCGGCTAACCCTCGGACGCGGCTCGGCTGTGGCGCAGGCGCGGTGTACAAAAGACATTCCGCCCTACTCTTTGGCGCGCAGGCAATCTG  
CGTGGTGAAAAAGATCTGCCGGAAGGT

## SEQ ID 1182

MESKFFILLRFAGSVLPPSYMRGIGVRRVRGFLARRVSPHIGRGVNIERGAYVFPDITVLGDSGIGANCBICRGLVVGKVMVMGPECLLYSTNHKFDRENKRFEGYTEIRPTILEDV  
WPGRRVIVMAGVTVGRGSVVGAGAVVTKDIPPYSLAAGNPAVVKNLPEG

## SEQ ID 1183

AAACCAATTTTCAGACGGCATTTGTCCCTTAAACACGTTTTTTCAAGCGCGACCATACCAACACCCACAGGTGCGCTTCCACCTTCGTACAACTTTGCTCCATCAACAT

## SEQ ID 1184

KPIFRHLSLKTFRFKRDETHKPQVAFHPSYNLCISKH

## SEQ ID 1185

TTGATTCCATCAAACTTCCCTCAAAAGAACTTTTACATTTTATCGAATATCCTCTTGACGAAACAACAGAAATAGCGAGAATGCCGAGCTTGTCT

## SEQ ID 1186

LIPSNLPQKNFLHFIEYPLDETTENSEAELV

## SEQ ID 1187

TTGAAAGGAATCAAAATGAAACAAGGTATTCACCCGAATACCCGGAAGTTAACGTTACCTGCTCTTCCGGCAACAATTCGTAACCAATTCGCAATGGAAGAAAGAACTTTAACATCG  
AGGTTTGTCTCCCTGTGCCACCCGTTCTATACCGCACCCAAAAATCTGTCGATACACCGCGCGGTGGACAAATTCACCAAAATTCGCGAACCTGTCTCAACGC

## SEQ ID 1188

LKGNQMKQGIHPNYREVNVTCSCGNKFVTKSAMERENFNIEVCSLCHPFTYTQIXIVDTTGRVDKFNKFGNLFKR

## SEQ ID 1189

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## SEQ ID 1190

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## SEQ ID 1191

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## SEQ ID 1192

LLIHYIDKSVQILKSPAIEHMAGLNSCKAAISV

## SEQ ID 1193

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## SEQ ID 1194

MGCFMIQNVVTSIILYSFVAVDILLTPNVIFCQKSRKDIINIYLGQFLGSVSLILLSLPAFVLDYIPSKELGLGLIPFLGLKVLILGSDGSIKAEGLRKDNKILIFLWAMITFA  
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## SEQ ID 1195

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## SEQ ID 1196

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LAGSPTPLVAHLFGQTDFGIPFVYLWAAAFKHLSPWAADFYDAARFAGVFPVIGLTFCCGAGPNFLGRHGRSVVLIHIGCIGLIPVAHFLNPAFAAAGLVLHGYSLARRRVIAA  
SPLLGTGWTLMSLAAYPAFALMLPLPVLMPFRPQSRRLMLTAVASLAPALPLMTVYVYLLAKTQPALFAQMLVYHVPFTGGVRIHQAPSLPYLKNLLHFPALPALVHTVCTR  
LPSDWDILGIVMLAVLVLAPNQRQDNLVWLLPPLALFGAQLDSLRRGAAPVNWFGIMAFGLFAVFLATGFPAMNYPWPAKLAERAAVSPYVYVDIDPIPMVAVLPPLVWLA  
ITRKNIRGRQAVTNAAAGVFLWALLMLTFLPWLDAAKSHAPVVRSEASPSPELKRSLSDGIBICIGIGGDLHTRIVWTVQYGLPHRVGDVRCRYRIVRLPNADAPQGWYTVQGARPR  
NRKSPALIRKIGENILRTD

## SEQ ID 1197

GTGCGGAAATCCGTATAATTGCGGATTAACCCCTTATATAGTGATTAATTTAAATCAGGACAAGCGGACGAGCGGACAGTACAAATAGTACGGCAAGCGGAGCGCAAGCGCGT  
ACCGGTTTAAATTTAATCCACTA

## SEQ ID 1198

VPEIAYNCAIKPLYSLMLNQDKATKPTQVQIVRQGEATPYRPFKNPL

## SEQ ID 1199

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## SEQ ID 1200

MHTLYSGITCPFSHRFRVLYEKGMDFRIKIDIDYNKPEDLAVNPNYQVPLVVRDLVLHESNIIINEYIDERFPHQPLMPGDPVMRGRGLVLYRMEKELFNHVQVLENPAANKBQAKA  
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## SEQ ID 1201

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## SEQ ID 1202

VPECENACKTAGFASISDLFAHGFPGGQCFDKGFALEDITLGVFEQRRTFAQFDIVWNEPPQQRQGNINHRKIFAEQVFAFAERRGKHRQAVADGFAFPCLFLVGGGVQVNLVDVVEQF  
FFHTVQHQPFAAHNGIAGHKLRMGEAFVDVFDVGLVQHIALDQHGDLVVRVHDGEVFGFVNIDIDFPKIHITFPVQNEAAAFAEGAGNAGIEGHNNCRSCVMPARRLIYSGINLNR  
YGVASPCRTICTVCGFVALS

## SEQ ID 1203

TTGCAAAACCCGCGCTTTTCAGGCATTTTCACATTTCAGGCACACCCACGGAACCCATCATGCCACCTCAACCAAAACCTTACATCTCCGCGCACTTTGCGAATGGTCAGCGACAACA  
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CAACGATTGATCAGCTTTCCGCGCTTTCGCGGACAAGCGCAGCATATGATACCTGTCGACAGCTCTTCAGCCTTTTCGCAAGGAGACCGGAGAGATGAGGTTTGAATG  
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## SEQ ID 1204

LQNPFFCRPHIQAHTFPIPTSTKPYILRALCEWCSNLSLPHILVWNEHTRVPMQVVRDNEIMLIGATQNLRIDNDWISFARPGQAHDTIHPVGHVLSLPARETGECSGPEL  
EYRPDTPSENTSAETAPRAPKGLKLVK

## SEQ ID 1205

TTGCATCGATTTCATCCCGATATAGCGAGGCTTTCTCCAGCCATTTCCCTTCCAAACAAAGAACAAAAAGCGCGCGGCGAGCGGATGCCCTTCTCTTACAGGTTCCCTTATTTT  
TAAACCGCAGCGACGACCGGTTTGGCGGGCTTTTGGTGGCGGCGCGCGGAGCGAGCTGTTCTTTCAGCTTCCGCGAGCACCGCGGACCGATGCCCTTCACTTGTATCAATCGTCCAC  
AGACTTGAACGCGCGCTTTTGGCGCGGATTTCCGCAATGGCTTCCGCGGCGCTATGCCCGGCGCTATGCCCGGCGCGCTCCAGCTTCTGGTGGGAACCCGATTTGAATGTTAAACCGCGAAAGGAGAA  
GGCGCAGGAGAACAGCATACAGAACATACAAACATTTTTCATGGTTTTCCTTTAAGGTTGCAAAACAAACCGCATCTTCCGACGATATGCGCGAT



## SEQ ID 1206

LHRFIPRYSAGLSPAISLPNKEQKSAGGSRCPFLYRFPYFLTAGSTGLAGPFGAGAPTEANSFSFASTAGMPFTLIKSSDILNAPFCARYSAMAFAGMPFGSASSFWNSTRNLNVRKGE  
GAGEQHTBQYKHFHGFSGKCKQQTASCDMDAD

## SEQ ID 1207

ATGACACAAAGAACCCGCTTTGGGCGCGGCACTGAAATCCGCCGTCCAAACTATGAGCAAAAAGAAACAGACCGAAATGATCGCGGACCACTATCGGCAAAATACGATGATTCAAACGCT  
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## SEQ ID 1208

MTQETALGAALKSAVQTMKKKQTEMLADHIYGYDVKRFKPLALGIDQDLIALPQYDSALJARVLNHCRRPRYLKALARGGKRFDLNRRFKGEVTPBEQALQNHFPVQALQQA  
QAAETPSVEAEAESSAAE

## SEQ ID 1209

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CGCGCGCAGCGAATCGCGCTCATCAAAGCCAGCGCATGAGCACAAAAGCTGCTGTGTGATCTGTCTCAGTTTCGCTTTTATTTTGTATTCGCGCGCTCGCGCTCGCGCAATGGGTT  
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## SEQ ID 1210

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MSVGBELTTYIRHLQXNSQNTQIYALAWWRKLIVPAAMWALVAFAPFTPTTRHNGMLKFGGICLGLLPHLAGRLFGFTSQLYGTPTPLAGALPTIAPALLAVWLIRKQEKR

## SEQ ID 1211

GTGTTTCAGACGGCATTTTGTCCGATGGGCGCAACGGAATCCGTTTGTGCGCAAAACCTGTTTCGCGGATTCGAACCGTGTTCGCCCTGCCGATTCGATATTAGGACATTGAAATGC  
CGTCTGAACCTGCGATACGGGCTTCAGACGGCGTTTGTCCGATATTCGGGCAATCAGCGGCTCAGTACGTTTCAAGATTTTGT

## SEQ ID 1212

VFTAFCPMKRKNPVGKTCFVSKPCCPCRFDIRTLKMPSEPAIRASDGVLSDIRAIRRSVRFSPRC

## SEQ ID 1213

ATGAAGACACACCGCAAGACCTGCTCTCGCGTGTGTTTGTCTTTTCAGACGGCATCGAAACCGCGCTTCCATCCGACATCCGACGAGGACATCATGAGCCTGAAAACCGCGCTTACCG  
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## SEQ ID 1214

MKTHRKTSACVCFAPQASKPAVSIHRPSEDIMSLKTRLTDMKTAMRAKDQVSLGTIRLINAABKQFEVDERTZADDAKITAILTKMVKQRKDKAKIYTEAGRQDLADKENAEIDVLHRY  
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## SEQ ID 1215

ATGCTGCAATCCCGCTAAAGAGAATGAACCATTTGAAGTCGTATGCGCGCTTTCAAACCGCGCGTAGAAAAACCGCGCTGCTGACCGAGCTGCGCGCGCGGAGGCTACGAAAAAC  
CGACTACCGAACCGCAACCGCAAAAAGCGGACGCGCTAAACCGCTGCAAAAACCGCTGCGCAGCCAACAGCTGCGCGCCCAAAATGTAC

## SEQ ID 1216

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## SEQ ID 1217

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## SEQ ID 1218

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## SEQ ID 1219

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**SEQ ID 1220**

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 FIGASRNVGLAQGLMCPATAREIAGKIGMDAAQLYPADGNTRMGTWYMDTKRRLQNKELATAGYNAGPGRARWQADPTLEGAVYASTIPFSETRDYVYKVMETNAAYTASLPGAPHIP  
 LKQREGTVPAR

SEQ ID 1221

TTGGAAGAAGACAAAATGCGCGTCTGAACAGCGCGTTTGCCCGAAATATATGCGGAAACTGCACCGCGCTTTGGAATGTTTCCGACATAAATTTATATTTTTCAATCATTTGCCGTTTGGGTGCGA  
ACCGCTGCCCTTTGCCCGTTTCAGACGGCATTTGTCGAAATGGTTGCCCGCTTCCTGCTTTATAT

SEQ ID 1222

LEKTKRLNRRLPELYAETAPPLECFRNLVPSIIIRLGANRCLCPFQTALSEMVARFLLY

**SEQ ID 1223**

ATGTTAACCGCCGCAAGGGGAGAAGGCCGACAGGAGAACAGCATACAGAAACATCAAAACATTTTTCATGGTTTTTCCTTTAAGGGTTGCAAAACAAACCCGATCTTGCAGCATATGGC  
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SEQ ID 1224

MLTAERKQENSIQNTNIFPMVPLRVANNKPHLATIWRINKNRYGVAPPRLGNDSLR

SEQ ID 1225

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SEQ ID 1226

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SEQ ID 1227

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**SEQ ID 1228**

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**SEQ ID 1229**

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SEQ ID 1230

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GGNOGNHVSIIIPFDPADIDGYFWP\*SKLIGCKAVPSSPAEGRYRLSDVAATAKOGAGEA

SEQ ID 1231

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SEQ ID 1232

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SEQ ID 1233

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SEQ ID 1234

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SEQ ID 1235

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SEQ ID 1236

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SEQ ID 1237

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SEQ ID 1238

LETL SKIIVFP IOOSPMSDTTGAEDKAEIVGTL

SEQ ID 1239

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SEQ ID 1240

MYSGAGKSTLRLRLINLLRPDTGKVNVCQQLTALDAAALRQARQNTIGMVQFQNLNLSNTTVAGNVAFPLEIAGWPSEKIKARVACLEIVGLTERAGHYPAQLSGGQKQRVGIARALAP  
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## SEQ ID 1241

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CGGTCTTGCCATCGGCTTTTGTATACAGCGCGCGCGCAGCATGATAGCGCGCGCGCTTGGGCGACCTTCGCTATCCGCTACCGCTACTACCGCTACCAAAACGAAGTCATGCTT  
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## SEQ ID 1242

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NLREVPGVIEAAAAMGAPFLAIVLRLVLLNEARAGMVSSITVLAIGLLSYSAAGMIGGGGLDLAIRYGYRYQTEVIVFIVALLVLLVLIQSTGNALARKLDR

## SEQ ID 1243

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## SEQ ID 1244

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## SEQ ID 1245

TTGAAGAAGGTTTTCATATTTTCTCTGATGTTGTGGCGTTTCAACAAAAANTGACAGGCAGGAGTCTCCCTCCGGATTCCGCGTTACAGCGCATTTGCCCGAACAGGGGATTT  
TA

## SEQ ID 1246

LKKVFIISPDPVAVSNKNDRQGVLPSPGFGVQTAFANRGL

## SEQ ID 1247

ATGAAAACCTTCTTCAAAACCTTTCCGCGCGCGCATCGCGCTCATCTCGAGCTCGCGCGGTCAAAAAGACAGCGCGCCCGCAGCTCTCGCGCGCGCCCTTCTGCCGATAACGGCG  
CGCGGAAAAAGAAATTCGCTCTCGGACGACCGCTCGCGGACTTCGGCGATATGCTCAAAGAACAAATCCAAGCCGAGCTGGAGAAAAAGGCTACACCGTCAAATTTGGTTCGAATTTACCGA  
CTATGTGCGCCGAATCTGGCATTTGGCGAGGGCGAGTTGGACATCAACGTCTTCAACACAAACCTATCTTGACGATTTCAAAAAGAACACACCTTGGACATCACCAGAGCTTCCAA  
GTGCGACCCCGCTTTGGGACTGTATCCGGCAAACTGAAATTCGTTGAAGAAGTCAAAGACGGCAGCAGCTATCCGCGCCCAACGACCGCTCCAACTTCGCAACGCGCTTGGTGTATGC  
TGAAGAACTGGGTGGATCAAATCAAGACGGCATCAATCCGCTGACCGCATCCAAGCCGACATCGCGGAAACCTGAAAAACATCAAAATCGTGAGCTTGAAGCCGACACACTGCC  
GCGCAGCCGCGCGACGTGGATTTTGGCGTCTCAACGGCACTACGCCATAAGCAGCGGATGAAGCTGACCGAAGCCCTGTTCCAAGAGCCGAGCTTTGCTATGTCAACTGGTCTGCC  
GCTCAAAACCCGCGACAAAGACAGCCAAATGGCTTAAAGACGTAACCGAGGCTATAACTCCGACGCTTCAAAGCTACGCGCACAAACGCTTCGAGGCTACAAATACCTTCCCGCATGGA  
ATGAAGCGCGACGCAAA

## SEQ ID 1248

MKTFPKTLSAALALILACGGQKDSAPASAAAPADNGAAKEIVPGTTVGDPGDMVKEQIQAELEKGYTKLVEFTDYVRPNLALAEGLDINVPQHKPYLDDFKKEHNLDTPEAQ  
VPTAPLGLYPGKLSLEEVKDGSTVSAPNDPSNFARALVNLNLGWLKLDGINPLTASKADIAENLNKIRIVLEBAQLPSRADVDFAVVNGNYAISSGMKL/TEALFQEPSPFAYVNWSA  
VKTADKDSQMLKDVTFAYNSDAFKAYAKRFEYTKYPAAMNEGAAK

## SEQ ID 1249

ATGCCGATTATCAACGCGGTACCATCATCCGCTTTCCCATAAACCCGCTGCAACGGCAACCGGCTATTATAGTGAATAAACAGAAATCCGATAAACACGGATACAAATTTGCGGCAA  
CACCAATATCCGA

## SEQ ID 1250

MPIIKRRTIIRLSHKTACNGKPAIIVKKQKSDKHGYKLSATPNIR

## SEQ ID 1251

TTGTCCGACCGTTGGCGAGCAGCAATCCAAGCCGCGCCCAATCCGCTTTTACTTTTGCCATACCGCCCTCCCGTGCCTATTAGATAGGATGTTAAATCGGATTTTATCGGATAT  
TGGGTGTTGCCGACAATTTGATCCGTGTTTATCGGATTTCTGTTTTCATATAATAGCCGTTTTCGCTTGCAGGCGGTTTATAGGAAAGCGGATGATGTTACGCGGTTTGATAAT  
CGGCATCAGCGGGCGAGCGGTTTCCAATACGCGCTGAAGGCTTTTGAACTTTTCCGCGCGCAAGATGTCGAAACGCACTTGTGGTATCGAAAGGCGCGGAGATGGCGCGCTTCCGAA  
ACGGATTATACGAAGAAGCAAGTATATGCTTGGCTGATTTGCTCAATCCGATCGGCAATATCGGGCGGTGCACTGCGAGCGGTACGTTTAAACCGGACGGGATGCTGGTCCGACCTGTT  
CGATCGGACGCTTGCCTCTGTCGCGCACGGCTTCGCGCACAACTCTTGACGCTCGCGCGGATGTTGTTTGAAGGAAAGCGCGCGCTGCTGCTGATGTTGCGGAAACCGCGCTGAA  
CCTTGGCCATTTGGAATTTGAAGCGGTAACGGAATGGCGCGCTGTTTCCCTCTGTTCTCGATGTACCGCAAGCGCAGACGCGGACGACATAGTGGCGCACAGTATCGCA  
CACACGCTGTGCTGTTCCGAATCGATACCGCGATTTGGCGGAATGGCAGGAAATGGCGAT

## SEQ ID 1252

LSAPLASSESKPRNPPTTFAIPPSRAYSDRLNVRVYRILGVADNLYPCLSDPCFTTIIAGLPLQAVLWERRHNVRLIIGISGASGFQYGVKALELLRAQDVETHLVVSKGAZMARASE  
TDYTKDEVYALADFVHPHIGNIGACIASGTFKTDGMLVAPCSMRITLASVAGFGDNLTRAADVILKERRRLVLMVRETPNLHLNLMKRVTEMGVVPFPVPAMYRKPTADDIVAHSLA  
HTLSLFGIDTPDLAEWQMD

## SEQ ID 1253

ATGGCAAAAGTAAAGCGGATTGGGGCGCGCTTGGATTGCTGCTCGCAACCGTGGCGCAACAGCAGCGCGGACCGGTTGACTCGGCTTGCCTTAAAGATATCCGCGCCGCGCT  
ATCAGGCGCGCTGCAAAATGATGACGAAGCCTTGCAGGAATGCGAGATTGATTAAGCGCAAGGCGTGATACAGCCGCTCATGTCGCGCAACACGAGCTTCCGATACGAATGAT  
TGCAGCGCAACCGCTTGGCGCGCGCTCAGATTGCGCGCTGTCCGAATCCCGCGCTTATCAAAACCATCAGCGACGAAACCGCATTTGCAATGGGTTGATCGAAAACTCCAGCGC  
GAAAACTCAACCCATCGAAGAAGCACAGGCTTGAACGCTTTCGCGCAGGTTGGGCTGACCCACGAAACCATCGCCCAAGCCGTGCGCAAAAGCCGAGCGGATTTCCACAGCC  
TGGCGCTTTTAAAGCTTCCCGAATCCGTGACGAAATGCTTCAACGCGCGCTCGAAATGGGGCAGCGCCGCGCATGCTGACCTTCCCGCTGCTGCAACAGCTCGAATTTGGCGCAAAA  
GGCGCTCAAAACCGCTGGTGGTGGCGAAGTCAAGCGCGCAGCCAGGCGCGCTTCAAAACAAACGTCGCGACCAAAAAAAGCTGCGCGCGGACATCGCGCGCTGAATGATTG  
CTGACTGAAAAATGGGTGTCAACGCGGAAATCAAGACCGCCACCATAAAAAGGCAAAATCATCTGATTTTGACACGCGCGAAACCTTCGACCATATCTTGAAGCAAGTGGGCGATAG  
ATTACCGCGCT

## SEQ ID 1254

MAKVRGGLRGGLDSLILANGADNSSGDRITAVAVKDIRFGYQARVQIDDEALQELADSLKAGQVQFVIVREHLSRYELIAGERRWRAAQIAGLSEIPAVIKTIDETALAMGLIENLQ  
ENLNPITEAQGLKRLADEPLTHETLAQAVKRSJAISNLSRLLSLPESVQEMLYQRRLEMGHARALLFLPVVEQLELAQKAVKNGNSVREVERRSQAALQNKRPKKTAAADIGRLNDL  
LTKLGVNARIKTANHKKGIILHFDTPETFDHILKQLGIDYRP

## SEQ ID 1255

GTGGGAAATATAATCTATGACATTTTTCTGCTTCCGTAAGAAATCGTTTCTGTTTTCATTTTAAATTTTCGAGGAAATATGAACACACGACATCAACTTTACGCACTGTGGGTAA  
GCGCG

## SEQ ID 1256

VGNIIILTFPLLRVIVFLSFLIFEEDMVRINFTQLWVSA



ATGGATCCGATTCGTGTTGTATTCCACATTATTGCCGGTTGGCATGGGCGATTTCACATATTTTGGTGATTACCTGCAGGCAATTAATTTTCATGGCGTTGGCGTTCGTCTATATCGGGC  
AGGCGCACGATGCCAC

**SEQ ID 1272**

SEQ ID 1272  
MAGSTITAADYIKHHLQSLTSLSDVTQGGGLKNLIDFSPINLDVFFAVLLGVIGSFLMWRGAKKATAGVPRFQAAVEILFEFVDDMCKSLIHSKSKAVAPLGLTLFVWIFLMNDM  
LPVDLLPMWQGITGNHALLRIVPTADLNTALALAVGVLLICIYYNIKIKLGGWFHELFPAPFGAKLAPANFLNLNVEFLSKTYSHGMRIFGMYAGELVFLLLIALLGRSWAASGSVEV  
MDPILPVFHITAGLAWAIFHILVITLQAFIFMALAFVYIQAHDAH

**SEQ ID 1273**

SEQ ID 1273

GTGGCGCTGCCCGATATAGACGAACGCCAACGCCATGAAAATAAATGCGCTGCAGGGTAATCACCAAAATATGGAAAATCGCCCATGCCAACCGGCAATAATGTGGAATACAAACAGAATC  
GGATCCATGACTTCAACCGCTGCCGAAGCCGCCAAGAAGCGGCAAGCAAGGCTATCAGCAGGAATCCAGCTCGCCCGCATACATATGCCGGAACACCGCATACCGTGGGATACGGTTT  
TAGAAGAAAGAACTCGACCAAGTTCAACAGAAAGTTCGAGGTCGAGATTTCACCGAAGCGGCGCACTGAACAACTCGTGAAACCAAGCGGCCAAATCCTTTGATTTTGTATGTTTGAATAGAT  
ACAAATCAGCAACACCGCGCAGCAGGATGCCAAAGCGGTTCACAAATCGGCAGTCGGTACGATCGGCAGCAGGCGGTGATGTTGCGGTGAATGCGCTGCCATACCATCGGCAGCAAAATCG  
ACCGGCAGCATATFATCATCGCTCGCATCAGCGAAAATCCAAACAAACAGCGTCAGACCCAAACGCGCGGAGCGGCTTTTTAGACTTTTCGCTGTGAATGATGCTCTTACACATATCGTCCACA  
ATCAGCAACAGATTTTCCACGGCGCGCTGGAAAGCTCCGGGAACGCTGCGGTTGCTTTTTTTGCAACGCGCCACAACAGGAAGCTGCCGATTACGCCCAACAGGACGGCAAAAGCAAGCGG  
ATCAAGGTTAATAACGAAAATCAGCAATGTTTTTCAGTCCCTGACCCCTAGTAAACATCCGACAACTGGTCAAGCTCTGCAAGTGGTGCTTGATGTAGTCGGCAGCGGTAATGGTTTTCA  
CTGCCATAATCTTTCACTCTCAACATATCTAAAAAAACAGATGGC

**SEQ ID 1274**

SEQ ID 1274  
VRLPDLIDRQRHENKCLQGNHQNMENRPGQTGNVVEYKQNRHDFNAAGSRPRATAKQGYQQEYQLARIHTAEQPHTVGYGFRKKLDVQQQKVRRCFCTERRTEQLVKPAAQSFDVDDVID  
TNQOHADSECSGQVIGSRYDAQQGVNVAGNALPYHRQQIDRQHLHRVHQENPKRQRTQRRDGFRLPFAVNDALTHVHLEQDFHGGLETSGNACRCFFCTAPQOEADYAAQDQKKG  
IKVNRKKSINVFQSLTSLNRQTQALQVVLDDVVGSGNGFTCHNLSTLTKKPDG

**SEQ ID 1275**

SEQ ID 1275  
ATGGGGTTTGATGTCATCGCATGTGGTTTGATCGTTGGGTGCAATGGGTGCATCTATCGGTATCGCAATGGTCGGTCTAAATATTGGAAGTCTCTGCTGCGCAACCTGAACTGA  
TGGTCCGCTGCAAAACCAACTGTTCTGATGCGCGTCTGATTGATGCCCGATCTTGATCGGTGTCGCAATGCACTACTGTTTCGGCTTCGTCAACCCGTTTCAGGTGCA

SEQ ID 1276

SEQ ID 1276  
MGLIALACGLIVLALGALGASIGIAMVGSKYLESSARQPELIGPLQTKLFLIAGLIDAAFLIGVAIALLLFAFVNPFFGA

SEQ ID 1277

SEQ ID 1277  
TTGATATTTCACGTTACTTAACTTCGTATTGGGGTTAATCAAAACAGGCTGCACCTGTACGAACGGAGCAATCCGTCCTGATTATGCACTGCAAAACGGGTTGACGAAGGCGCAACAGTAGTG  
CAATGGCGCACCAGCATCAAGAATCGCGGCATCAATCAGACGGCGAATCAGGAACAGTTTGGTTTGCAGCGGACCAATCAGTTCAGGTTGGCGAGCAGAGACTCCAAATATTTAGAACCCGAC  
CATTTGCGATACCGATAGATGCAACCAATGCACCCCAATGCAACGATCAAAACCATGCGATAGCAATCAAAACCATTTTAAACTCCTTTAAAGAAACAAAGSTTTAAACTCAAAAAACAACTA  
CTTGGGAAAAATCAGTGGGCATCGTGGCCTGCCCGATATAGACGAACGCCAACGCCA

SEQ ID 1278

SEQ ID 1278  
LIFTLLNLRLIGVNGTCTCTNGRIRPDYAPANGLTKANSSAMATPIKNAASIRPAIRNSLVCSPISSGWRAEDSKYLEPTIAIPIDAPNAPNATIKPHATAIKPILNSLKKQRLNYKNKL  
LGIKSGHRAPARYERTPTF

SEQ ID 1279

SEQ ID 1279

GTGAATATCAATCAACATTAATTCGCTCAAATCATCGCTCTTTTCGGTTTGGTATGGTTTACCATGAAATTGTGTGGCCGCCGATTGCCAAAGCTTTGGATGAGCGTCCGCCAAAATCG  
CCGAGGGCTTGGCTGCCCGGACGCGTGGTAAAGCGCAITTCGAGCAGGCTGAAAAAAGGTTGCAGAACTTTTGGCAGAAGGGCGTAATCAGGTTTCCGAAATGGTTGCCAACGCCGAAAA  
ACGTGCCCGCAAAATTGTCCGAGAAAGCCAAAGAACAGGCTTCTTCCGAGGCCGGCGCATTCGAGCTCAGGCCAAAGGCCGATGTGGAGCAGGAATTGTTCGCGCACCGCGAATCCCTGCGC  
GATCAGGTTGCCGTGTGGCTGTCAAAGGTGCCGAATCTATTTTGCGCAGCAGAGTCGATGCTTCCAAACACGCAAACTGCTCGATACCCTGAACACAGGAGTTG

SEQ ID 1280

SEQ ID 1280  
VNINATLFAQIIIVFFGLVWPTMKFVWPTIAKALDERAAKIAEGLAAAEERGKSDPQAEKKVAEALLAEGRNQVSEMVANAETRAAKIVEEAKQASSEAARTAAQAKADVQELFRARESLR  
DOVAVLAVKGAESTILRSEVDASKHAKLLDTLQEL

SEQ ID 1281

SEQ ID 1281  
ATGCCAGAGTTCGCAACGATCGCCAGACCTTATGCAAAAGGCATTGTTCCGGTCTGGCTCAGGAAAAAAACCAATTGAGTCTTGGTTGGCGGACTGGAAAACTTCGCGCGGTGTGTTCCAG  
AAGGGAAGTGGGCTTCATTTGATTGACCGTCTGAAACGAAATGCTTCAGAAAAAGCAGATATPCTCATCGATTGGGTGCGTTTGAAGAGCAAGGAGTTAAAAAATCTTGTTATCGCTTGGC  
CGGGCAGAAACGTTTTCGATATTCGCCGAAGTGTATGCTCAATATCAAGACTTGACCTTATCATTTCAACCATATCAAACTTCGCGGTCAATTCACAGTGCGCTATCCGTTGACCGACAACAG  
GTCCGCGAGTTGGCGCAAAATGCTGAATAAGCGTTTCGACAGCGAGCTGAAAAATCTCTGTGCAAAATCGAACCGAGACTGATTGGCGGCATAAAAGTTGAAGTGGGTGATCAGGTTTGTGATT  
TGTCTGTACAAGGCAAACCTGAGTGCTTTGTACACGACTATGACGAAT

SEQ ID 1282

SEQ ID 1282  
MAEPATTAIRPYPKALFGLAQEKQNTESWLGGLKLAADVQGEKVASLIDRPETNASEKADILIDLVLGKDKELKNFVTVLAGQKRLSILPEVYAQYQDLTSLFNMHIKSAVTYSAYPLTDKQ  
VGLAQMLNKRFDSEKLSVRIEPELIGGIKVEVGDQVLDLSVQGKLSALYTIMIN

SEQ ID 1283

SEQ ID 1283  
ATGCTTTTCAGCGCTTATCTCTTCGGAACCTTAGCTACCCGGCTATGCAACTGGCGTTACAACCGGTACACAGAGGTTCTGCTCCACTCCGGTCTCTCGTACTAGGACGAGCCCCCGTCAAAAC  
TTCCAACGCCCATCTGCATAGGGACCAAACTGTCTCAGCAGCGTTTAAACCCAGCTCAGTACCACCTTTAAATGGCGGAAACAGCATACCCCTGGGACCGACTACAGCCCCAGGATGTGAT  
GAGCCGCACTTCGAGGTGCCAACTCCGCCGTGCATAGAACTCTTGGCGGGAATCAGCTCTGTTATCTCCCGGAGTACCTTTTATCCGTTGAGCGATGGCCCTTCCATACAGAAACACCCGGAT  
CACTATGTCCTGCTTTGCACTCTGCCGACTGCCGACTTGTCTGCTGTCTCGAGTTTAAGCTATCTTTTGCCATTGCACCTATGCAGTCCGATTTCCGACCGGACCTAGGTAACTCTTGCAGACTCTCTCGTTAC  
GCTTTGGGAGGAGACCGCCCCAGTCAAACTGCCCTACCATGCAGGTCCTCCGACCCGGATGACGGGTTGGGTTAGAACCTCAAAGACACACAGGGTGGTATTTTCAAGGACGACTCCACAGAG  
ACTGGCGTCTCTGCTTCCAAGCTCCCACTTATCTTACAGAG

SEQ ID 1284

SEQ ID 1284

SEQ ID 1285

SEQ ID 1285

ATGTTAGAAAGCTATCGTAAAGCCGCCGCCAGCGCGCGCCCTCGGCATTCCCGCCCTCCCTTTGAATGCGCAGCAAAACCGCGATTGGTTGAGCTGCTGAAAAACCGCCCGCAGCGG  
AAGCGGAGTCTTGGTTCGAGCTGCTTGCCCAACCGTGTTCCGCCCGGTTGGAGCATGCGCCCAAAGTCAAAGGCTCATCTCGCTGCGGTTGCGGCAAGCAGCGCATCCAGCCCGCTGGT  
TTCCCCCAAATATGCGACCGCAACTCTTAGTACGATGCTCGCGGTTACAAATATCCAGCCTTAACTCGAAGCTCTTGGACGACGACAACTCGCGCCATTTCGCCCAAGGCTTGAACAT  
ACGCTCTCTGATGTTTCGATTCTCTCCACGACGTTTCAGGAAAGAACCGAAAAAGCGACAAATACGCGCGCAGGAAGTTTGGCAATCTTGGGCAGATGCCGAATGGTTCCGCTCCCGTGCCTAAG  
TTCCCCGAAAAAATCACCGTTACCGCTCTTCAAAGTTGACCGCCGACAAACCAATACAGACGACCTCTCTCCGCGCCGACGCGTGGAGTGGTCCGCGATATTCGCTGCACGCGCTGGCCATGCT  
GAAAAACCCCGCGCAGCGCATCGCGACCAACACCGGCGGAAGTCGTCGGAATTAATTTGTTGAAGAAGCTCAAAGCCAAAGGCCATCCGCTTGCCTACGTCGGTGACGTGGTTCGGTAC  
GGTCTTTCACCGCAATTCGCGACCAACTCCGTCATTTGGCATACCGCGCAAGACATCCCGTTCGTGCGCAACAAACGCTTCGGCGCGCTGTGCTTGGCGGTAAAAATCGCGCGCAATTTCT  
TCAACACTCAAGAAGACTCCGCGCGCTGCGGATTTGAAGTCGATGTTTCCCGCGCTGAAAAATGGCGGATGTCGTCAATATCTTCTTATGAAGTAAAACTGCGAAAAACCGCGAGACTGT

TGCCGAGTTTGAATGAAATCACAAGTATTGCTGGACGAAGTGAAGCGCGCGCGGTATCAACTGATTATCGGTCCGGTCTGACCGCCAAAGCGCGGAAGCCCTGAAACTGCTGCC  
TCTACTGATTCGCCCTGCCGCAAGCGCTGCCGAAAGCAAAGTCGGTTTACCTTGGCGCAAAAAATGTCGGTCGGCTCGCGCTGTCGCCGGAAGGACAGCGCTGCCGTCGGTACTT  
ACTGCGAACCAGCGGATGACAGCGGTGGCTCGCAAGATACGACCGCGCGGATGACCGCGGACAGGTGAAAGACTTGGCTTGTGGGCTTCTCCGCGGATATGGTGATGACAGTCTTCTG  
CCACACCGCTGCCATATCCGAAACCTGTGATGTAATAACCCATAAAGAACTGCCCGCTTTATTCTACCGGTGGCGCGGTGTCCCTGCGTCCGGGCGAGCGGTGATCCACTCATGGCTC  
AACCGCTGCTGTTGCTGATACAGTCCGTACAGCGCGGACAGCCACACCGTTTCCCATCGGTATTCTTCCCGCAGGTTGAGGCTTGTGCTTTTCCCGCCCAACGGCGTAA  
TACCGCTGATATGCCGAGTCCGTATGTTAGCTTTTACGGGCAAGCTGCAACCGCGCGTAACCTGCGCGGATTGTTGAGACGCCATCCCGCTTACCGGATTAACAAAGGTGTTGCTGAC  
CGTTGCCAAAGCGGTAAGAAAAATCTTCTCGGCGCATCTTCGAATCGAAGGCTGCCCGATTGAAAGTGAACAAGCCTTGAATTGACCGACGATCCCGGCAAGCTCCGCG  
GCGGCTGTACCGTGAAGCTCAATAAGAGCGGATTCAGATACATGAAATCAACGCTGTTGATGAAAAATGATTGCTCAACGCGTATCAAGATCCGCGCGCTTGAAGCGCGCA  
TCAAAGCTATGAAAAATGGCTGCAAAATCCGAGTTCTCGAAGCGGATAAGATGCCGAATACGCGCGCGTGAATTGAAATCAACATGACGACATCAAGAGCGGATTAATCGCGTCCG  
GAACGACCGCGACGAGTATGCTTTATGTCGGAACGCTCCGCGACCAAAATCGACGAAGTGTTCATCGGTCTTGTATGACCAACATCGGCCACTTCCGCGCGCTCCAAACTTTTGGAA  
GGCAAGAGCGACATCCCGTCCGCTGTGGGTAGCGCGCGGACCAAAATGAGCGGAAAGAGTGTCCGACGAAGTCACTACGCGTACTCGCGCGCGCGCGCGGTATGAAATGC  
CGGCTGTTGCTGTTGATGGTAAACAGCCCAAGTACGCGAAGGTGCAACTGTCTATGTCACCTTCCGACCGCAACTTCCGAAACCGCTTGGGTAAAAACACTTCTGTTTACCTCGCGT  
GGCAGAGTTGCGCGGATTTGCTCCAAACTTGGTAAATCCGACCGCTTGAAGAATATCAAGCAATATCGGCATCAACGAACAGCGCGGATAAATCTACCGCTATATGAATCAAC  
GAAATCGACGCTACAAAGAGTAGCGGAGACCGTGAATGTT

## SEQ ID 1286

MLEAYRKAALAAALGIPALPLNAQQTADLVELLKNPAGGEGFLVELLHVRPVPVDAAKVKASFLAAVAAGSASSPLVSPKYATELLGTHLGGYNIHALIELLDDRLAPIAARKLH  
TLNMFDSFHDVQEAERKGNKYQEVLSWADAENWASRAKVEKITVTVFVKGDETNDLSPAPDAWSRPDIPLHALANLKNPRDITPDKPGEVGPILKEELKAKGHPVAVYVGVVGT  
GSSRKATNSVIMFTGEDIFFVFNKRFGVCLGGKIAPIFNTQEDSGALPIEVDVSALRMGVNHLIPYEGKIVKNGETVAFELKSVLLDEVQAGGRINLIIGRLITAKAREALKPLA  
STAFRLPQAPAESKVGFTLQKRVGRACGLPBGQVRFPTGYCEPRHTTVGSDTTPMTRDELKDLACLFSDHVMQSFCHPAAYPKFVDVKHRELPAFISTRGGVSLRPGDGVHSHL  
NRLLLPDTVTGSGDSTRFFIGISFPAGSLVFAAATGVIPLDHPESVILVRFSGKLQPGVTLRLDNLVNAIPLYAIKQGLITVAKAGKNIFSGRIEIBGLPDLKVEQAFELTDAASERSA  
AGCTVILKNKEPIIEYKNSVNLKMHIANGYQDPRALERIKAMEKNLANPELLEADKDAEYAAVIEINMDDIKREPIIACPNDDVCFMSESRSTKIDDEVPIGSCMTNIGHFRASKLLE  
GKSDIPVRLWVAPPTKMDAKELSDGHYGVLAGRAGARMEMPCCSLCMGNQAVQREGATVMSTSTRNFPNRLGKNTFVYLGSAELAAICSKLGIPTVEEYQANTIGIINBQDKITYRYBNFN  
RIDSNEVAETVNV

## SEQ ID 1287

ATGCAGCTTAATCTGCTGAAATTAGCGATCTGATTAAAGCCAAAGATCGAAATCTGTCTGTAATGCCGAAGTGAATACCGTGGTACCGTGATTTCGGTAACGCGTATCGTTCGA  
TCCATGGTTTGTGATGCAATGCAAGGTGAGATGCTCGAATTCGCCGGAACACTTTAGGCTTGGCGATGAACCTGGAGCGGACACTCCGTCGGTCCGCTAGTGTGGGCGAGTACGAACA  
TATTAAGAAGCGGACACCGGTACCTGTACCGCGCGTATTTAGAAAGTCGGGTGCGGCGGAATTTGGTGGACGCGCTGTCGATGCAATGGGTCGCGCTATCGACGCGCAAGGTCGCGATT  
AATACAACTTTGACCGCGCTCTGCGAAAAATCGCAGCGCGGTGATTGCAACGAAATCGGTTGATGACGCGGATGCAACCGGCTGGAAGCGGATGACTCTATGATTCTCTGCGGTGCG  
GTCAGCGTGAGTTGATTATGGAGACCGTCAGACAGGTAAACCGCGGTAGCATTTGGATGCCATCGTCAACCAAAAGGTACGGGTGTTATCTGTATCTATGTCGTATCGTCAAAAAGC  
ATCTTCTATTTGCCAAGCTGGTCCGCAATTTGAAGAGCATGCGCGGATGGAACACACAGGATTTGGTGTCTGCAACTGCACTCTGAAGCGCGCGCATTCGAATATATCGCACCTTATTCAGGT  
TGTACGATGGGTGAATCTTCCGCGATCGTGGCGAGATGCCCTTGATGTTTATGACGATTGTTCCAAACAGGCTGTGGCTTACCGTCAAAATTTCCCTGCTTTTGGCGCGTCCGCGCGG  
GCGAAGCTTATCCCGCGGATGTTTCTACCTGCACCTCCGCTGTGTTGAACGTCGCGGACGCTGCAATGAACACGAAGTGAAGAAATTTGACCAACGCGGAAGTAAAGGCAAAACCGGCTC  
TCTGACCGCGTTGCGGATATCGAAACCCAGCGCGCGGACGATCTGCTTTCGTTCCGACTAACGTCATTTTCGATTAACGACGCGTCAAGATTTCTTGGAAACCGGACCTCTTCAACCGCGGT  
ATTCGCTCTGCAATCAATGCGCGGATTTTCGCTATCCCGGTAGGCGGTGTCGCAACCAAAAGTGAATTAAGAGCTGGGTGGCGGTATCCGTTTGGCGTTGGCAATATCGTGAATTTGG  
CGGCGTCTCGCAATTTGCAATCCGATTTGGATGAAGCTACCGCAACAGTGTGAGCATGCGGAAGTCTGAACCGAACTGATGAACAGAAACAGTTCAGTACGTTGAATACCGCTGAAT  
GGCTTTGACCGCTTTGGGCAATCAACACCGGTTCGATTTCTGATGTTCCGCTTGCCTAACGCTTGAAGTCTGAATTTTGAAGCTTTTGGAGCTTTTCCGATACCAACATCCGGAAGTTTGGAA  
CGCGTCAATGCTTACGATGCAATGTCGACGAGAGCGGAGAAAAAGCTTGAAGCAGCGCATGAATTCCTTCAATCTCTTACCGCTATCAGGCA

## SEQ ID 1288

MQLNPABISDLIKAKIENLSVNAEYSTRGTIVISVTDGIVRIHGLSDAMQGMELFPGNLTGLAMNLERDSVGAIVLGEYEHKEGDTVTCTGRILEVPGRELVRVVDALGRPIDGKPI  
NTTLTAPVEKIAPGVIAKRSVDQPMQTLKAIDSMIPVGRGQRELIIGDRQTKTAVDALIVNQKGTGVICIVVAIGQKASSIANVVRKLEHGAHEHTVVAATASEAAALQYIAPYSG  
CTWGEFFRDRGEDALIVYDLSKQAVATRIISLLRRPPGREAYPGDVFIYLSRLLEAAARVNEHEVEKLTNGEVKGTGSLTALPIITFQAGDVSAPVPTNVIISITDQIPLFETDLFNAG  
IRPALNAGISVSRVGGAAQTWIKLGGGIRLALAQYRELAAFSQFASDLDEATRIQLEHGEVVTLEMKQKQFSTLNTAENALTWAINNGSYSDVPKALAFEFELFSFVRTQHPVEVLE  
AVNAGSAMSESEKTELAAMKSFKSSYAYQA

## SEQ ID 1289

ATGGCAGTAGGAAAGAGATTCTACCAAAATCCGAGTGTTCAGAATACCCAAAAGACTACTAAAGCGATGCAAAATGGTGTCAACCTTAAATAGCGGAAGACTCAGGAACGGATGAGTT  
TGGCGCGTCCGTATGCCGAAAAAGTGGTATGGTGATGAGCCATCTTGGCGAAACCAATACCGATCATGGTATTCGCTTACTGGAATCTCATCGGAAATCAGACGTGCTGCTTTTATTTT  
GATTACGCTGATGAAGGTTTGTGTGGCGGTTTGAACGCCAACGTGCTGAAAGTTTTGGCACAAGTTCAAGAGTATCGGAATCAAGGTATTAAGAGGAAATCGTATGCTCTGGCAGT  
AAAGGCTCTGATGGCGTCTCAGAGCATTTGGTCTGAATGTGGTGGCAGTCCGCTAAATTTGGGCGATACCCAAAAATGGAATGCTGCTCGGACCTTTGACAGAACTTTTCCAAACGATG  
AGAAATAGAAATGACAGAAATCCATCTGGTGTATTCGGGTTTGTCAATACCATGCGTCAAGAACCAGGAGTGAAGTATTTGCTGCTATCGGTGAGAACGTTATGGCGATTACGCTCC  
CAATCAACGCTTACGCTGGGAATACCGCTACGAACCGACTGCACTTGCAGTGTGGAATATCTGGTTCCGCGCTATTAGAGTCTGCTGGTTTATCAGCGGTGAGCGCAATATGGCATCC  
GAACAGGACGCCGATGGTGGCAGTGAAGCTGCAACAGACAAATCGAGCAATGCCATCAAGAGTTCGCTTGGTATATACAAATCCGCTCAAGCTGCGATTACCAACGGAATTTGTCAG  
AAATGTAGCAGGTGCGGCGCGCTC

## SEQ ID 1290

MAVGKELLTKIRSVQNTQKITKAMQMVSTSKMRKTQERMSLARPYAEKVRVMVSHLAQTNDHGIPLLESHREIRRVGFILITSDKGLCGGLNANVLKFLAQVQVEYRNQGIIEETVCLGS  
KGLMACQSIGLNVVASAVNLGDTPKMEHLLOPLTELFORYEKHEIDRIHLVSGFVNTMRQEPMEVLLPIGENVIGDSAPKSPFSWEYRYETPALAVLEYLVRRYLESVVYQALSDNHAS  
EQAARMVAMKATDNAGNAIKELRLVYNKSRQAAITTELSIVAGAAAV

## SEQ ID 1291

ATGACCAAGCGAAATCGTACAAATATCGGTGCGGTGTTGACGTGGAATTTCCACGCGACATGATTCCGCGCGTTTACGACGCTTTGAAATAGACGAAACCGCTGACTTTGGAAG  
TCCAACAGCTTTTGGGTGATGGCGTAGTCCGTACCATGCTATGGCAGCTCGGACGCTTGAAGCGCGGATGACTGTGAGCAATACCTGGTTCGCCCATTACTGTGCGCGTAGGTAAAGG  
TACGTTGGACCGCATTTGTGATGATTGGGAACCGCTGTTGACGAGGCAAGTCCATTTGATACGACAGAGTCTGCTCCATCCCAAGACCGCTCTTAAAGTTGACGAATCTGCTTCCACA  
ACCGAATGCTCGAAACGGCGATTAAGTGATTGACTTGTGTTCCGTTTCCAAAGCGGTAAAGTAGGTCTGTGCGCGGTGCCGCTGGGTGAAACCGTGAACATGATGAATTTGA  
TCAACACATCGCCAAAGCGCACAGCGCTTGTCCGTGTTCTCAGCGGTGGGTGAGGTCACCCGCAAGGTAAACGACTTACCAACGAGATGAAGATTCCAAGTATTTGGATTAAGTAGC  
CATGGGTATGGCCAAATGAAGCAACCTCCAGGCAACCGCTGCGCGTCTTTGACCGGTTGACTATGGCTGAAATCTTCCGTCAGCAAAAGACGAAACCGTAAAGGTGCTGACGTA  
TTGTTCTTCTGACAACTACTACCTTACACTTGTGGCGGTACCGAAGTATCCGCACTGTTGGGCGGTATGCTTCTGCACTGGGTACCAACCGACATTTGGCTGAAGAAATGGGTGCTT  
TGCAAGAGCGTATTACCTTACCCAAACCGGTCCATTTCTTCAATCAAGCGGTATATGATCTCGGATGACTTGAAGTACCGCTTCCGCGCACTTTCCGCGCACTTTGACGCGAC  
CGTGTATTTGACCGGTGATTTGCTCTTTGGGTATTTACCCGCGAGTTGACCGCTGACTTCTACTTCCGCGCAATTTGGATCCGATGGTATTTGGGTCAAGAGCACTACGACGTAGCGCG  
GGTGTACAGTCTACTTGCAAAAATACAAAGAAATTCGCGACATCATGCCATCTTGGGTATGGAAGAAATTTGTCAGCAAGACAACTGGCTGTAAAGGTGCCGTAATACCAAGCT



TCCTGTCTCAACCGTCCACGTTGCCGAAGTGTTCACAGGTTCTCCAGGCAAAATATGTGCGCCCTGCGCGATACCATTCGCCGCTTCAAAGCCATCTTGAACGGCGAATACGATCATCTGCC  
CGAACAGGCATTCTATATGTGTCGCGAGCATCGAAGAAGCGGTTGAGAAAGCGAAAACCTTAAAC

## SEQ ID 1292

MSQKIVQIIGAVVDVEFFRPMI PRVYDALKLEENGLTLEVQQLGQGVVVTIAMSGLKRGMTVMSGSPITVPGKTLGRIVDVLGTPVDEAGPIDTKSRATHQAAPKFDLSST  
TELLETGKIVIDLCPFAKGKVGVLPGGAGVGKTVNMMLINNIKAHSGLSVFSVGERTREGNDYHEMKDSNVLKVMVYQMEPPGNRLRVALTGLTMAEYFRDEKDEWKGKRV  
LFFVONIRYTLAGTEVSALLGRMPSAVGYQPTLAEMGRLOERITSTQTSITSIQAVVYPADLDTPSPATTFARLDATVVLSDIASLGIYPAVDPLDSTSRQLDPMVLGQEHYDVAR  
GVQSTLQKYKELRDI IALLGMDLSDEDKLAVMRARKIQRFSLQPFVVAEVTSGPGKTVLRDITAGFKAILNGEYDHLPEQAFYMVGSIEAEVAKTLN

## SEQ ID 1293

ATGCAAGTTGAGGTTGTAAGTGGCGAGCAGAAAATCTATTTCAGGCGAGGCAACATTTATCGTTGTTCCGACTGTACAGGCGAACTCGGTATTTATCCGCGACAGAGCCGATTATGAGTT  
TGGTGCCTCCCGGTGCGTTGCGTTGACCGTTCCGGGCGAGGATAAAGAGGTTTGGTTCGTGTTCCGGCGGTATTTTGAAGTACAGCCTGATAAAGTAACGTCTTGGCGGATGTTGC  
CGTCCGCAAGTCCGAAATGAGTCCGGCAGTCCGGAAGAGCGGAGGCGGCAATTTCCCAAGCTAAAGACGATAAGGCTTTGGCGGAAGCACATAAGCATTTGCTGCC  
GCAATTGACAGCTCAAACCTTTGGACTATATCCGTTCCGCAAGAAA

## SEQ ID 1294

MQVEVVSGEQKIYSGEATFIVVPTVQELGIYPRHEPIMSLVRPGALRLTPVGEDKEVLVAVSGGILEVQPDKVTVLADVAVRSAEMDRARAEEAKKAAEAGISQAKDKALABAKALAA  
AIAQLKFLDYIRSHK

## SEQ ID 1295

TTGCAGTTTGAAGATGATTGTTCGAAGGTAAGCATGGCTTATGTTCGATAAAAATAAGGTTTTATTCTACTGTTTCCATAGCCGCTTGAATAGATTATCTCGAAGACAGCC

## SEQ ID 1296

LQFEDDLLEGKHLPLDKIKVLFYCFHSRLNRFISKTA

## SEQ ID 1297

ATGGAAGTCGGTGCCTGCACATCCCATCCGCGACCTGCCCTGCGCGCTCGGCCCCGAGCCTTGGTTTCCGCGCTACGTCCAACCCAGCCGCGCCCCAAAGAGCGCCGCTACGCGGACA  
ACCCCAACCGCTGCAACACTATTACCAATTCAGTTCGCGCTCAAACCGCGCCCGCAATATCCAAGACCTTATCTGACTCCCTGCGCGAATTTGGGCTCGATCCCAAGTCCACGA  
CATCCGCTTTGTGGAAGACGATCGGAAACCCACCTCGGTGCGTGGGGTTTGGGCTGGGAAGTCTGGCTCAAGCGCATGGAAGTAACCCAGTTTACCTATTTCACAAAGTCGCGGT  
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TAAGCTACGGCGACGTGTACCATCAAAACGAAGTCGAGCAATCTACTACAACTTCGAATACAGCATGCGGACTGGCTGCTGCGCGAGTTCAACGACTACGAAGCGCAAGCCAAACGCT  
GTTCCGCGAAGAAAACCGCGGCTTGCCTTACCTGCCCTACGAGCTGGTCTCAAAGCGGGGCTACGTTCAACCTTTAGACGCGCGCGCGGATTTCGTAACCGAGCGGCGCACTTAT  
ATTGGAGCTATTGCTGATGTAGCCGCGCGCTGGCGCAAAAATATATCGAAGCGCTGAGAACTGGGCTTCCGCTTGATTAAAAA

## SEQ ID 1298

MEVGAGTSHPATCLRALGPEPFAAYVQPSRRPKDGRYDNPRLQHYIYQFVALKPAPANTQDLYLDSLRELGDIPKVEDIRFVEDDWENPTLGAWLGWEVNLNGMEVTOFTTYPQVGG  
IDCTPVLGEITTYGIERLAMYLGVENYDLVWAKTPDGNVTSGDYVHQNEVEQSTYNFEYSADMLLRQPNDEAQAQKRLFAEENAGLALPAYELVLKAGHTFNLIDARGAISVTERATY  
IGRIRALSRAVAQKYIESREKLGFPLIK

## SEQ ID 1299

ATGACACCCCAAACCTTTTAATCGAACTCCTTACCGAAGAACTCCCGCCAAAAGCCCTGAATATCTGGGCAACCAATTTTCCGCTTCCGTTGCCGAAGGCTTGAAGAAAGCGCACTGG  
TTGACGCGCGCGCGCAATTTACGCTTATGCTTCGCGCGCGCGTTTGGCGGTTCAGTCAAAAACGTTGAAGCGGCTTCAAGCGCATCAGAAAATCGTGAAGAAAGCGCGCTGCGGTGCGGAA  
TGCGGTAAAGACGCTACGCGGACCAAGGCTTTGGAAGGTTTGGCGCGCGCGCGGCGGAAATCGAAGACCTGACCATCTCCACGACGCGCAGGACGCTGTACGCTTACGAATAC  
GTCCAAACCGCGCAGACCTTTGGCGGAGCTTTTGAAGAACTATCAATCAAGCTGTTAAGAGCTCGCGATTCGGAAGTAATGCGTTGGGCGCAGCAGCAGTTTACCTTCTGTCGCGCGCTG  
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CGCGGACAGCTACGCGGCAAAATGCGCGGCGCAAGGCAAGTCTGCTGCTTGTGTTTGGCGCGCGCGGCGGAAAGCGCGGATTCAGACGCGCAITGGAAGCGGCGACCGCTCTGAACCGGACCGCT  
GCGCGGATGAAGCGCTTGGACGAAGTAACGCGCTGCTGGAATGGCTGTTGTTTGAAGCGCGGTTTGGAGAACACTTCTCGCGCTGCTCAAGAATGCTTGATTTTGACGATGC  
AGCAAAACCAAAATTAFTTCCGCTGCTCGACCAAAACCGCAAGCTGATGAACCGCTTCTGCTGTTTCCAACTGCAAAACGAGACCGCTGCGCATCATCCGAGGCAAGCAAGCGCT  
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GAACGATCGAAGCGCTGCAAGCATCGCGCGCATATCGCAAGCAATTTGGCGCGGATGCCGCGCGCAGCGGCGCGCGCGCTTGGCAAGCGGCACTTGGTAACGAAATGCTG  
GCGAGTTCCCGCAACTGCAAGGACGATGGGCAAAATACATACGCGCGCTTGGACGCGGAAACGAAAGTTCGGAAGCTATTAGCAACACTACCAACCGCGTTTGGCGGCGCAAGCT  
GCGCGAAGCAAAATTTGCCGCGCGCTGGCACTTGGCGCAAACTGGAACCTTGTGCGCATTTGATTCCTACCGCGCAGCAAGAGCCCTTACGCGCTGCGCGCGCG  
GCTTGGGTMTTTCGCGATGCTGATGAGTACGTTTGGACGTGAACGAATGATTCAGACGCGCATTCGACAGCTTCCGCAAGGTTTGTCTCAACGAAAAACGCGCTGTGAACCGCG  
ACTTTATGCGAGCGCGCTTCCGCTGCTGCTGCAAAACGATTATCCGCAAGACATCGTTCCGCGCTACTCGCAACAGCGCGCGCTTGGAGATTTGACGCGCAAACTGACGCGGT  
CGCGGTATTCAAACACTGCGCGAGCGCGCGCTGCGCGCGCGCAACAAACGCTGCAAAACCTGCTGAAAGCGGATGCGGAGTTGGCGCGGTTAACGAAAGCGCTGCTGCAACG  
GACGAGAAAAAGCGCTGATGCTGCGCGCAAGGTTTTCAGCGCAAAATCGCGCGCGCGCTGCGCGAGGCAATTTCCAACTGCTTTGTCCGAACTGCTTCCGTCAGCGCGCGGTTG  
ATGCTTCTTCGACGCGGTGATGCTGATGCGGAGATGCCGCGTAAACAAACCGCTGAACCTGCTGAACCGCTTGGCAGGCGAGTGAACGCGGTGCGCGACATCGCGCTTTTGGG  
CGAG

## SEQ ID 1300

MTPTLLIIEELPPEKALNNLGNHFAASVAEGLEKAQLVDGAEEFTAYASPRRLAVQVKNVAVQADQKIVKGPVAVNAVVDOTPTKALEGFARGAGAKIEDLTIIVHDERQDWAYEY  
VQGRPLGLLENTINQAVKLPKPKVWRGSSSTFTVVRVHGLIVLHGGDVVNVSVLGLQSGNQLGHRFLSDGEIIEADSYAQMRRGQKVVASFAGKAAIQTALBQARRLNATV  
AADEALLDEVTALEVPVLEAGFEHFLAVPQECILITHQONQYFPILLQNGKLMNRFLLWSNLQTEDESHIIRGNRVLRLARLSAEFFYKQDQKATLESRLPKLANVYHNKIGSQA  
ERIERLQSTIAAHAKALGADAAAAAERARLAKADLVTEMVGEFPELQTMGKYARLDGETEIEAIEQHYQPRFAGDKLPSKIAAVALADKLEFLVGIWIGLIPITGDKDFYALRRA  
ALGILRLMQLYGLDVNELIQTAFDSFPQGLLNEKTPSETADFMQARLAVLLQNDYQDI VAAVLAKQPRRLDLDTAKLQAVAVFKQLPEAAALAAANKRVNLLKADAEGLAVNESLLQ  
DEERALYAAAGLQPKIAAABAEGNFTALLSELASVKPQVDAFPDGMVMAEDAARVKNRLNLLNLAGQMNADIALGE

## SEQ ID 1301

TCCTGCCACCTGTGTCGGTTTGGGTCAGGTTTCGATCAAACGAGCTTACTGGCTTTTCCGGAAGCGTGGTATCGGTTGCTTCCGTCGCTGCGTAGACACTCGTCATCAC

## SEQ ID 1302

SCPPVSVCGTVRFKLKLSGFSNKRIGICFVSVDTREH

## SEQ ID 1303

ATGCTTGAACCATACCGTCCGATTTGTCAAACCGTCCGATTTGTGGGAAAAATCCCAAGATTGAATTTAAGCGAGGCGGACACCGGTTGGACAGGGAAGGCTATCGCCCAATGTGCGTA  
TTATCTTAATTAACGAACGTAACGAAGCTTTTGGGTAAGCGCGTTCGCGCAACATTCATGGCAGTTTCTCAAGGCGGATCAAGCGCGGCAAGCCCGGAAACCGGATGTACCGGGA  
ACTTTACGAAGAAGTCGAGCTTTCGCGCAACACGTCAAAATCGTGGGCGGACGCGGCTGCTGCGTTACGAGCTGCCGAACACTGGGTGCGCGCGAATGGCGCGGCTCTTATGCG  
GGACAGAGCAGATTGGTATCTCTCGCGCTGACCGCGGAGATTGCGATGTCACCTGCGCGCCACCCCGCAACCCGGAATTTGACGCGTGGCGTTGGCATCAATATTGGGCGCGGCTG  
ACGAAGTATTGATTCAACGCGCAGCTTTATTGGAGGCGTTGAAAGAACTCTTCCCGCTTCTGCGCGGTATGGAAGTTATGAAGACTTTGCGCGCGGCAACCTTCCGCGCAACCG

## SEQ ID 1304

MLPYPYRIPCQNRPICGKIPRIANLTGDTVLDRGYRPNVGIILINERNEVFWGRVREHSWQFPQGIKPGESPETAMYRELYBEVGLLPQHVKIVGRTRDMLRYDVPNNVVRREWRGYSR  
GQKQIWLRLR/IGRDCDNLRAIRHPEFDGRWQYNAFVDEVIDFKRDVYLALKEKLSRFLRGMSYEDFAARQPSGNR

## SEQ ID 1305

ATGCCGCTCGAAGGTGTGTCAGACGGCATTCGGGTCAATCCCTTACTCCATACGGATGACGGGGATCAACATTCACGGTCTCGGCTACTTCGTTG

## SEQ ID 1306

MPSEGCSDGLAVNPLHDTDDGDTFTVSATSL

## SEQ ID 1307

GTGGCGGAGATGGAAAAAGACCGCAGCATCATTCGGATGGGCGCGTGGTGGAAATTTGTGGAAGAAAAGACCGCAACCGGCTGGCGCGCATCAAAACACGGCAAAATTTGAAAA  
AGCCGACCCGGCAGGAAGACATCGCCGCTTTTCCCTTTGCGCAACCCATACACAACAACACGATGATTATGCGCGCGCAGCGTCATTGACGGCGGTTTCGGTTACAAACCGCGCGGA  
TTGGGCGGAAGATTACCAATTTTGGTACGATGTCAGCAAAATGGGCGAGGCTGGCTTATTATCCGGAAGCCTTGGTCAAAATACCGCTTCACGCAATCAGGTTTCATCAAAACACAGCGTC  
CGCCAAACAGAAATCGCGCAAGGCATCAAAAAACCGCCAGAAACGATTTTTCAGCTCTATGGGTTTAAAAACCGGTTGACAGCGCTAGAAATACCGCAAAACAAAGCAGCGCGGTACG  
AATTGCCGGAAGGATTTCGCGGAAGGATTTCGACCGCGCCGCGGTTTGTACCGATGCTTCAACCGGACGACACCGCCCTCCGCGCGGTGGCTGGATTTCGCGCGCAGACGG  
CAGGATGAGCGCGCTGTATTACCTTGAGGCAATCTTCGCAATTTGTACCGCTGATTAACAAACCGCGCGGAGCGCGGTTCGCGCAGGAAAGAACAGGAGATT

## SEQ ID 1308

VGMEKDRSI IAMGANLELSEKDNRLARHKKIKWKPTRHEDIAAPFPFNP INHNTIMRRSVIDGGLRYNIGRDWAEDYQFWYDVKLGRLAYYPEALVKYRLHANVSSKHSV  
RQHELAQGIQKTARNDFLQSMGFKTRPDSLEYRTKAAAYELPEKDLPEDEPARRRFLYRCFKRTPTTPSGAWLDFAADGRMRRLFTLRQYFGLIYRLIKNRQARSASAGKBPXI

## SEQ ID 1309

ATGCAAAACACGTTATCAGCTTGGCTTCCGCGCGAGAACGCGAGGCGCACATTCGCCCAACCTTCGGCAGTCGCGGCATCCGTTTTCAGTTTTCGAGCGCATGTCGCTCTGAAAGGC  
TGAACACGGCGATGCGGGAACCTGCTCCCGGCTTGTGCGCGCACCCCTATTGAGCGGAGTGGAAAAAGCTGCTTTATGAGCCAGCGCTATGTTGGGAACAGCGGTGGATGAGGTCT  
GCCGTATATCGCGCTATTGAGGACGACGTTTACTCGCGCAAGCGCGGAGCAGTTCCTTCGCGAAGACTTGTGTTGAAGAGCGTTTGTATAAGGATTCCGCCCTTATCGTCCGTTG  
GAAACGATGTTTATGCAAGTCTGACCTCGCCCTCCGCGGTGGCGGACTACGCGCGGCGCGCTTTCGCTTTTGAAGCGAACACTGCGCGGACCGCGGCTATATTATTTCCGAAAGG  
CGATGCGTTTTCCTGGAAGGTTTTCGCGTTTTCGCGCGCGAACGCTGCAACCTGTGCTGATTTGATGTTTCGCGCAACCTGACGACAGGGAAGGAAATGCCGCTTTCGCGCTCAATCC  
CGCTTGTGCGCGCAAGAGCTGCATTTATGCCAAGTTTCAGGACCAAAACAGCGCATTTGGCAGCGCTGATCGAATGACCGCGCGCTGAACCGCAACAGCAATGCCGCGATTCCCGCGC  
AACACATTCAACACCGCTGATCCGCGCTTGACCAAAATCGCGAGGAAAGGAAAAACGCCGAAAGCGCGCAACAGACAATCGGCAAAATTTATGCTCTTTCGCA

## SEQ ID 1310

MQNHVLSIASAERRAHIAATFGSRGTPQFFDALNPSERLBQAMAEVPLSAHPYLSGVEKACFMASHAVLNEQALDEGLPYIAVFEDDVLLEGAEQFLAEDTWLEERFDKDSAFIVRL  
ETMFHVLVPSGVDYGGRAFPLLESEHCITAGYIISRRAMRFLDRFAVLPERLHPVDMMPGNPDREGMPVCQLNPALCAQELHYAKPHDQNSALGSLTEHRRRLNRKQWRDSPA  
NTPKHLRLALTKIGRERKRRKREPTIGKLIIVFPQ

## SEQ ID 1311

ATGGACATCGTATTTCGGCGACAGCAACTATGCCGCTATCTTTCGCTTTCGCGCAAAAGCGTGAAGCGGCCCATCCGATACGGAATCAGGTTCCAGCTCTCGATGCCGCGATCA  
GTGAGGAAACCGCGCGCGGTTGCCGCCAATTTGCGGGGGGGGGGGG

## SEQ ID 1312

MDIVFAADNYAATLCVAASVEAAHPDTEIRFVLDAGISZENRAAANAIRGGGG

## SEQ ID 1313

TGCGCCCAATTTGCGGGGGGGGGGGGTAATATCCGCTTTATAGACGTAAACCCGGAAGATTTCGCGCGCTTCCCTTAAACATCAGGCACATTTCCATTACGACTTATGCCGCGCTGA  
AATFGGCGAATACATTGCCGATTCGACAAAGTCTGTATCTGATACGACGATTTGTCAGGAGCGGCTGAAGGCTTATGGGATACCGATTTCGGCGGTAACCTGGGTCGCGCGTG  
CATCGATTGTTTTCGAAAGGCGAGGAAGATACAAACAAAAATCGGTATGCGCGGACGGAAGATATTATTTCATCGCGCGCTTATGCTGATCAACCTGAAAGGTCGCGCGCGCAGAT  
ATTTTCAAAATGCTCGCAATGGGTGGAACAATACAAGGACGTGATGCAATACAGGATCAGGACATTTGAACGGCTGTTTAAAGCGGGGTGTGTATCGCAACAGCGGTTTCAACT  
TTATGCGGACCAATTTATGCTTTATGCGCAAGCGGTTTCGCTCCGCGCATCCGACCCGCTTACCTCGACCGTAACCAATACGCGGATGCCCGTCGCGCTCAGCCATTTATGCGCGCTCGGC  
AAAGCGGTGGCACAGGACTGCACCGTTTGGGGTGGGAACGTTTACAGAGTTGCGCGGCGCTGACGACCGTTCGCGAAGATGGCGCGGCAAACTTGCCTCCGCGCGCAAGCGT  
ATGCTTCAAGATGGCGCAAAAGCTGCTGCGCAGATCTTACGCAAGATTAT

## SEQ ID 1314

LPPICGGGGNIRFIDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCKVLYLDTDLVLDGLKPLMDTDLGNNVWACIDLVERQEGYKQKIGMADGYYTPNAGVLLINLKKRRHD  
IFKMSCEWVEQYKDMQYQDQDILNGLFKGGVCYANSRFPNPHNYAFMANGFASRHTDPLYLDRTNTPMVAVSHYCGSAKPWHRDCTVWGAERFTELASLTTPVEBWRGLAVPTKR  
MLQRWKKLSARFLRKTY

## SEQ ID 1315

TGCGGTCGCGCGGCAAAAGCGTATGCTTCAAAGATGGCGCAAAAGCTGTCTGCCAGATTCTTACGCAAGATTATTGACGGGCGAGCGGCTCTGAAGCTTCAGACGGCATCGGACGTA  
TCGGAAGAGAGAACGGATTGACGCTTTAGTCAGCGTATTGATTTCGCGCTCAACGCTAGAAAAATATTTCGCCAATCATTCGCCCGCTCGTGAATCAGACTTGGCGCACTTGGATA  
TTTGTATGTCGA

## SEQ ID 1316

LPSSRRQSVCFKDGAKSLPDSYARFIDGAGRLKPSDGIIGRIGKEKRIAAFSQIRIDLRLQREKIFCPIIGRRRESDLAQLGYFDCR

## SEQ ID 1317

TTGGATATTTGATTGTCGATGACGGCTCGACGGACGGCAGCGCCGCTTTCGCGCGGCTTTCGAAGAAGACGACGGCAGGATCAGGATAATTTCCAATCCCGCAATTTGGGCTTTATCG  
CTCTTTAAACATCGGCTGGACGAATTCGCAAGTTCGCGGGGGGGGGGGAATATATTGCGCGCACCGATGCCGACGATTTGCTTCCCGCGCTGGATTGAGAAAAATCGTGGGCGAGAT  
GGAAGAACCGCAGCATCATTCGATGGGCGCGTGGTGGGAAGTTTTCGCGGAAGAAACATAAAGCGTGCTTCCGCGCATTCGCCGAAACGGCGCAATTTGGGCAAAACGACCGCG  
CATGAAGACATGTCGCGGTTTTCCTTTTCGCGCAACCCATACACAACAACAGGATGATTATGAGGCGCACCGCTCATTCAGCGCGGTTTCGCTTCGATCCAGCTATATCCAGCGCGAAG  
ACTATAAGTTTGTGACGAAGCGGCAAACTGGGCGAGCTGCTTATTATCCGAAAGCTTGTCAAATACCGCTTCCATCAAGACGAGACTTCCTTCAAAATACAACTGCAACAGCGCAG  
GACCGCGTGGAAATCAAGAGAAATCAGGCGGGGTATTTGAAGCGCGCAGGACATGCGCTCGGGGCGGACTCCCTGAATTACGGGCTTTGAATCAACGGCATATCGGTTGTACGAA  
AAAGCGCTGTGCGGACAGGATATCGGATGCTCGCTGCTGTACGAAATTTCTTGTGCTGGAAGGATATCTTTGACCGATTGCTGGATTCTTGACAGACCGCGTATCAGGA  
AGCTGTTTTCGCCACCGCAATATAGGAAATCTGAAAAAATGTTACGCGCTTGGAAATACCGCAGCTAT

## SEQ ID 1318

LDIILVDDGTDGTPAIAARRFQEDGRIRIISNPNLGFIAISLNLGLDELAKSGGGGEYIARTDADDIASPGWIEKIVGMEKDRSI IAMGANLELSEENKSVLAAIARNGAIDMKPTR  
HEDIVAVFPFNP INHNTIMRRSVIDGGLRDPATYIHAEDYKFWYBAGKILGRLAYYPEALVKYRPHQDQTSKYNLQRRRTANKIKKEIRAGYWKAGIAGVADCLNYGLLKSTAYALYE  
KALSGQDGLRLFLYBYFLSEKYSLTDLLDLDTRVMRKLFAAPQYRKILKKMLRPHKYSY

## SEQ ID 1319

ATGCTTCACATCTCAATTAACCTTCGCGCACCGGCGAGCGTCACACCTTATACGTCACCTTTCGTTTGGCAGAGTCTGCTGTTTTTAATAACAGTCGACGACCTATCTCTCGG  
ACCTCCGGGCTTACGGAGCAAGTCTTAACCTTAGAGGCGATACCTTCTCCGAGATTACGATATCAATTTGCCGAGTTCTCTCCCGAGTTCTCTCAAGCGCTTAGAATCTCATC

CTGCCACCTGTGTGGTTTCGGTACGGTTCGATTCAACTGAAGCTTACTGGCTTTTCCTGGAAGCGTGGTATCGGTTCGTTCTGTTGTCGTTAGACACTCGTCATCACTTCTCGGTGTTA  
AGAAAACCCGGATTTCGC

**SEQ ID 1320**

**SEQ ID 1320**  
 MLHLQLTFRHRAGVTPYTTSTFVLAECVFNKQSQPPILCDPPGLTEQVLNLRGHTFSRSYGINLPSSFSKVLSSALEPSSCPPVSVCTVRFKLLSGFSNKRIGICFPVSDTRHFSVL  
 RKPQFA

**SEQ ID 1321**

SEQ ID 1321

ATGTTAGATATCCAATTGCTCCGACAGCAACACCGCGCGCGTTGCGGAACGGCTTGACAGCGCGGGTTATGACTTTTGATACCGCACGTTTGTAGCGCATGGAAGAACGACGCAAGTCGGTTC  
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TAGACGCTGCAAGGCAACGGTCAAGTCCGCCAAATTTGCAGAAGATTGTTCCACGTTACCCGCGCGCGCGGATGAAACCAAAACCGCAGCATCTGATTTACCGCGCGGAGGTATACCTG  
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GATTTCCAAGCAGCGCGCATGAAGGCGCGTTTCAAAGACGAAAACGGCAAAACCGCTTGGTACATACCTTAAACGCGCTCCGGTTTGGCAGTGGTTCGCACTTTGGTTCGCGGTTTGGAAA  
ACCATCAAACCGCGACGGCAGCATCATATATCCCGCGCGCACTGCAACCGTATATGGGCGGTGTTTACCAAGTTGGAAGTGAAA

**SEQ ID 1322**

SEQ ID 1322

MLDIQLLRNNTAAVAERLARRGYDFDTRPDALEERRKSVQVKTTELQASRNSISKQIGALKGQGKHEEAQAAMDQVAQIKTDLQAAADLDVQGKELDANLLSIPNLPHESVPPGKDETE  
NVEVRKVGTPPREPDEFIKDHVDLGEPLGLDFEGGAKLSGARTVMRGQIARLHRALAQFMLDTHMLQHGTYTHYTPYIVDDTTLQGTGQLPKFAEDLPHVTRGGEDETKTYQLIPTAEVTL  
TWTVAGSIIIPSEQLPLKLTAFSPCFRSEAGSYGKIDTRGLRIHQHQPDKVEMVQIVHPKSYGALEEMVGHAENILKALELPYRVTITCTGDMGFSAAKTYDLEVMVPAQNTYREISSCSNCE  
DFQARRMKARPKDENGKNRLVHTLNGSGLAVGRTLVAVLENHQAQNDGSINI PAALQPYTNGVVTKLEVK

**SEQ ID 1323**

SEQ ID 1323

GTGAACCTGAAAAACCCGCAATTTTCGAAACTTTTGGAGCTTCACGCGGAAGAAATACCACTTACCTCGAAGCTTGC CGCGAGTTGAAAGACGCCAAAAGCGAGGCGCGAGATTTCAGC  
GGATGAAAGGAAAAACATCGCCCTGATTTTGA AAAAATCCACGCGCACAGCTGTGCGTTTGAAGTGC CGCGCACGCGACCAAGCGCGGATGCAACCTATCTGGAACCGTCCGCCAG  
CCAAATTCGGGCAACAGAAAGCATTTCAAGACACGGCGCGCTCTTAGGCAGAATGTACGATGCCATCGAATATCGCGGCTTCGCTCAGGAAACTGTGCAAGAAATTGGCAAAATATCGGGGC  
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CAGGAACGCATCGATTTGCTGAAAGATTACCGGTTACGCCCGGAATGTCGCGGCATTCGGGCAATTCGGGCAATTCGCGCAAGTCAAAATTCATGCAGTGCCTGCCCGCTTCCACAACCGCGAAACCAAG  
TCGGCGAATGGATTTCAGCAAACTTCGCGGCTGAACCGTGTGGAAGTTACAGAAGAAGTATTCGAAAGTCGGCGCGCATCGTGTTCGATCAGGCGGAAAACCGTATGCACACGATTAAAGC  
GGTAATGGTCCGGCTCTGGGCGAC

**SEQ ID 1324**

SEQ ID 1324  
VNLKRNHFLKLLDFTPEEITTYLLDLAAELKDAAKAGREIQRMKGKNIALIFEKTSSTRTRCAFEVAARDQGADATYLEPSASQIGHKESIKDTRVLGRMYDALEYRGPAQETVEELAKYAG  
VPVFNGLTNEFHPTQMLADALTMREHSGKPLNQTAFAFYVGDARYNMGNLSLLGAKLGMDVRIGAQPSLWPESEGIIAAAHAAAKETGAKITLTENAHEAVKVGCFIHTDWWVSGEPEKFW  
QERIDLLKDYRVTPELMAASGNPQVFMHCLPAPHNRETKVGEWIYETPLGNGVEVTEEVFSPAGIVFDQAENRMHTIKAVMVAALGD

**SEQ ID 1325**

SEQ ID 1325  
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ACGATGATATTGCCGTATTGTGAGGATGATGTTCTGCTTGGCAAAGACGCGAAGAAAGTTCCTTGC CGAAGATACTTGGTGTGAAGAGAGCGTTTGTGAAGGATTCGCCCTTTATCGCTCCGTTGT  
GAAACGATGTTTGGCGAAAGTTATGCTCAGACCGGATAAAGCTTCGAAATTATGAANAACCGCTGATTTCCTTGTCTGAGAGAGCGAACATCTTGGGACGCGTGCCTATATCATTTCCGCTGAGG  
CGATGCGGTTTTTCTTGGACAGGTTTGGCGTTTTCGCCCGCAGCGGATTTAAAGCGGTGACATTGATGATGCTTTACTTATTTCTTTGATAAGGAGGGGATGCCTGTTTATCAGGTTAGTCC  
CGCCTTATGTACCCCAAGATTCGATTATCGAAGCTTTCTCAGTCAAAACAGATGTTTGGGTAGCGATTTTGAAAAAGATAGGGAACAAGGAAGAAGACACCGCGGTTGTTGAAGGTGATG  
TTTGACCTGAAGCGTGCTTTGGGTAATTCGTGAGGAAAAAGAAAAAGATGTAGAGCTCAAGGCGAGGCGGAGCTTGAGAAAGTTTACCGCAGGCGGGTCAATATGTTCAA

**SEQ ID 1326**

SEQ ID 1326  
MNHVISLASAAERRAHIAATFGSRGIPQFFDALMPSERLQAMAEVPLSAHPYLSGVEKACFMASHAVLWKQALDEGLFYIAVFEDDVLGKDAEKFLAEDTWLEERFDKDSAFIVRL  
ETMFAKVIIVRPDKVLNLYENRSPFLLESEHCAGTAGYIISREMRPFLDRFAVLPPERIKAVDLMATTYFFDKEGHPVYQVSPALCTQELHYAKFLSQNSMIGSLDEKREQRRHRRSLKVM  
FDLKRALGKFGREKKKMERQQAELKVKYGRVILFK

**SEQ ID 1327**

SEQ ID 1327  
TTGGGGCGATTTTACCTAGCAGATGAAAAACACGGGATTTTATCCGAAAAAGCAAAATCCCCCGCCGTCATCCCCGGAAGCGGGAATCTGGAATTTTAATCGCGCAAGAATTTATC  
GGAAAAAACCGAAGTTTAAAGACCTAGATTCGCCCTGCCCGGGAATGACAGTGTGTCCATTTCTGATTTTAATCCCCATATTTTACACAAACTATT

SEQ ID 1328

SEQ ID 1328  
LGRFYLADEKTRDFIRKSNNPPAVIPAKAGITWNPMAARTYRKKPKFKDLDSRLRGNDSVSISDFNPLYFTQTI

**SEQ ID 1329**

SEQ ID 1329  
ATGCCAGATTCTACCTGCCGAAAAACCTTTCCGTCGGACAAACCGTCGACCTTCCCAGCAACATCGTCGCCACCTCAACGCTCTGGCGCTCCGCCCAACGAAACATCACCCCTCTTG  
ACGCGAAAGGCGAAGGCACATACCGCAGCGCTGACCGTTTGGAAAAACACCGCGCGAAGCGGAAATCCTGCAACGAAGACACACCGCAACAGAGTCCCGCTCAACATCACGCTCATCCA  
ATCCATTCTCCGCGCATGCGATGGATTTCACCTTCGCAAAAAGCGCTCGAATCGGCGTAAACCGGCATACAGCCCGTCATCAGCGAAGCGTGCATGTCGCGCTCGACGGAGAACGCGCC  
GCCAAACGCGCTCGACGCTGGCAGGAATCGTCATCTCCGCTCGCAACAAAGCGGAGGAACACCGTTCCTCCCGCTACTGCCCATCATCGGCTACCGTGAAGCACTCGACAAATATGCGGT  
CTGAAACACGCAAGCTGATTATGAGCATCAACCGCGCTGCAAACTCGGCGACATCCGCCACCGCTCCGGCGCAATGCTCTTTATGGTCGGGCCCCGAGGCGGCTGGACAGAACAGGAAGA  
ACAACAGGCATTTGAAGCCGGCTTTCAGCGGTTACACTCGGAAACAGGATTTTACGCACAGAAACCGCCCACTCGCGCCATCGCCGCGATGCAGACGCTTTGGGGCGATTTTACC

**SEQ ID 1330**

SEQ ID 1330  
MPRFYLPENLSVGGQVLDLPDNIIVRHNLVLRPNENITLFDGKGKAHTARLTVLEKHRAEAEILHEDTTDNESPLNITLIQSISSGDRMDFTLQKSVELGYTAIQPVISERCIVRLDGERA  
AKRLARMOEIVISACEOSGRNTVPPVLPFIIGYREALDKMPESEWIKLIMSINRACKLGDTHPSPGAIIVMVGPEGGWTEDEEQOAFEGQAVTTLGKRIIRLTETAPLAATAAMQTLWGDFT

**SEQ ID 1331**

SEQ ID 1331  
GTGTTACACCGTTTGCAGAAAGTCGTGCGCCATATCGCGCAAAACCGAAATATATGCGCGCTTTTGTGAATACGCGCTCCGCCCGCAAGGAACAGCGTTTCGATGTTGAGCGAGGCGGCACATTG  
CCGCGCAGACGGCCATTTCGCGCGCGGTTGCCGCTTCTGATCGATTGCCCGATGTTGGCGCAGGAAATGTCCGCGCAGGAACAGTCGGCTTTGTGGGAACAATATTCCGGGGAAAAAGGGCT  
GTGGATGTCGATCGATAGACGGGACCAACAATTTGTGTCACGGCGTGGCCGCAITTTGCGGTGTCGGTGGCGTTGTGTCGCAACGGGCGCGCGAATTGGCGGTAACTACAAATCCGGTC  
AAGCGTGAATGTTTATATGCGCAACCGGGCAGGGTGCTTTCCTTAATGGGACACGCTGCCTTTGCGTCTCGTGATAAAAAATCTCAATGAGGCGATTGCGGCGGTGGAAATCAAATATC



TGCGTTTCGGGCAAACTTCCAGCCGATGAGTACGCTCGCGCTTTCCGGACGATACGAGTATGGGACGACGCTGGACTGGTGTATCTGGGCTCGGGCGTTATGATGTTTATGT  
CCACGGCGGGCAGAGCTGTGGGATTTATGCTCGGGTGGCTGATTTTCAGGAGGCGGGCGGCGAGGCTGACGACTTTGGAAGGCGAGCGGTTTGGAGTGGTGAACCGTGTTCAAACCG  
TCGGTCGTCGCGCGCTGCAACCGAAGCTGTTTGAACGCTGGGTCGGTGGATACGGGAAAAACG

## SEQ ID 1332

VHRLQKVVRIHAQTEINPRFLNTPSRKEDGSHLSEADIAAQTAFAAALFLLIDCPHLEEMSRQEQSALHBYSGERGLWTVDPIDGTNNFVNLPHFAVSVAPVRNGRAELGVITYNPV  
SGECFYAERGGGAFNLNTRLPLRLVDKKNLEAIGVEIKYLSGLSSRMSTLAPFGTIRMSSTLDCYLCAGRYDVYVHGGQKLDYAAALIFEEAGGRLTLEGGDFWSEHVPKR  
SVVALEPKLFERNVGVIRENQ

## SEQ ID 1333

TTGGCTAAGTCTTCCACCTACCGGCTTAAACAAGCTATTCCACAGCTTGCCAACTTAACCTTCTCGCTCCCACTCGCATTTGAATCAAGTACAGGAATATTAACCTGTTCCCATCGA  
CTACGCTATTCTGCTCGCTTAGGGGGCGACTCAACCTACGCGGATGAACGTTGCGTAGGAAACCTTGGGCTTTCGGCGAGCGGGCTTTTCCCGGCTTATCGCTACTCATGTCACAT  
TCGCACTTCTGATACCTCCAGCACACTTTACATGCACTTCATCAGCCTACAGAACGCTCCCTTACCATGCGGTAAACCGGCATCCGAGCTTCGGTTATAGATTTGAGCCCCGTATCA  
TCTTCGCGCAGAGCACTCGACCACTGAGCTATTACGCTTTCTT

## SEQ ID 1334

LPKSSYRLKQIPTACQPNLLRPHLAPESSTGILTCFPTTHFCLALGADSPYADERCVNGLSASGLFTRPIATHVNI RTSSTLYNAPSAYRTLPHYAGKPAASAVIDLSPVT  
SSAQDDSTSELRFL

## SEQ ID 1335

ATGAAGTTCGCGCTTAAAGCGCACACTCTGTTAAACCGTCCGAAGCGCTCAACATTTTAAAGCTTCGACAAACATTTACCTTAAAGGAAATCAATGCAAGTCTATTACGATAAAGATG  
CCGATCTGCTCCCTGATCAAAAGGCAAAACCGTTCGCTATCGGTTACGGTTCGCAAGGTCATGCCATGCTGCCAACCTGAAAGATTCGGGTGTAAACGTTGGTATCGGTCGCGCACGG  
CTCTTCTTGGAAAAAGCCGAGCAGCCGGCCATGTTGTTAAACCGTTCGTAAGCGACCAAAAGAGCCGATGTCGTTATGCTGCTGCTGCTGACGAAACCATGCTGCGCTCTATCAC  
GCCGAAGTTGACGCAATTTGAAGAAGGCGGACGCTGGCATTTGACACAGGCTTCAACGTCGACTACAAACATCGTTCCGGTGGCGACTTGGACGTTGATTTGTTGGTGGCCCCAAAG  
GTCCGGGTACATACCGTACGAGTGAATACAAACCGCGCGCGCGCTGCTCTGATTCGCGTTTACCAAGACAATTCGCGCAAGGCCAAGACATCGCCCTGCTTATGCGGCTGCCAA  
CGCGGCGACCAAAAGCGGTGTGATTGAAACCACTTTCCGGAAGAAACCGAAACCGATGCTGTCGCGGAACAGCGGATTTGTCGCGTGGCGTGGCGGAGTTGATCAAGCAGGTTTGA  
ACCTGACCGAAGCGGTTACGCGCTGAAATGGCTTACTTCGAATGCTGCACGAAATGAAACTGATCGTTGACCTGATTTTGAAGCGGTATTGCAATATGAACTACTCCATTTCCA  
ACAATGCGGAGTACGCGGAATACGTTACGCGCTGAAATGGTCAATGCTTCAGCAAAAGAGCCATGCGCAATGCCCTGAAACGCAATCAAAACCGCGGAATACGCAAAATGTTTATCCA  
AGAGGGTAAATGCAACTACGCGCTATGACTGCGCGCGCGCTTGAATGCGGACCAACAGTTGAAAGTCCGCGCAGACTGCGTCCATGATGCTTGGATTACGCGCAACAAATG  
GTTGACCAAGACAAAC

## SEQ ID 1336

MKLPFRHRLFPNSEAAHFKAATTTIYLGKQMVVYDKDADLSLIGKTVIIGYSGQHAAHANLDSGVNVVIGLRHGSWKKAEAGHVVKTVAEATKADVVHLLPDETMPAVYH  
AEVAANLEKATLAPAHGPNVHYNQIVPRADLDVIMVAPKPGHTVRSYKRGGVPSLIVYQNSGKARDIALSYAANGGTGGVITFTFREBTBTLDFGQAVLCGGVABLKAGFB  
TLTEAGYAPENAFTECLHEMKLIVDLIFGGIANMYNISNNAEYGEYVTGPFVNVASSKEAMRNALKRIQTGEYAKMFIQEGNVNYSNTRRRRLNADHQUEVKVGRILRAHMPHTANKL  
VDQDNH

## SEQ ID 1337

ATGAACACTCACCAACCCCGCTGCGGTTACGGCACAAGCTATGCGGCTGCTGCCGACCGCTTCATCTGCGGCAATCTGCGCGCCACCGCGCAAGCCCTCATACGTTCCG  
GGTACGCGCATATGCTGCACTTATCGACTACATCATGCTACTACCGTTCCGCGCAACAAACATCTCTGATGCCCGCAACTGATGCGAGTGGAGCAGAGAGCCGAATGGCTGGG  
CTTGAATGTCATCGCACCCCAACCTCGGCAACAGCAGCGCCAGTGAATTTGAAGCTACTTCCAAGACGCGGAAACCGAAGTGCATACGAGCTGTCGCGCATCTGCGAAATA  
CGGAGCAATGTTATTCATGATCCGACTGTTCCGCTGCTTACATGAACAGCCCTGCAATTTGCGGTTCCGGCAAAAAATTCAGAGCTGCTGCGGCAAAATATCTGCAACCTGTCGCA

## SEQ ID 1338

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AEQNYIFDTPVPLPMKQFCICGSGKFKACCGKYLQFVA

## SEQ ID 1339

GTGGTGGTGAAGTGTCTATTTGTTTGGGAATGCAATGCCGTCTGAAAGGGCTTCAGACGGCATGGTTGAAAGCCTGTCCGTTAGGGCATCAGCATGCCGCGT

## SEQ ID 1340

VVSVHFVWECKRLKGLQTAWLKSLSVRASACRR

## SEQ ID 1341

ATGTCACGCGCAAAACCGCCGCCCATCGAGTGGGAATAAACAGCAAAACAGGGCTGCACCGTCCGGCGCAGTCTTCGATTATCGGAAAAAGGAAAAATATGAGCACACAAGATTAA  
GCGGCAAAATCGCTTTGGTAACCGCGCATCGCGCGCATCGCGCGCAATTCGCGACACACTGCGCGCAGCGGTGCCAAATCATCGGTACGCGCAACCGCGAGAGCGGTGCGCGGC  
GATTACGAAACGCTCGGCACATGGGCGCGGCAAGCGCGCTATTAAATTCGCGCAACCGCGAAACCGCTGAAACCTGATTGCGGCATCGAAACCGCTTGGCAAACTCGACATTCG  
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TATGGCGCGCAAGTCCGCGAGCGCGGCTTACCGTCAACTGCGTCGCGCGCGCTTTATCGATACCGCATGACCGCGCGCTGCGCGAAGAAACCGCGCAACATTTACCGCGCAAC  
GCTTGGCGAGATTCCGCGACGCGCAAGACATCGCGGATCGGTTCTGCTCGCTTCCGATCAGCGGAAATACATTAACCGTCAACCGTCAACGTCAGCGCGCGCATGCTGATGCC

## SEQ ID 1342

MSAANRPPSSGNKQQTGLHRPAQSFYRKKGNMSTQDLSGKIALVTGASRGIGAAIADTLAAAGAKIIGTATGESGAAAIKRLAQWGGGRVLSNAEPETVENLIADIETKTFGLDIL  
VNNAGITRDLNLLMRKEREWDIMQVNLKSVFRASKAVLRGMKQRAIRIINTSVGVGMNAGQWYAAKAGLIGFAKSHAREVSGRITVNCVAPGIDTETRALPEETRTTFAQT  
ALGRFGDAQDIADAVLFLASDAQYITGQTLHVNGHLMF

## SEQ ID 1343

ATGACCCAGACAAATCTCATCTCGACTTCGGTTCTCAAGTTACCGGGCTGATGTCGCGCGCGTGCAGGAGCCACGTTTACTGCGAATGCACTTCTTCGATATGCTTTGGACG  
AAATCAAGCGCTTCAACCCCAAGGATCATCTTTCCGCGCGCCCTAATTCGTTTACGAATTCGACATCAAGCCGATACCGGTATTTTGGATTGGGCACTCCGGTTTGGCACTG  
CTACGCGATGCAATTTATGGCGACCACTTGGGTGGGCAAGTGCAGCCCGCAACAGCGCGCAATTCGGTTACGCGCAAGTCAAAACCATTCGACAGCGGACTGACACCGCGCATCAAGAC  
GACGCGCCCAACACACTCGAGCTATGATGAGCCACGCGGACAAAGTGTCCAACCTGCGCGAGCGTTTCGCGCTATCGCGGATACCCGCTCTGCGCGATGCAATGATGAAACGCG  
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AGTTTATGGCGAACTCGCGCGGTGACCGACCTGAGAAAAACGCAAAATCATCGCGCGGAATTTATCGAAGTATTTGATGCCGAGAGAAAAACTCACCACGCCAAATGGCTGGC  
GCAAGCGAGTATTTACCCGAGCTAATCGAATCCGCGGTGCGAAACCAAAAGCCGACGCAATCCACCAACAGTCCGCGCGCTGCTGAAATATGAAGCTCAAACTGCTT  
GAGCCCTGCGCGACTTGTTCAAAGACGAAGTGCAGGATTGGCGTGGCTTTGGCTGCGCGCGAATGTTGACCGCACCCCTTCCGCGCGCGGTTTGGGTGTGCGCATCTTGG  
GCGAAGTGAAAAAGAAATACCGCGACTTGTGCGCTCAGCGGAGCATATTTTCATCCAAGAAATACGCAATACCTACCGAGCAAAACGCGCAGCTCTTGGTATGACCTGACCGACCGAGCAT

TGCCGTATTCTCGCCGTCAAATCCGTGGCGTGATGGGCGACGGCCGCACTTTACGACTACGTCGTGCGACTGCGCGCAGTCATCACCAGGCATTTATGACTGCACACTGGGCAGAGCTG  
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**SEQ ID 1344**

MTQDKILILDFGSGVTRLIARRVREAHVYCEHSHFDMPLDEIKAFNPKGIIISGGPNSVYESDYQADTGIFDLGIPVLGICYGMQFAHRLGGEVQPGNQRFGYTAQVKTTDSGLTRGIQD  
DAPNTLDVVMHSHGDKVSKLPDGFVITGIDTPSCPJAMHENAEBQFVGIQFHFVTHTKGGRALNRRFVLIDICGAPQWTPMPTYIEEAVAKIRBQVGSDEVILGLSGGVDSVAALHRAIG  
DQITCFVDFHGLRLNKGVMVMDMPARNLGKVKVITHVDAEBSQFMAKLAVGTDPEKKRKIIIGAEFIEVFDAAEKKLITNAKWLAQGTTYPDVIESAGAKTKKAHAITSKHNNVGGLPENMKLIL  
EPLRLDKFDEVRELGALGILREMYVHFPPGPGGLGWRILGSEVKKEYADLLRQADDIPIQELRMTDENGTSWYDILTSQAFVFLPVKSVGVMGDGRTYDYVVALRAVITSDPMATHWAEL  
PYSLLGRVSNRIINEVGKILNRVYVDSGKPPATIEWE

**SEQ ID 1345**

ATGATAGAAAAAATGACTTTTCGGACTGTTTAAAAAAGAAGACGCGCGCAGCTTTATGGCGCTGATGGCGTACGTTCGCGCCCTACAAAAATCGGCATCGTTGCGCGCCCTGATTTGCCATTTTCG  
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CTGATGACTTTGGGTCTCCGTGATGACCATCAAGCAAAAATCCGAAGAATATGTTTGCCAAATGCTGACCTTTCTCTCCGCTACCATCAGCAAGCGCTCGCGACCGCTGATCTGATGAAT  
TGCTCAACTCTGACGGAACAGTCGCTGCGTCAACGCGCAGCGACATCTTCAACGCTCTCAACGCGCGACACGATGATGCTTACCGCGCTGACCATCTGCTCTGCTTTACCTCAACTGGCAGCTCAG  
CCTCATCTGCTCTGATGTTTCCCGCTGCTCTCCCTGCTCTCGCGCTACTACCGCGACCGCTCTGAACACAGTCACTTTCCGACTCGCAAAAAAGCATAGGCACGATGAACAACTGATTTGCC  
GAAACCCATCAGGGACACCGCGCTCTCAAGCTGTTTCAACGGGCGAGGCGAGCGCGCAAAACCGTTTCGACGGGCTCAACCGCACCATCTGCTCGGCTCAGCAAAAAAATCAGCAGGCAACGG  
CGGCACATTTCCCGTTCAGCGAACTGATTTGCCATGTCGCGCTTCGCGCTCTGCTCATCTTCATGCGCCTTGCGGCAAGGCCAAAAACGGCTACACCAACATCGCGGAAATTTATGGCATTCATCGT  
CGCGACTGCTGCAATGTAGCGCCCTGCAAAAGCCTTTGCCAACATCAGCATCCCTATCGACAGATGCTTCTCTCGCGCGCGCGCGCGCTATGTCGCACTTTCTCGACACCCCGCGCAACAGGAC  
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CCC GCGCATTTTGAAGACGCGCGCATATTATTTGGACGAAGCCACCGCACTTGGACAACGAATCCGAACGCTCTGTTCAACAAGCGCTCGAAGCGCTGATGGAAGAACCGCACCGG  
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ATCATGCTGGAAGAACATCTCCGGAAGAAAGATACCGCGCGCTTTCAGACGGCA

**SEQ ID 1346**

MTEKLTPLGFKKEDARSPMLMAYVRPKYKRLVAALIAIPGVAATESYLAFTIAPLHNHGPSAPAAPFDLSAAAGILSTLQNWREQPTVMVWGTEKIKWTVPLIILVIVIRGICRFTSTY  
LMTVWSVMTISKIRKDMFARMLTSSRYHQETPSPSTVLMMNLMTLQSVSNASDIPITVLTRDTMTVPLGLTIVLLYLNMQLSLIVVLPFLLLSLSRYTRDRLKHVIDSQKSGTGMNVIA  
ETHGGRHVVKLFNQQAQANRFDAVNRITVRLSKKITQATAHSPFSELIASIALAVVIFITALNQSNGYTTIGEPMAFIVANLQMYAPIKSLANISIPMQTMFLAADGVCAFLDTPPEQD  
KGTLPARQVEGRISDFPNVDVEYRSDGIKALDNFNLDIRQGERVALVGRSGSGKSTVVNLLPRFVPEPSAGNICIDGIDIADIKLCLRAQFALVSDQVFLFDDTLFENVYRSRPDAGEAEVL  
SALQAANQLSLDISAPNGLHQPTIGSNGSLSGGQRQVATARALIKDAPILLDEATLSDNNESERLVQQAELRLEMNRTGIIVAHRLATVESADRIIVMDGKKIEQGHQDQLMFQNGY  
TLRLNISGKITAAVQTL

**SEQ ID 1347**

TTGACTTCGTTCCGCAAAAAGCAGCGCTGCCCTCTTCAGGCTGCTTTTCAAGTCCGAAACGGCAAAACAGCGCATATTTGCGCTATAATFCCATCCCTACCAAACCAACCGACAGCGGCTCGCGT  
TGCAGTTCGCCGCCCTACCGATATGATAGAAAACTGACTTTCGGACTGTT

**SEQ ID 1348**

LTSFRKKQPALFRLLFTSERQTAAYLRYNPSLPNHRQRLPLQFPYRYDRKTDFTV

**SEQ ID 1349**

ATGTCCTTTCGCATCTCTCTCTCCCGGACAGGGTCTCCAAAGCCTCGGCATGATGAACGGCTTTGCCGAACACGTCATCGTCAAAAACACATTTGACGAAGCCTCCGCCATATTGGGGCAGG  
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SEQ ID 1350

024 12 1999  
MSFAFFPPGQSSLGMMNGFAERHIVIVKPFDEASAILGQDLWAMINGSDAETIGQTVNTQPIMLAAGVAVTRYALEVGGKTPAAVAGHSLGEYTLVAAREALDFADAVKLVRLRAELMQS  
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SEQ ID 1351

GTGGATGACCGCGAATTTCGGCGTGTGATTTCACACGGTTTTCAGTGTTCGCGCAAGTTTTCGCGCGCGGGTTTCATCAGGCTGCAATGGGAAGGAACCGATACCGGCAGCGGCAGGGCG  
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SEQ ID 1352

VDDADRLRLDFFNGFECPGKFPVGGGPHQAAAMCRNGYRQYRQGAFGPSGFFGGSHGASDGGGVACNHDLSGEVEVDGDFHPALCGFGFTNLPDLFTFPQTQNGRHCAYALRYGGLHQFGQAQADEFDG  
IGIKYQCFGGCKRGVFAEAVSNGGRRPAAHFQIQIAGVNGNAGGEEENGLGVCLDTPDQIAAVNHPQVLPQYGGGFVKCVFDDDDVFGKAVHAEALGTLSGREECECHSTPLLGWIVRDVAR  
VLOKVRAEFNNNSGCRSPGHCKPROSDTAQONAFSPFYA

SEQ ID 1353

TTGGTGGTTCGGCACTCAAAACGGCGCGGGCAGTCATAGACGCGTAGTTGACATTACCCCTCTTGGATAAAACATTTTTCGGTATTTCGCGGCTTTGGATGCGTTTCAGGGCATTGCGCATGGCT  
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CAGATCGGTTTTCGGTTCTTCGCGGAAAGTGGTTTTCATCAACACCCGCCCTTTGGTGCCCGGCTTTGGCAGCCGCAATAAGACGGCGGATGCTTTGGCCCTTCCCGCAATTTGCTTTGGTAAACG  
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CGTGAAGCCGCTGTGCAAAATGCCAGCGTCGCCCTTCCTTCAAATGGCTGCAACTTCGGCGTAGATAGACGGCAGGCATGGGTTTCGTGACGGCAGCAGCAGCATTAACGACATCGGCTTCCTT  
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TGACCTTCCGAACCGTAAACCGGATGGCAACGGTTTGCTTTTGATCAGGGACAGATCGGCATCTTTATCGTAATAGACTTGCATTGTGATTTCCTTTAAGGTAAATGGTTGTGGAAGCC  
TAAATGTGCGCGGCTTCGGACGGTTTAAACAGAGTGCCCGCTTAAACGGCACCTTCATTTCATCAATACGATTTCACACGCTTCGGTTTTCGCCGTGACGGCATGGACGAAGGCTTGA  
AATGCCGCTGGCACTTTCGTCAA

**SEQ ID 1354**

LWVGITPAAGSHRRVVDITLLDKHFCVPAGLDAPQGLAHGFFAGSIDHFRAGNVFAVLRLVGVNGVVHIGTAPENQVNDQPHFVQAEVSHFRVVTGFGQFKTCFDQLGHATAQYGLFAB  
QIGFGFPAESGFNHETAFGAAGVSGRIRQGVFLAGLIVLVNGNQRRHAAAFVFTAYGCTRTPTGGNNHNVQVGTENDLVVVEEVAVCKCORRAFFQIGCNFQVIDGRHGFVRQOQHNDIGFF  
GRFSNGFNMGACPGFFPRRAVAQTDHHVYTRIPVGSNGMTLRTVTTDNGGPAFDQOQIGITPVIDLHLISPAVNGCRSLKMLSGFGEVRKQSVPLKRQLSSIRFPTLRFCRRRTGRRLQ  
NARKHYVRQ

**SEQ ID 1355**

AGTAAGCAAAC TTGAAATCCCTACTTTGATAAAGCTTACTGCTTTGTTGTGTCCTAATCCTGCCPTTTGTGTTTCAGGATTAAGTCGATACAA

**SEQ ID 1356**

SKQT\*NPYFDKAYCFVVS\*SCLLCFRIKSIQ

**SEQ ID 1357**

ATGAAGCGCGAGGCTTTCTTCAAACCGATGGCGTGTGCGCATTTCTGTCCGCGGTTTCGTGCGGCTCCCGTAFTGGGCGCGTGTTACGCAATATTGTCCCTCATGCGTTTGCACTTT  
ACGGCATCGACAAACGGCGTGGCGTGGCGGGAAAACGCCGATTTCCCGAACACCGGCTGCTCTCGCTGCCTTGTGTTGGCGGTTGGACGGGCGCATACTTGGGTAGTAGGATGTTTCAGGCA  
TAAAAACGGCGAAAAAGCGTTTTGTGTGCTGTGTCGGTCTGACTGTTTCGGGCAATGCTCTGGCGACCTGCATCTGATTGATTATTTCGTTCCGCGCGAACCTTTTGTAAAACTCGGCGAA  
CATCTC

**SEQ ID 1358**

MKRQAPFKPHCAAFLSAVSLRLPVLGACTAILLSYAFALYGIDKRRRAVRGKRRIPEHRLLLPALPGGHTGAYLGSRHPEHKTAKKRPVVLFRLLTVSGNVLATCILIDYFVPPPELFVKLGQ  
 EL

**SEQ ID 1359**

ATGTCAGTATGCGAAAAATTTCCGGCAGCGGCAGCTATCTTCTGCCAACCGCGTCAGCAATGACGACCTTGGCCAAAAGGTAGATACCTCTGCAGAGTGGGATTACCGCGCGTACGGGCATCA  
AATTTCCGCCATATGTCAGCCGAAAAAGAAAAACACGAGTATCTTGACGCCGAAGCGGCGCGCGCGCTTTGGCAGATGCCAAATTAATATATAACGACATTTGATTTGATATATCTGGCGAC  
GGCAACGCCGATATGTCAGTTTCTTTACCGCCACCATCTGTGACGAAAAATTTGGGCAATCACCAACCGCTGCCCCGCGTTGACGTGCAGCGCGGTGTGCGCAGOCCTTATGTACCGCGCTG  
ACTACGGCAAAATGCTTACATTTAAAGCGGTATGGCGAAAAACCGCTGGTCATCGCGCGCGAAACCTTCAGCCGCATCTGTCGATTGGAACGACCGCAACACCTGCGTGTCTGTTGGCGGAG  
CGCGCGGCGCGGTGGTTTTAAGCGCGTCCGACAAACCGCGCATCTCCACAGCAAACTCAAAGCCGACGGCAATTTGCTTGAACCTTTAAAGCTCCCCGGGCAAAATCGCTTCGCGCAAGGT  
TTCGGTTCGCCGTACATTTTCGATGGACGGTCCCGCGTGTTCAGGTGTGCCCTCAAATTCGCTGTCCAAAATGCGCGATGACCTTATCGCAAGAAGACGGTTACCGCTGCGGACAAATCGAC  
TGGATTTGTTTCCCATCAGGCAACCGCGCATTTGCAATGACCGGAAAACTTTGGGTTTGGATGATGCGCAAAAGTCTGCTCTGACCTGCAAGACACCGGCAACACGTCCGCGCATCTCA  
TTCGCTGCTGCTTTGGACGGCGGATCCCGCAGCGGACAAATCAAACCGCGGTCAAACCTGCTGCTCGAAGGCATAGGCGCGGTTTCGCGTGGGCGCGGTGCTGTGTGCAATAT

## SEQ ID 1360

SEQ ID: 1596  
 MRYAKISGSGSYLPANRVNSDDLAQKVDTSDEHTTARTGIKFRHIAAENEKTSDLAAEARRALADAKIININDIDLIIVATATPDHFPSTATIVQQRKLGITNGCPAFDQVQACGAFHYAL  
 TTNAYIKSGMAKNAKALVIGAEFTSRIVDNDRTTCVLPGDGAGAVVLSASDKPGTIHSLKADGNYLKLINVPQGLACGKVSQSPYISMDGPGVVKFAVRMLSKIADDVIEEAGYTAEQID  
 NIVPHOANRIITSAKHLGLSDKQVVLVQDHCFTSAASIPALDAGIRSGQIKRGQHLLEGIGGGFAMGAVLLQY

SEQ ID 1361

ATGCCGCTCGAAGCAGCTTGGGCTTTCAGACGGCATTTCCTTCACTTAAACACGCGTATCGGCAACCCGCCGCCCGTCCACGGCAATCCGCATCTGAAACCAATCTGTATGCCAAAC

**SEQ ID 1362**

MPSEAAWAFRRHFLHLAORIGNPAPPVKNPHLKTICHPNHTPIPVSVICTLPVLGNERRFFAYNSRI

SEQ ID 1363

ATGCCGCTCTGAAAGCCCAAGCTGCTTCAGACGGCATCTTGATGTGTGGGTTTCCATCAAAATTTATATTGTGTCGGGTGTTTGTGTTTTTGTCATGATAAAATTCGGAAATGATATTTTGAATTGTA  
GAAATATTTTATAGAGATATCTGTTCAATAGGGTAGGAATCTCCCAAGATTTCCTTACCTTCCCGCTGTAATTTTCGTGTTTAAAGGTTTTTTACTTTTAATATCCCGCGCTTC

SEQ ID 1364

MPSSPSCFRRHLDCHVSIKLYWCRCFLSDKFGNDILNCRNIFRDMFNVRVGISODFPYLPAVIPCCKVFYFNIPAF

**SEQ ID 1365**

PTGCCAATAATTCAAACAATTTTGAAGGGCGGGGATATTAAAGTAAAAACCTTAAAAACAGAAAATTCACGGCGGAAGGTAAGGGGAATCTTGGGAGATTCCTACCTTATTGMACATATCT  
TCAAAAATATTTCTACAATTCAAAATATCAATTTCCGAATTTATCAGACAAAAACAAACACCGGCCACCANTA

SEQ ID 1366

LPILOTLEGGDIKVNKLTENYSCKVRREILDSYPIEHLKNI STIONILSEFIROKOTPAPI

SEQ ID 1367

TTGATAGAAATGAAAACATCGACGGTCGCTTTTGGCGGATTTTATATGCGAGACAACGGGGAGCGAATCCAAATCCCGGTTTGGAAAACTCTGCATTAGGGAATCAATCGCTTTTTT  
CCGTTATCAAAATTTTCAGAAAAAAGCGCGCTCTGTGTTTCAGAAATCATCCCCGAGCGGGAATTTGGCAATACCGAATTAACTGTCTATTTTGAAAAAGGATATTATAGTGGATTACCAA  
AACCGGTACGGCGTTGCCCGCGCTTAGCTCAAGAGAACGATTCCC

SEQ ID 1368

1.I.PMKTSTVVEGGFFMADNGERTOIIPVLNPDLREINRFFSVSNFEKKAGVLVFRLLPEPEFGNTLTVYFEKGYSSGLTKTGTALPRLSSKRTIP

SEQ ID 1369

TTGTGCTTAACTCCTGCCCTTTGTGTTTCAGGATTAAGTCGATACAATCATCACCCAAATACTATGTTTGTGTTTCTTTCTCTCTGCGAGAGGTTTTTATCCTTTGCAAAGAAATAAAAAATC  
AAAAACAACCTCATGTGCTTTGTGTTG

SEQ ID 1370

LCINPAFCVSGLSBYNHHPNTMFVFFSLARGFYPLORIKNONKLIVFVC

SEQ ID 1371

SEQ ID 1371

GTGTCGCCCTTAAACGGCAACTTCATTTCATCAATACGATTTCACACGCTTCGGTTTTGCGGCTCGACGGACTGGACGAAGGCTTGGAAATCGCGCTGGCAATTATGTTGTCGAATAGCTGCT  
TGGGATTTCCAAATTTTCCACGAAAAACAAACGGTTTCGGTTTTGCGGATTTCCTGATGGAGATGTAGCTGATGTTGCCCTCTTCGCGACGGCTGGCTTTGACCAAGTCTTTAAACTGTGCTG  
CAACGCTTTGCGGATTTTCGGTTTTGACGGTAAACGACAGTCGACAAATTTTAATGTTGACATAAATCTCTCCCTCGCGCTCGTTTTTCAGACGGCAATCAAAATACCATGCGGCTC

SEQ ID 1372

WCRI NGNPTBOYDFORPGFAVDGLDEGLEMRAGIMFVNSCLGFPPIPHENKTVRFADFLMEIVADVALFRTAGFDQPFKLCCQCFRVFRFDGNQCDNFNVREKSLPPVFQTAPEYHAV

## SEQ ID 1373

ATGCCGTTTCTCAACCATAGACGACAACTGGACATATTGATGAAGATTGGATTACGGTACGAAAAGCTATGACCGGAACATTTTACCGCGCCAAACCGGCAATTCGGCTTGGAGCTGG  
AGTTTTTTGATTTCATGCTGGATGCGAAACCGGCAAAATGCGGAAGCGCGGAGCGGCTGTATTTTGTAAACGACGACGCGAGCGCGCGCTGTGGAAAAATGGCGCAAAATGG  
CGTGAACATCTGGCGTTGCGTTGTCGGCTTCAATAATGTGGATTGAAGCGCGCTGAAGAGTTGGGCTTGAAGTCTGTCGGCTGCTTATTCGCCGAATCGGTTGGCGAACAT  
ACGGTCCGCTGATGCTGACTTTGAACCGCGCTATCCACAAAGCTTACAGCGTACCCGCGATCGGAATTTTTCGCTGAAGGTCGACCGGCTTCAATATGTACGGCAAAACCGCGGGCG  
TTATCGGCACGGGAAATCGGTATCGAACGATGCGGATTTTAAAGGTTTCGGTATGAACCTGCTGGCTTACGATCCGTTTTCGAACCCCGAAGTGAAGAACTCGCGGCGAGGTATGT  
GGATTTGGACGAGCTGATGCGCGATCGGACATCATCGCTGCAATTGTCCGCGCACCGCGAAACCACTATATGCTGAACGAAGCGGCTGACAAAAATGAAGACGGCGGTGATGATT  
ATCAACACCGCGCGGGCGGCTGATTGACAGCGCGCGCGCATCGAGGCGTTGAATGCCGGAATTCGGTCAATTGGGCTGATGTGTACGAGAACCGCGCGAGCTGTTTTTGAAG  
ACAAATCCAACGATGTGATTACCGACGAGCTGTCGCGCGCTGCTGCTTGTCTATACTGTTTACCGGACATCAGGCATTTTTCGGAAGAGCGGCTGGGTAAATTTTCGAAGT  
TACGCTGTCCATATCCGCGAGGTGCGACAGACCGCGGATTCGCGCAATCGCGTTCGTCGCCGAGGT

## SEQ ID 1374

MPFLNHRQLDILMKIATYGTSDYREHPTANRHFGELEFFDMLDAKMAEGAEAAACIPVNDASRPVLEKLAQIGVKTVALRCAGFNNVILKAAEELGLKVVVPAYSPESVAEH  
TVGLMLTLNRRHKAYQRTDANFSLGLTGFMYKTAGVIGTGKIGIATMRILKFGMNLALAYDPFNPVEVEKLGGRYVLDLYARSIIITLHCPATPENHYMLNEAFAFRMDGVMI  
INTSRGLIDSAAIEALKCRKIGALGMDVYENERELFFEDKSNVDITDDVFRLLSSCNVLFTHQAFILTEALGNISEVTLNIREVGTGDCGNVVRADG

## SEQ ID 1375

ATGTTTTCAATCTATCAAAATCAATGGCTTTATGTTAATCGGACGTCTTCTATCTCAAAATCTCTTGTGATAAAAGAAATTTCCCGGATCTCTGTTCCGTCAGCGGATATCGAAA  
TCTTCGATATAAGTACACAGGATGTCAAAGCCAAAAACGTTCCGAATAATGAATAATAATCAATCGGATTCATCAGACGGCATCAAGCTTCCCTCAAGGATTTTCCGAACTTCA  
TCATCCGTTTGT

## SEQ ID 1376

MFSPLSNHLVYWLIGRIFYLKFLVDKRNFGFLFRQPDLEIFDISTQDVKSQKTFRRIMNIQCGFNQTLKPAKGFSELHPPV

## SEQ ID 1377

ATGAAGACATTAGAAAAACGGATGAAAGCTCTAGACAAACGGATGATGAAGTTTCGAAAAATCCCTTGAAGGCGAGCTGATGCCGCTGATTGAATCCGATTTGGATTATATTCATTAT  
CGGAACCTTTTTTGGCTTTTGACATCTCTGTACTTATATCGAAGATTTCGATATCCGCTGACGGAACAGAAATCCCGGAAATTTCTTTATCAACAGGAATTTGAGATAGAAAGCAC  
GTCCGAT

## SEQ ID 1378

MKTLEKRMKALDKRMKPGKSLGRDLARLTESALDYIHSERFLAFDILCTTIEDFDILRTBQESRELSFINKEFEISTSD

## SEQ ID 1379

ATGACCGGCGACGAAACGACGCTCCGCCAAGCCCTGAACCGCGGAGGCGCGCGATGGAACGCGATCGACATCTGCCATACCAACCAAGTTGTGCGCATGGATGAATCCCTCAGTCCGCC  
TAAAGAACAAAAATACCTCTCCATGCGCGTTGCCATCAACCAAGTTAAAGAAAGCAAGCCCAAGCCCGCTATCCGACGGCAACACGGGCGCGCTCATGGCAACCGCACGTTTCCTCT  
CAAGACCATACCGCGATCGAACGCCCGCCATCGCCAAATTCCTTCTCTCGACACCGGACACGTTACCTTCGCCCTCGACCTCGGCGCAAAACGTCGACTGCACACCGGACAGCTTGGC  
CAATTTGCCGTCATCGCGCAGCGAACTCGTCCACGCGCTCCATCTCAAAAGGACAGCGCGCGCTGGTCAACGCTCGGCAAGACATCAAGGTACGGATACCGTCAACAAA  
CCTACAACTGCTGCAAAACAGCAAACTCAACTTTATCGGCAACATCGAAAGCAACGCGATCTGTACGCGGAGGAGATGCTGCTGCTCGCGGACGCTTTTTCGGCAACGTCATGCTCAA  
AACCATCGAAGGCGCAGTCAAAATTCATGAGCGGAGCATTCGCGCGGAATTCAGAGCAACCTGTTCAACAACTTGGCGCGCTTCCGCGCTTACCGCGCTCAAGGCTTGAAGCAAAA  
CTCGATTCGCGCAAAATTCACGGGCGCATCTCTGCTGGGCTGCGCGGATCTGTCATCAAAAGCCACGCGCGGACAGACAAACCGGTTTCCGCTACGCACTCGAAGAGCTTACCACGAAG  
CCAAGTCCGCGCGCTTTTCAAAATCGAACAGCGCTTGGCGAACACTCGCGCACCTGGAAGCGCGCCCAAAACGAAACCGCGCGGCTG

## SEQ ID 1380

MTGDETQLRQALNAGAPMERIDICHTTQVVMDESPQALNKKYSNMRVAINQVKEKAQAASVAGNTGALMATAFVFLKTIPIGIERPAIAKFLPSDTHVTLALDLGANVDTPEQLA  
QFAVIGSELVHALHPKQKQPRVGLVNVGTEDIKGTDTVKQTYKLLQNSKLNFIINTESNGILYGEADVVDGFGVGNVNLATIEGAVKFMASIRREFQSNLPNKLAAVAALPALKGLKLNK  
LDPRKFNGLAILLGLRGIIVKSHGTDKTFRYALEEAYEAKSAGLSKIEQVVAEQLALEAAQNETAASL

## SEQ ID 1381

TTGGGGCTTTTGAATATTTTACGGGGTATTATACGGAACGCTTTGCCCTCTGTGTTGACGTATGGCGAAAGTTTGGACGGATGGTGGCTCAATGCAAAAAAGCCAG

## SEQ ID 1382

LGILEYFHVLYGTLCPCVLYGESLDGWCVCCKKSQ

## SEQ ID 1383

ATGAACAGAAAAATCTGTACACCTACGATGACATCCACCGGCTCATCAAGCATTTGGCAGAAAAATTCGGAACCGCGCGCTCAAAATACGATGCCATGATCGCTATCGCGCGCGCGGCT  
TTATTCGCGCACGATGCTGCGCTGTTTCTGGAATTCGATTTTATGCGGTAAACACCGCTATTACGACGCGACAGCGAAGGACAAGTTACCGAAGAAGTCAAAAAATGCAATGGCT  
AGACCCCGTCCCGAAGTCTCGCGGGCAAAACGCTGCTGCTGATGAAGTGGACGACGCGGCTAACCATGGAAGTCTGCTGAAAGAACTGCTCAAGGAAGACTTCGACACTGTC  
GGCGTCCGCGCTCGCACGAAAAATCAAAGCAAGCAGGCAAAATCCCGAAGGATTCCTTATTTACGCGGCAITACCGTAGAAGACTGGTGGATCACTATCCGTTGGGACGCACTCG  
ACATCGACGAACACACCGCTTCCGGAAGCGATCGAGCG

## SEQ ID 1384

MRQKIWYTYDIDHVRKALAEKIRNAGVKYDAMIAIGGGFIPARMLRFLBIPYAVTTAYYDSDBGVTEEVKVKQWLDVPEVLEGRKNVLVDEVDSDRVTHFCLKELLKEDFTV  
GVAVLHEKIRAKAGIPEGIPYFSGITVEDWVWVWDALDIDENRLAEADR

## SEQ ID 1385

TTGCTTTGTTTGTGATTTCGGCTTTCCAAATTTGTTAAAGATCGATGCGTGTATTTCTACTTCGCAAAATCAAAATAAGCTGCTAAAAACAGCAAACTGCTTTTCAATTTGTTAAAGTTTGG  
GTGAGGCAAAACGGATCGAACCGATGACCCCTGCTTGCAGGAGGCTGCTTACCAA

## SEQ ID 1386

LSLFVDFGFPIC\*RSNRYSTSQIKISC\*KQTCFHL\*SPGGGKRDRDTPLLAKQVLYQ

## SEQ ID 1387

TTGTGTTTGAATGAAATGCCGTCATGAATCAATTTTAAATCCGCCATATTCTACTGATTTGTTTGAATTCGGTGTATTATGCGGTTTCTCAACCA

## SEQ ID 1388

LCFEMEMPCMKSLIRHILLICLSNYYVAVSQP

## SEQ ID 1389

ATGGTATTTGAATGCGCTCGAAAAACGAACGGCAGGAGAGATTATGTCGAACATTAAAAATGTCGCACTGGTTACCGTCAAACCGAATACCGGAACACTGGCAGCACAGTTTAAAG  
AACTGCTCAAAGCCAGCGCTCGGAAGAGGGCAACATCAGCTACAATCTCCATCAGGAATTCGCGAAACCGAACCGTTTGTGTTTCTGTTGAAATTTGAAATCCCAAGCAGCTATGACGA  
ACATAATCCAGCGCGCATTTTCAAGCCTTCGTCAGTCCGTCGACGCAAAACCGAAGCGTTGGAATTCGATTGATGAATGAAGTTGCGGT

## SEQ ID 1390

MVFECLKNRQERFMSNKKI VALVTVPKPEYTTETLAAQFKELVKSRAEEGNI SYNLHQEIGKPNRFVFPVENWKSQAALDEHNASAHFQAFVQSVGDKTEALEIVLANEVAV



## SEQ ID 1391

GTGTACACAGATTTCCTGTTTCATCGGAATTCCTTGGTGGTTGGGGCTTTTGGAAATTTTCACCGGGTATTATACCGAACGCTTTGCCCTGTGTGTGACGTATGGCGAAAGTTTGGAC  
GGATGGTGGCTCAATGCAAAAAAGCCAGTAATTCATGGCAATGTTCTGGCTTTTCAGTCAGTCGAATAGGGATTTATGCGCTTTGGCTTTGACCATTTCGCGCGCGGTACATACC  
GTTGGGGAGATGTGTGCGGGCGGTGTACTTCGCGGTGTGTGTCGACAAACAGTGGCGCGCGTCAGTCGCTGTGCGAACGGTGATACCGCGTTTGAAGGGGATTTTGTGTT  
TGT

## SEQ ID 1392

VYQIFCFIGISLVGAFIFSRGIIRNALPLCDVWRKFGRMVRPMQKPVIAWQCSGFFSQSNRDYSPLALTTLRPRYIPLGEHWGCRCTSPVVLSTNSAGAVSASCERCIPRLEGDFL  
C

## SEQ ID 1393

ATGCACCGTTCCACGACGCACTGACCGCGCCCGCACTGTTTGTGACAGCACAACCGGGAAGTACACCGCCGCCACCATCTCCCCAACGGTATGTACCGCGCGCGCAAGTGGTCA  
AAGCCAAAGCGGAA

## SEQ ID 1394

MHRSHDALFAPALFVDSSTGEVHRPHHSFNGHYRGRKVVKAERG

## SEQ ID 1395

ATGTACAGACCTTAATTTGATTGACCGGAAATTTTTCGCGCGAAAGCGAGAACCTGCAAGGCACTTTTCGTGCGAAGAAATGGACGAGCGAGTCAGTTTGACAGATTATCCCGCGGACA  
GGCGGAACAAATATCTTTTACACTGACCGCGCGTGCAGACCGGCTGCAACGCTGTTCCTCGACCTGAACGTCAGGCGGATATGCCCTGATTGCCAGAGATGTATCAAAACCATGCGC  
GTTTCATGCTCGATGAAAGCAGCGCTATCATCTGTTTTCGACGAAGAGTCTTGGACGAATCCATGCTTGGCGAGAAAGTTCGAAGGCATACCTGATTGAAAAAGAACTCGACGTGCGC  
GCATTTGTAGAGACCAATCTGATGTCCTGCGCTTTTCGCGCGACGACGACACTGCGGCAATACCCCTTCGGAATCCGCCAACAGACAAACCAACCCCTTTGCTGTTTTCGCGG  
GTTTGAAGACGAGT

## SEQ ID 1396

MSDNLIDPELFAERQHLQGSFLLEELDERVSLHDYPADRRNKISPTLTGGRDLRLFLDLNVKADPLICQRCIKPHPHLDESSRIILFSDEESLDESHLADDELEGILIEKELDVR  
ALVEDQLHSLFFSPRHGCGNLPESANQDKFNPFAVLGLKSS

## SEQ ID 1397

GTGTTTCGCGCATGGCTGGATTTTACCGCCCTTCGGGCGTGTTCACAGGTAAGGAGGATGGGATGGGTTTGGAACTGCTTTGGTTTGGGTACGAGTTTCGGTTTTCGCCCGCGAAC  
AGATGGAAAGGCTTCGGCAITTCCTTTCAGCGCGCATCCCGGATTTTACGAAACCGCGATGTTGGGGGAATCCGCCCTTCAGACGCGATTGCGCTTCGCCAGGGTAAGGCGCGTCTGTT  
GACCGGGCGTTTTCGCCGGCGCTTGTATGTCGTTGCGGACAGGTGGCGTGGTGGCAGCGCAGGTCGGGCAAGCGATGAACCTTCGCAACGCGCAAAAGATGTTGATGCAATTTGAGC  
GCGAGGAGATTTGAGTTTACAGTCGGTCTGCTGCTAAATACGGTTACGGGCGAGGATGCAATCGGCATATCGATAAGACGGTGGTCTGTATGAGGCGAGTTGGACGAGCTGCACATCTCTCC  
GCTATTTGGAGCGCGAGCGGATGCGGTTTATTTGTTTCGTGTGCGCGAAAGCGAGGGCTTGGGCGCGCTGTTGATCGAACGGATTGAAAGTACCGATCCGAATGCGCTTGTATGCTGCGC  
GGTTTTCGCTGCTGCAATTTTGAAGACGAGGCGTGGATGTTTG

## SEQ ID 1398

VFRMAGFYRPFGRVFNKEDGMLFLVLGTSSVFRREQMERLGIAPQASPDFDETFLGESAPQALRLAEGKARSLTGRPPGALIVGADQVWCDGRQWQKPMNLANAQKMLHLS  
GREIEFYSAVVLNVTGMRHRHIDKTVVMRQLDELHLILYLERKPDVAVCSCAAKSEGLGALLIERIESTDPNALIGLPVFRVLVDPLKNEGVUVL

## SEQ ID 1399

ATGAGTGAGGGAATGATGCTCTCTGTTTGTATTGATTCTACGCTTTGGGTACGCTGACACGCGGTGCTGTCAGCATGAACAACGGCGGTGTGTCGGCTGACGGATTTTGTGCG  
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TACGATTTGACGTTGCCGACTCAGTTGGTGGTCAATAACGGTTGCGGATTTGGCGCAGGATGAAGGAATGCCAATCTGAAAAACGCGCGACGATTTTGTGATGTATGCGGT

## SEQ ID 1400

MSRGMSPVLYLIPITPLGTPDTPCLLQHEQRAVVGLTDFVVEAKTARAHLKHLGTTPIREINLQTLNEHTDLKTLPELLKPLQEGRSNGIVSEAGCPAVADPGANLVALAHKHGFVFRP  
LVGPSSLLALLAMASGANQNFAPNGYLPSEKNERIQSLNALEQRSQCGETQIFJETPYRNDALLADAVENLHPETRLCTADTLPLTQLVSVKTVADWRHRKHPNLKRPITFVMIYAG

## SEQ ID 1401

TTGGCGCAGGATGAAGGAATGCCAATCTGAAAAACGCGCGACGATTTTGTGATGATATCGGGTTGAAGATTTCCGCCCGATAGGGGGTGAACAA

## SEQ ID 1402

LAQDEGNAQSEKTPDDFCVCGLKISAFIGGEQ

## SEQ ID 1403

ATGCAGGTTTCCACCGCATCGGCAAGCAGCGCATCATTCGGGTAAGCGGTTTCAATAAAAACTGCGTCTCGCGCACTGCGCGGAACGTTGCTCCAAAGCAATTCAAACTCTGAATGCGC  
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TCAACAGCGCGCCCAAGCCCTCGCTTTTCGCGCGACAGCAATAAACCCGATCCGGCTCGCGCTCCAAATAGCGGAGGATGTGCGAGTCTGCTCAACTGCTCATCAGACACCGCTCTT  
ATCGATATGCCGATGCACTTCGCGCG

## SEQ ID 1404

MQVFHRIKQRIIAVRFPKNLRLAALPRTLLQSIQTLNALIFFRQITIKRKVLPIRTSRHQQQAGRADQRPYFKTVFHRQCHQIRARIGNSRATRLADNPHTAPFLQRFQFQSLQ  
IRVFIQRLQIQFAYRRYPQLQMRTRRFPFDKIRQPDNRPLFMLQARRVRRYQRRNQIQNRHSLTHRLKMPSEPPRRHKRAVTKHPRPRPSKNRFDGKPADQSRHSRDYFQSVR  
STARPSPRFSPHTNNKPHPARAPNSGCCAARPTASSRPPSTRYADASC

## SEQ ID 1405

ATGCCCGACGATGAAAAATGCCGCTGAAACCTGTTTCAGACGGCATTTTATTTGTTTACCCCTATCGGGCGGAAATCTTCAACCCGCATACATCAAAAAATCGTGGGCGTTTTC  
GATTGGGCAITTCCTTCATCTGCGCAATCCGCAACCGTTTACTGACCAAC

## SEQ ID 1406

MPQHKCRLLKPVQTAFLFTPTTGGMLQPAYITIKVGRFFRLIGLSFLRQSATVLLTIN

## SEQ ID 1407

ATGGATTTTAAAGACTCACGGCGTTTTCGCCATCGCGCTGGTATTATGATCGGCTGGGAAAAATGTTCCCAACCCGGAACCCGTCGCCCGCCCCAACAGGCGGCAAAAAACAGG  
CAGCAACCGCTTCGCGGAAGCGCGCTGCGCGCGCAACGCGGATTACCGTAACGACGACACGCTTCAAGCGGTTATGATGAAAAAGTGGCGACTTGGCGCGCTGACCTGCTCAA  
ATACAAAGCAACCGCGGACGAAACAAACCGTTCTGCTGTTTGGCGAGCGCAAGAAATACACCTACGTCGCCAATCCGAACCTTTTGAACGCGCAGGCGAACCAATCTTGAAGCGATC

GGCTTTAGCGCACCGAAAAACAGTACACCTCAACGGCGACACAGTCGAAGTCGCTGAGCGCGCCGAAACCAACGAGCTGAAATCGACAAAGCTATACCTTTACCAAGACAGCT  
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CCGAGTGGCACATCAACCGCAGCATGAAAAACAACGCGCCCAAGCGAAGTCTGTTCC

## SEQ ID 1408

MDFKRLTAFPAIALVIMIGWEKMFPTPKFVPAPQQAQQAATASAAALAPATITVTTTQVAVIDEKSGDLRLRLTLKYKATGDNKPFVLPDQKEYTYVAQSELLDAQNNILKGI  
GFSAPKKQYTLNGDTVEVRLSAPETNGLIKDKVYPTKDSYLVNVRFDIANGSGQTANLSADYIRVRHSEPEGGYFTHSYVGVVYTPBGNPQKVSFSLDDDAKSGKSEABYIRKPT  
GWLGHIEHFMSTWLIQPKGQSVCAAGDCRIDIKRRSKLYSASVPLAAIQAGKAETPAVNLVYAGPQTTSVIANIADNLQAKDYKGVHVPASPLFWLNLQHNHIGWGAIVLVTI  
IVKAVLPIPTNASTRSNAKMRAPLQITKEKYGDDBMAQQMMQLYKDEKINPLGGCLPMLLIQVPIGLYVWALPASVELRQAPWLGWITDLSRADPYIILPIIMAAHFAQYTLNPP  
PTDPMQAKMMKIMPLVFSVMFFFFPAGLVLYVWVNNLLIAQONHINRSIERQRAQGEVVS

## SEQ ID 1409

CGACAGAGCTGACGACAGCCATGCAGACCTGTGTACGCTCCCGAAGGCATCTCCGCTCCGAGGATTCGCCCATGTCAAAACCAAGGTAGGTTCTTCGCGTTCATCGAATTA  
ATCCACATCAT

## SEQ ID 1410

RHEI/TAMQHLVYSGRRHSSVSGGFRCTQNVRFALHRINPHH

## SEQ ID 1411

ATGCGACATATCTTATCTGTCTGATCGAAAAACGAATCAGGTGCGATGAGCGCGTGTGCGTGTCTCTGACGCGATTAACAATATCGAATCTTTGGCGGTTCGCGCGACCGGAAGCA  
AAACCGCTGACCGATGACCATCGTTACCCACGCGGACGAGCAGGTATCGAACAATCACCACCACTCAATAAATGATGAAAGTGAATTAAGTGGTTCGATTTGAACGAAAGCGGTT  
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ATTGAAATTACCGGCTCGACCGCAAGCTGGATTCCTTTTGGAAACCGTCCGACGCGCCAAATTTGGAAACCGTACGTACAGGTGCGCGCGCATCGGTGCGCGTGAGCGTATTTGA  
AAAT

## SEQ ID 1412

MRHLSVLIENESGAMSRVVGLFSARDYNIDSLAVAPTEDKTLRMTIVTHGDEQVIEQITKQLNKLIEVIVVDLNESESRFVERELMLVKVRAAGKDRDEFRLITETIRGSIIDVIDRSTT  
TEITGSTDKLDSFLETVGRALILETVRTGAAGIGRGERILKI

## SEQ ID 1413

ATGATGGGGCTTTGCTGAAAAATTGGAAGCGCTGCTTATTTGTCCGCAATCGGTTCTTCGCGGTTCTTGGCAGCTGGACAGGCGCGCGCAATACCGTCCGCGATACGGTCCGCGG  
TGTGCGAGGTTTCGAACCGCTCAAAGCGCGCGCGTCAACACGCGCAACACCGCGCAATCTGCGCGCGTATCAGGCGCAAAAGCGCGCGGAGGAAAAAGAGGTTGCGCTA  
TGTCAACCGCTTAAATCATPTGAAACCTGTGTACCGCAATGCTGTTTGTGATGCTGACGCGCGTCCGCAACTCAACCGCGCGGTTGACGACGCGGT

## SEQ ID 1414

MTGALLKNWKLILLSAIAFFAVSWQLDRAAQYRRGYGAHVSEVSERLKAAAEVHAZHARKSSAAYQAQKAAREEKERVYVQTLKIIEKPVYRNACPDAGVRELNAAVDDGG

## SEQ ID 1415

GTGCAAACTCCGCGTCGATATGAACCTTTGGCGGAATCAAGCTGTATCCCGGAGTACCTTTTATCCGTTGAGCGATGGCCCTTCCATACAGAACCCGATCACTATGTCTGC  
TTTCGCACTGCCGACTGTGCTGCTGCGAGTTAAGCTACCTTTTGCCATTGCACTATCAGTCCGATTTCCGACCGGACTAGGTAACCTTCGAATCTCTCCGTTCAGCTTTGGAGGAG  
ACCGCCCACTCAAACTGCTTACCATGCAGCTCCCGACCGGATGACGGGTGCGGTAGAACCTCAAAGACACAGGCGGTGATTTTCAGGAGCACTCCACAGAGACTGGCGTCTT  
GCTTCAAGCTTCCACTATCTTACACAACTGACTTCAAGTCCAATGCAAGCTACAG

## SEQ ID 1416

VPNSAVDMNSWAESSLLSPEYLLSVERMPFHTPEPDHYVLLSHLPDLVSQSLSYLLPLHYQSDFRPDLGNLRTPLRFRRRPQSNCLPCTVDPDGGSGLEPQRHQGGIFKDDSTETGVF  
ASKPSTYPTQVTSKNALQ

## SEQ ID 1417

ATGGGACAGTACAAGAAGCTGTGTAATCTGCTGTTTGGCGTTCTGGCGTATGCTTTACCATCTTTGGCTATATGGGACGAGGTTTATAAGAAAGCCCGCTTACCCGCAACAGGTG  
TTTCCGCACTCCGCAAGGCTGATGACGAAAGACGATATTTTGGCAGGTCACTGCGTGGCAGATACCGCGCATGGAAGTCCGTTGATTTCTGGCTACCGCGCATATCAGGCTCC  
GACTGGACCGCGGCTGCGCTGATGAGTTGTCGCGCTGTTGATTTGACCGCGCAACAGACTTACGCGCAAAATTCGATGAAGTTTCCCTGAAGAACAGCGCTTCTGAAAC  
CGCTTGGCGGATGANTACCGCAATCAAGCGCTATTAAGAGACGCGCAGCGCTGCTCATGAGGATACGCGGTTGAAAGCATGAAAGCATCTGCTCTTACTATCAGCGGTTTACGCG  
ATGATCCCAAGTTCACCAACACCGCGAACACTTTGCAATGAAAAACACACATTTGCCAAGCCAAAGAGCGCGTGAAGAACTGTTCGACTTCTTCTTCTGACTTCTTGTCTGCTGCGAC  
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CGACTGCTTCCCTTACGCGCTGACCGGCTTGGCACATCCAATCCGCGATCTTCTGATTTGCAACCGGCTTTTACGCGGAGGTTTGTCTGCGCGGATTTGCAACGCGCGCAAGAT  
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TGGCGCGCTGCGCGCTTATGTTGTGGCGGCTTCCGCGGCGCTGACCAACCTGTACTTCTCCGCTTACTTCCGCTTACCGCGCGGCTTGTGCTGTGTACGCTTCTTGG  
GCGCTGCTGTGCTGGCGCGGAGGACATACGAGCACTGCTTACCAACCTGTACTTCTCCGCTTACTTCCGCTTACCGCGCGGCTTGTGCTGTGTACGCTTCTTGG  
CATTTGGCTTCTGATTTGTGTTGTGCGGCTTCTGAAACCGAGCGCGGTTTACGACAACTGATGACTTGGGCTTCTGCTGTCTCAACGCGGCTTGTGCTGTGATTTGCCATCAG  
CTGCTGCTGTGCGGCTGATTCAGGATACGCGCTTATCAGCAGCGGTTTGTGCTGTGCGCGGAGGATTTCTGCAATGGAATCTCGACACCTGCGCTGGGTACGCACTGCG  
CCGACTTAACTTTATCGCGGTTGCAATCTGCTTGCATCCAGCCACTAAATCGTATTCGCGCGGACAAA

## SEQ ID 1418

MGQYKILWYLLFAVLAVCFITLGYMGSEVYKAPPYEPQVVSASGKVLMTKDDILAGQSAWQSTGGNEVSGILHGAQYAPDWTADWLHRELSAWLDTAQQTYGKKFDEVSPBQAVLKT  
RLADEYRNQSRKEDGSVVISDTRVKALESILPYTHGVYGDPLQITREHFAMKNLTPSQEAREKLDFPFTWSASTNRPGEVFTTNNWPEHLINNVPTTENYNSFTSVLLIM

GIGLLMNGSYFLTKREBEVSEDPISKIQLTPSQKALGKYVFLTVALFVVQVLLGGLTAHYTVBQGFYCIDREALGFHSDWFPYALTRTWIHSALFWIATGFLTAGLFLAPIVNGKD  
PKFQRAVGNFLYIALFIVVGGSYAGNFPALTHILPEFNFVFGHQGYEYLDLGRFWQLLMVGLLLMLFLMLRCTVSAPKRGVDENLLAIFVASMVGVGVFYAPGLFYGEKSPIAVHEYH  
RWWVHLWVEGFFEVFAATAFAFVYINMGVVRSTASTALAAAIFMLGGVPGTILHLYFSGSTSASMAIGACFSALEVVPVLVLLGREAYEHWSTYHLSDNAKRLRWPLMCFVAVAFHHR  
IGAGVPGFLINPPLISFYIQGLMNTSAVHAHAALPGVYGPLALGFLVLLVARYLKPNAFDDKLMTWGPHLLNGGLVGMTAISLLPVGVIQAYASITHGLWYARSEPLQMEILDITLRNVRTA  
PDLIFIGGAICVAIQATKRVFGRDK

## SEQ ID 1419

ATGCCGACGGTTCGCTGTCCGATAGACGGGGAATAAGGCGGGCTTCATACCGACGGCGCTGCCGACGCCGGAAGGTTACAGCGCATTTATAGAAACCGATGGGAAATAAAGGAA  
ACCGTCAATT

## SEQ ID 1420

MPQVACSDRRGIRAGFIPDGRAASPKVQATALYRNHRHKGKRAI

## SEQ ID 1421

ATGAACCTCTCTATTGTCCAACTGCTGCTGGGGCTGATAAGGTTTACCAATCTGCATCAGCCGCTGAFTCCGCGCGCTGCCGTTATACGCCGACCTGTTCGCAATACCGGTCGAAG  
CGGTCAAAAAATACGGCGCATTTCAAAGGCTCCGGCTCGCCATCAAGCGCATTCACGCTGCCACCTTTTCGGCGGACACGGACACGACCCCGTTCC

## SEQ ID 1422

MFLLSKLLGLIRFYQYICSLIPFPCRYTPTCSQYAVEAVKYGAFKGLRLAIRIARCHPPFGHGHDVPP

## SEQ ID 1423

ATGAACGCACTTATCAACCTTCGGTTACCAACGCAAAACGCAACCCACGGCTTCCTGCTGCGCTCCAAAACACGCGCGGACGCGCAGTATTGGCCGACGCGCTGCCAAAGCGCGCAAC  
GCTGGCAGTG

## SEQ ID 1424

MKRTYQPSVTKRKTHGFLVRSKTRGGRAVLAARRAKGRKRLAV

## SEQ ID 1425

TTGCAAAAAGCGGCAATTTGAGTGTAAATTCACGGTTTAAATATCTACCAATCTTATTTTAGGAACCATCATGAAACGCACTTATCAACCTTCGGTTACCAACGCAAAACGCAACCCACGGC  
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AAAAACGGATGATTTTCATCCGTTTTCGATTCAGAAACGCGCGCAGCGCGACCTGCTGCAAGTTTCGCGCTCAAAACGCGCAACGGGCTGGACCATCCCCGATCGGCTGTGTGGTGGC  
AAAAAACCGGCAAAACGCGGCAACGAGCGGAATATATGAACGCGCTCATCGGCACTGTTTCAGATTGAACAAAACCGGCTGCCGCTCAGGATTTCGTGTGGCGTCCGCGGCAAT  
TCGACAGGCTACGCGCAAAACAGGCAAGGCGGAACCTGCCCAACTCATGTTGGCAACCCGCAACCGGATGCGGGAACAGGTA

## SEQ ID 1426

UTKAANWVINGLIYPPFYRNHETHLSTFRYQYQTHPRLPALQNRTRTSIGRTPCQRPQTGSGVILDYRFRQYRLKTDFFSSVFAFNRRSRDLQVSRNNGNLDHPRIGLVVG  
KTKAKRANERNYMKRVIRDFRLNKLPPQDFVVRVRKFDRTAKQARAEALQIMFENPATGCGKQV

## SEQ ID 1427

TGCGCTGGGATTTCTGCCGCTTTCTGTGGATAAATTTTGCACGGTGTGGATAAAATATCGCGAGTCGGTATAATCGGTTGCTGCGTTTGAACCGACGCTATTCAACAGATT  
GTTTCTCTTTTGAAAATATATATTTCTTTGTTTCGATTTCATTTTACGATTTCGAGCCTATCCA

## SEQ ID 1428

LPADFCLSVDFLHGLWKYRRVGIIGSLRFEPTRIQQICPLFENLIFSLFISPLIRAYP

## SEQ ID 1429

TTGAATACGAAAGCGGACGCGCGGACGCAACTCTTCCCTTACCGCTTCTATTTTCGCGCAAACTGGCTCTTGAGCATATTGCAGGCAAACTGCTTCTTCCGTACACCCCATACG  
CCACCTCTCTCACCAACCGTAAGGGGCGCAATCCATTGCGCAAACTGCCGCTGAGGCAACATATCGTGAAGACGCGGAGGACAGCGGCAAACTCTGC

## SEQ ID 1430

LNTKGTAGSQLPYRFPYSGKLALEHLAGKLVAVHHPYATLL/INRKNRNLRLKLPVRQHVKTAEARPELC

## SEQ ID 1431

ATGACATTAGCAGAGTTTGGCGCTGTGCTCCGCGCTCTTACGATATGTTGCCCTACGGGCACTTTCGCAATGATTGCGCCCTTACGGTTGGTGAAGAGGTTGGCGTATGGGTG  
TGTACGCGCAAGCAACGATTGCTGCAATATGCTCAAGAGCCAGTTTGGCGGAAAAATAGAAGCGTAAAGGAAGAGTTGGCTGCCGCGCTCCCGCTTTCGTATTCAAACCGGAGAG  
CGTGGCTTA

## SEQ ID 1432

HTLAEFWPLCLRLRLDMLPHGQFAQNIAPLTVGEEGVWVYVGNQFACNMLKSQFAGKIEAVREELAAGRPAFRIQTGRERAL

## SEQ ID 1433

ATGCGCGCGGTGAAGGTGCTGTGCAACCTGCCGAGCGCTCTTGCACGCGGGCTCGGAGGAGATGCCGCTGCAGGAGGTTCTGTGACGAGCTGCCGCTGAAAAGCCTGTCAAACCG  
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AAGACGAAGCGCGCTGTTTATGCAATCTGATCCGTTCCAACTGCGGCACTGGAAGCGCGTTCAACCGTGTGAGCGGAGCAGCGCTTTATGAACCGTCCCGTCACTCGACATCGA  
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## SEQ ID 1434

MAAVEGAVEPAEPLHAGSEEMPQVEVLLDELSEKPVKPAASKTAADILAEKMLPHEPRQAAGPASRPESAARVARTDAQRDAEAREYBQYNLSFDYTFDTLVEKGNRLAAAAQA  
IAENPGQSYNPFYLGSTGLKTHLVQAVGNELKNRPDAKVRYNHSDDYIRSPKAVRNNTYDVFKQYQYDLIIIDDIQFIRKDRTHREFFLYLNHFNHKKQLILFCDVLPKIEG  
MDDLKSRFSWGLTLELEPPELEMRILAIQKAEAGISIEDEALFIANLIRSNVRELEGAPNRVGASSRPMNRFPVIDIDLARTALQDIIAEKHVITADIIIDAVAKYRIKISDVLGK  
KTRNRIARPRQVANSILTKELFTLSLPSIGDSFGGRDHTTVMHGIRAVAKLREEDPELAQDYKELLILIQN

## SEQ ID 1435

TGGTAAATCTGTTTGTGTAAGAGCGTTCGAAATATATAAGTATCCCTTCCGCTGTCTAAGATATCTCTCGATATTCGACATTCCGCTATATCTTTTCACTTCTGCTCGCGCTTCG  
GCAGCGCGAAGAACCGAATATACGCCCGCAGGGGAAAACAGTCAATATCTTACGCGGATTTTTTCGGGAAATTCGTCAT

## SEQ ID 1436

SVICPVKERCEIIXPPLSKISLSDIPCYTTFQVRRFGSGEENPYTPAGENSQYFQDFFGEIRH



**SEQ ID 1437**

SEQ ID 1437

ATGAAGCGGCTCTATCTTAGAAAAACTGCAACAACCTCGGCCAGCGGTTGGAAGAAGTTACCCACCTTTTAGGGCAACCCGAAGCCACATCCGATATGGACAACCTACCGCAAGCTCAGCGCG  
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AATCGAAGCGCGCAAGCCAAAATCGACGAACCTGGATACCGAATTGCAAAACCTTGCTGTCTGCCAAGATGCCGACGACGACAAAACATCTTTATCGAAATACGCGCGCGCACGGGGCGC  
GACGAAGCCGCGCTGTTTGCCGCGATTTGCTGCGTATGTACAGCCGCTACGCGGAACGCAACCCGCTGGCAGGTTGAAATCGTGTCCGCCAACGAAGCGGAATTTGGCGGGCTATAAAGAAG  
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AACGCGAAGTCCAAGCCAAAGAAGCGCGGCAACGCAAAATCCCTCATCGGCAGCGGCGGACCGCAGCGAACGCATCCGCACCTTACAACCTATCCCCAAAGCGAGGTTAACGAGCCACCGCATCAA  
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**SEQ ID 1438**

SEQ ID 1438  
MKPSILEKQLQIGDRLEEIVTHLLGQPEATSDMDNYRKLTRHAEITPVVEVFQNYRLAQSDLADEEMLSDPEMKDFAAEETEAAKAKIDELOTELQKLLLPKDAADDKNITETIRAGTGG  
DEAALFAGDILLRMYSRYAERNRQWEIVTSANESIELGGYKEVIARIVGLGAYSRKFESGGHRVQVNPATESQGRHITSACTVAVHPEADELEIDELNPADLRTDTTFRASGAGGQHINKTDS  
AVRTHILPTGVVEVECDGRSOHANKAQAMKVLAAARLNDQKREVOAKEAAERKSLIGSGDRSERIRTYNPQGRVTDHRIHLTKLDFVMDGLARITDALLAEHQAEILAAAGD

SEQ ID 1439

SEQ ID 1439

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GCTGCTCTCCGGTGTGCTGTGTGTGCTGGAATTTGGGACGACAAACCGTCTGACCGTGAAGGCGGGCAAAATCGCGTTTTCGCCCTGCAAAACCTGCCTGCGCCCGGATTTTCGATGATGAATGTC  
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GCTGTTCTCGCAACCCGGCTGTTGAGCTGCTGTCGACGACACGACGAGGAGGAAGCGCGCGAAGAAATCGAAATCGCCTATCAGGGCGCGGAACTCGAAGTCGCTTTCATATATCG  
CTATTTCATGAGACGCTGTCGCAACATCCATTCCGACGATATGCACTGCTGCCCTCGCGCAGCGCAACCGCTGACGCGCTGTTTACCGTGCAGCAACATCGGAATTCCAATATATTTGATG  
CCGATGCGGATT

**SEQ ID 1440**

Seq ID 1440  
MLILQAEKRSILKPLQAFPTGIVERLHTPLILSNVLTBGRGGQFKLLATDLEIQIDTAGPEGGAGDFRITTNAKKQDQILRALPAGALVSLWDWDDNRIITLKAGKSRFALQTLPAADFPMNV  
GEDI SATFSILGQERFKTMLSQVQYMAVQDIRYTLNGLLQVGGSQLRLVATDGHRLAYAACAIDALPRAEVILPRKTVLELPLKLLNVPDDPIQIELLDKQVRFQCNQTTIVSKVIDGKF  
PDPNRVIPLENDKRI FVLSRAELLGALERVSVILANEKFRGARLFLOPGLLSVVCSSNNSEQEAREEIRIAYQGGEEVGFNIGYILMDVLRNIHSDDMQLAFGDANRSTLFTVPNNPNPKYIVM  
PMRI

SEQ ID 1441

SEQ ID 1441

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AAGAGCTACAAAACCTCCGCGCGCGCATTTCAAACGAACTGCACGACCGCGAATACCGGCACGCGGTGCGGCTCGAAGTTCGCTCTCAGCGGCACGAGCATCTGACCGTTGACGAAG  
GCAATTCAGGCTGACCGACGCGCAATCTATCATGCTCAAGCGCTCAACCTCTGCGGCTCAACGCGCTCCCGGACCTAGTCAACCGCCCGAATTGAAATTTCCGCGCGCACACGCG  
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AATGGCATCTGGCAGACAATACCCACGCGTGCTGTATGACGCGGACGCGCGCTATATCCGCGCGCGCCCGCGAAGCGAAGCGACCGACTGCAAAAACGATTATTTGGGATTTGCTC  
CGAGGC

SEQ ID 1442

SEQ ID 1442

LPRCLKQTVRHVMPPETGADAAKPSDGIVRPLRPNNHNLWENLMTFQNRILCRELSLLAFNRRVLAQAEKKNVPLLERLPLCTVSSNLDEFFEVNMAHLKRENKLPFRRRPDNGKMPSET  
IADVTEAARSLIRHQYDLFNNVLQPELARESITHFYRRNRWGTQKKWIEDYDFRELLPIITPIGLDPSHPFPPLPKNSLNFAVELOGTDAFGRPSGMAIVQAPRIPLRVVPLPSELGGGH  
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IRREDGVLKRYAHLGTGNYHQGTSRIYTDPLGLTDADEQITDAVNLFLMEITGLGKPGRLNKLYQSPFTLHKMNVIGRIARETEHAKAGKGPARTAKMNSLIRPTVI EALYRASAAGVQIDLI  
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RG

SEQ ID 1443

SEQ ID 1443  
GTGACGGACGGTCTGTTTCAGGCATCGGGCAATGTGAAACCGGATACCGGTACGTCGGGTATCGTCTGTTTCAAATCACTTCCAAACAAAATAATGACGCAGTTTTTCGTACACCGCA  
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CGCCCTCTCTGCTTGAACCGATGACTTTCGCCGCCGTAACCGGGCTTGTGCGTACTGTTTCAGCGCTCAGTCCGAACGTCCTCCCTTGGGTGTGCGAGTGCAGATGAGGACGGGGTGGCAGTGAAG  
GTCTGTGCGCAAAACAGAGTTTCGCGCTTGGATGTGTGACGATGACTTTTTCTTTTGAATATAGGCACTGACCGCATCCGGCTGCCCCCTGTGCGAATACGGGGCAGTCTGTACGAGGCAG  
CAACAATATCCC

SEQ ID 1444

SEQ ID 1444  
VTDLFQASGQCEGYRYTVRPSVSNHPQHKINTQFFVHRIADVDAAVGHNPVGHGRGGDAFVSPFGKYLIPNAVQGEKKIALLETDDFAAVTGLVGTQVQRQSERFLGCGSADEGVALP  
VWGKTEFLGCVDDDFILNIGTDIRLRPLCEYGGSRQQAQYP

## SEQ ID 1445

ATGCCGCCCGCTCTGCTTCAGGGATATTGCTGCTGCTGACGACTGCCCGCTATTCCGACAGGGGACGCGGATGCGGTAGTGCCTATATTCAAAGAAAAAGTCATCGTCGACA  
CATCCAAGGCGGAATCTGTGTTTTCGCGACGACCGTCACTGTCACCCCGTCTCATCGGCATGCCACACCCAGGGGACGTTCCGACTGACGCTGAACAGTACCGACAAGCCCGTTACGG  
CGCGGAAGTCATCGGTTTCAAGCAGGAGGGCGATTTCCTTTTCCGCCGTCACCGCGCTTGAATCAGATACCGTCCGAAAGCGAAACGAAACGATGCGCTCCCGCTCGGTGCGACAGG  
ATTATGACCAACGGCTGCATCAACGTCAGCGATGCGGTGTACGAAAACTGCGTCATTATTTTGTGTTGGAAGTGATT

## SEQ ID 1446

MPRLLSGLICLLLTAPVFAQQQPDVASYIQKKKIVDTSKAELCFADDRQCHPVLIGTATPKGTFGLTNSDKPGYGEVIGFKQEGDFLALHRVWNPISERRNERIASPSVSDR  
IMFNGCINVSDAVYKRLHYFVLEVI

## SEQ ID 1447

ATGGGCCCGGCTGACCAAAGACGACATCTACAAAATCCCGGGCGCCCGCATACGACGAGGATGTATGACGCGTCCGGAATGGGATTACCTGTTCCACTTCCACACCCCGGCGGTGG  
GTATCGACCTGAAACACTTCCGGCGTGAAGGCGTTACTACCTGCCAATACAAAGTATTTTCGATAAAGACAAATTTGCCCGACGCTTCTACTGGAACCCCGCTTCCCGAAAGATGC  
CGTCTGCCCGCCCGCCACCCAAAGCCGAGCCGCAAGTCATCATCCGGAATCGTCCGCGCAAAACCGAAACGTTATCCGCCAA

## SEQ ID 1448

MRPGLTKDDIYKIPGRPHYDEMGYVRENDYLFHFHTPGVGIDPENTSGVEGVTTQYKVIIFDKKPFARSFYHNPVFPKDAVCPPPAPKAEPQVIIRKIVPAKPKRIRQ

## SEQ ID 1449

TGCGCGATACGTTTCGTTTTCGCGGACGATTTCGCGGATGATGACTTTCGCGCTCGGCTTTGGTTCGCGGCGCGCGGCGAGAGCGCATCTTTCGGAAGACGGGGTTCAGTAGAAGCTG  
CGGCAAAATTTGCTCTTTATCGAAATCACTTTGTATTGCGAGTAGTAAGCGCTTCCACGCGCGAAGTGTTCGAGGTGCGATACCCACGCGCGGGTGTGGAAGTGAACAGGTAATCC  
ATTTCGCGACGCGGTACATACCTTTCGTTAATGCGGCGCGCGCGGATTTCGTAGATGTCGCTTTGGTCAGACGCGGCGCATCTGATCCAGTTCGTATAGTCGGAATGTCCCGG  
CTTGTGTCGAGCGTTACGGAATAGGTTCCGCGAAACCGGATGTGCGGTGTCGCGCTTTCGCGTTCGCTTTATGTTGCGCAGGCGAGAGATGCTTCCGCGCAATCTGCCAA  
GCTCGGT

## SEQ ID 1450

LADTFPFCRHPFADDDRLGFCGRRADGIFREDGVFVEAAGKFVFIENHFVLASNAFHAGSVFVFDTHARGVEVBQVIFPAHAVHTFVVRARAADFVDVFGQTGAHLIQFVISRECA  
LVVERYGIGFRENRIVGRVGFVDAVHLRRQTECLPILPSSV

## SEQ ID 1451

ATGAAATCAACAAATCGTCAAAACGAGCTTGGCAGTATTGGCGGACGCGATTCTGTCGCTGCGCAACCATAAAGCAACGTCAAAGCCGACGCGACGACGACCAATCCGGTTTCCCG  
GAACCTATTCGTAACGCTCGACAACAAGCGCGGCATTCGCGACTTA

## SEQ ID 1452

MKIKQIVKPSLAVLAAGILSACATIKQRQSRHRDRQSGFPGLFRNARQARHIPDL

## SEQ ID 1453

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GCTGGGACATCCCTTGTGTTTCAGACGCGATTTCGCGAAGCAGGATTTCGCGTTTGAAGCCGATTTGTTGCGTTACCCCGGAGCGGTGGTTCGCGAAATCGGCTTGGATTTCGACGAC  
AAAACCCAAACCGCGCGCGAGCTGAACGGCAAAATTCAGTTTTCAGCCGCGAGCTTGCATTCGCGCAAAACCTGCGCGCGCGGTGATTCATCAATCTCAAGGCCACCGCGGACATCG  
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GCTCAATCCGAACGCGCGTAAGTTCGCGATACGCTTAAAGCCTTGAACGACGCGGATTTCGATTGGAACCGGATAGCCCGTTTCATGTTGGAACACCGCTCAATACGCTGCCAACATT  
CTTCGGATTGCGAAATTCGTCGCGAAATACGCGGTACCGCGCGCGGAAATCGCGCGGATACCGGAACGCAATGCGGACAGTCTGCTCCGTC

## SEQ ID 1454

MGRGRGETRVAUVAGVGMRLTDTCHLADSVLRGNLAQVLAERAGVWRPVPVATPCQDQDVAELSEMPSEHQIRIALGTHPWFSDGIAEQDFSGLEAVLVRYFRAHVGEIGLDFYD  
KTQTPPQRRERQIQVSRQLAQLTLLRRVLIHLKATADIAAAVKGTGTGGIVHAFSGSABEARVLTKLGFKIGIGSLLNPNARKVRDTLKLNDGDFVLETDSPFMLENTVNTPANI  
LRIAELAAERGTGAARLAAATERNADSLRP

## SEQ ID 1455

ATGCAGTATACAGGCGCGCAAAATCATAGTCGACAGTCTCAAAGCCGAGGCGTCGAGTACGTTTTCGTTATCCCGCGGTGCGGTATCGAAATCTACGATGCCCTGTTCCAACTCAATA  
AATTCAAACACATCTTACCOCCTATGACGAGGCGGACGATACACGCGGAGATGCGTATGCGCGCTACGCGGTAAGTGGCGGTGCGATTGTTACATCCGCGCGCGGCTTACCAATGC  
GCTGACCGGTATGCTACTGCTATACGATTCGATTCCGATGCTGTCATCAGCGGACAGTAGGCAATTCCTGATTGTTGTCGAGTTCGCAAGAGTTGATACGCGGTGATTAC  
CGTCCGCGGTCAACACAAATTTCTGTTTACGACATCAATGAGTTGGTGGAAACCAATTAAGAGCGGTTCCAAATTCGCGCAAGCGCGGACCGCGGCGCGGTGCTGCTGATGTCGCG  
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GAAATATATACGCGCGTTCGAGAGTCGGAACCTATTTTCGATTCTTTCGCGGATTTCGTCAAACTTCCGAGGATACGCGCATTCGCGCATTCGCGTTCGCAATTAATCTGATGTTGAAG  
GTGCTTGTGGAAGCATTAACCAAAAGACAGGCTGTTTATGACTTCTGACCGACAGAAACAGAAATGTGATGCTATGTCGCGCAACGCGCAAGGTTTGGACGAAATGCTACT  
TCCGCGCATATGCTACGACGGAAGCGG

## SEQ ID 1456

MQLSGAQITVQLKABGVVEYFGYPGGAVIETIDALFQNLKPKHILTRHEQA VHAADAYARVSGKVGVALVTSFGPVNALTGATAYTDSIPMVVISGQVGNLSIGTDAFQEVDFVIGT  
RPCVKHNLVTDINELVETIKKAPQIAASGRPGPVLDVDPKDVQAMAKFSYPQEDIFIRSTYQPVQGHIGQIKKAVQMLASAKRPVYFGGCVLGNASELTFRFRMTGAPCTGLMGL  
GATPSGRQPLGLMLGHGTTEANLAMQADVVLAAGARFDRVVSVPKFFKAKKVIHIDVPSIAIKRVKADIPVGDVKNLSENVALMQKQESVPSDALGKWKITIEWRSRDLN  
FDNGSEIKPQYVIQKLAEITGNSAITSDVQGHQMPAQYYPFERPQWNLSSGLGTGCVGLPYAIGAKLAAPDQDVPFCITGDSIQMNIQELSTCFQYRIPVNVITLNGYLGHVQWQ  
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## SEQ ID 1457

TTGTTGATTTCATATGACAGAACTCTTTTACCOCGATGCCGCTGCGCTTTTGTTCGGAAGACCGCATCAGGAGAGTTTAAACGTT

## SEQ ID 1458

LFDPMQNPFLPARLPFVRKSIRIRVILNV

## SEQ ID 1459

ATGCGTAAATTCGACGGCATCATTCGTATGCCGTACAAATACACCGCTTTTACTGATACGACGTTTTTATGCTAATATTACGAACCAAAATCAAACTTTAAACTCTCTGATGC  
GGCTCTTCGGAACAAAGGACAGCGGCATCGGGTAAAAAGGATTCTGCATA

## SEQ ID 1460

MRKPARASPMFYKYTAFTDTHVFYANITNQYTFKTLMLRFRKGRASGKKGFCI

## SEQ ID 1461

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GAACATTACAGCCCGCGCCATCGAGCCTGCCGCGCAGAAAAATGGGACGACGCCGATTTTCCAACTGCTCCGAAGACGCTTCCAAACCCAAATATTATGCTTTTGGATGTTCCCTT  
ACCC

## SEQ ID 1462

MRVRIYASCRQFADSPTSATCYNSSFKFLTSSSEKQNDHARTLPARRHRACGAEMGRFPYQRLRRFPQTQILLPFDVPLP

## SEQ ID 1463

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AGCTGCTCAACGATTGGGAACAGTGAACACTGGCCGGAACAGTCAAAACCATGACGCGCAACTGGATCGGCAATCTCGCGCATGACCGTGGCTTTCGCGTTTCAGACGACAGCAA  
GCAAGTTTGAAGCGATTACGCGAAATTCCTGCAAGTTTATACACCCGCGCGACACGCTGATGGGTGCGACTTATGTGCTGTTCGCGCGCAACATCCGCTGGCAACAGCGCGAGCC  
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GACGGCATGTATTCGCGAAGTCCGGAATATCGGCGCGGCTGCAACATACATCGCGCGCATGCAACACGCGATTTCGCACTCTCTGACGCGCGCTTTCACCAAACTGATGCGCG  
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CGCGTGC CGCAAGATATTGGAAGCGCGCTGACGCTGTTGTGGCCATCTGCGCGCACATCTGCGAAACCTGGAAGCGAATTGAACGCGCGCAACTGGAAGCAGGCTGGCGCA  
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## SEQ ID 1464

HPYPSPGLHGHVRYNTTIDGVLRSFKLLNGFVPMQWDAPGNPAENAKNNVAPAAWTDNIEMKPTQLKSLGFAIDWEREVATCKPEYRWEPWLFKLFKGIYVRKNGTVNWD  
VDQTVLANEQVINDGRGWSGALIEKREIFMYFYKIDYAEELLNDLKLHWPQVKTQMRNIGKSRGMTVRFVAVSDSKQLEGDYAKFLQVYTTTPTDLMGATTVAVAAEHLATAAA  
ADKPELQAFIAECKAGSVAEADMTMEKKGVPTGRYVNLNGDKLEWLVANYVLNGYGDGAVMAVPAHDERDFEFAKYNLPKQVLA VGDNAFDANRWQEWYGDKNGLVNLSDLDGL  
DPYTFADVAAGKIQSGAGRPFTQYRLRDWGISRQRYWGPPIPIVHCEKCGVDFVPADQLPVLVPEHVVDPDGMGSPFLAKMPEFYETSCPCCGGAARETDTMDTFHESWYFFRYMSPKFS  
DGMVSAESAKYWGAVDQYIGGIEHALHLLYARFTTKLMRDESLVNDPEPRLTQGMVVCETTYRENDKGGKWINPADVELTDDKGRFVSALVADGLFVVISGTERKMSKNNGV  
PQELINAYGADTARLFMFAAPPQSLWSDSGVEGAHRFLRLRWTVVEYLKQGA VKAPAGNQDGLSKELKDLRHLHSTTAKVSDDYGRQQFNTAIAAVMELLNQYDRTDTGSEQGR  
AVAQEVLEAARVLLWPIVPHICETLWSELNAGKLEWAGWPTVDEALVSEIEVMQVNGKLRGKITVAADASKADLEAALANBAGVKPMEGPKAKKITVVPGLVNTIV

## SEQ ID 1465

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AAGCAACCCCAAAATTCCTGTGTAATGAGCGAGGCTTGGCTGGA AAAACCGCTATTGCCCTGTTTCGCGAAGCAAGCCGATGACAGAGATTTCGCAATAACAACTGTTGACAGCTCTT  
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AACTTTTCTTCTTGTGATATAAAAAGCGGATTACTCATACGGCAATTTGTGCTGTGTAACCAAACTTTTCATACGCGCGGATATGATTTATCCCAAGAAATGAAGGCATTAAAAACCGAC  
CGCACCAATATGTTGTCATCAATCTCGCCCTTTGCCCTGAAAGCGGAAAAATATCTTAAATAGACGATTCCCGCATATTCGAACCCGAAACCGTCTGAAAAATGGAATCCAACT  
GTTTTCAGCAACCAAAATGCGGAGCGCAAGACTGGCTTTTGGCTGTTATGAAATGATTCGACCAACTACCGAAGAAATTCACATTTGCGCAATGTTATGAAATTTGAAACCAAACTATCC  
ATCCAAATTTCCCAAAACCAATATCAAGACAAAAATCCGCCAACAGTTGCAAAATTTGCGGTGATCAAAATATGATCGAAATTCATTGGTTCGCGGACTTTCAAAAAAATCGCAAAATG  
CACCCAACTCCCAAGCGCTTTGATTTCAATCATGATACTGAATTTACGAGAAATATTTATTTCTTCTGCCATTTCAAAAACGGTTGAAGTACACGCAATATTGCCCAAGGGCAGCAG  
TCGTA AAAAGTCGAGAAATTTATGGCAATTTATGAT

## SEQ ID 1466

LPCCLRLRLVLIPLVLLKINLKIQNNLFFDTQLGKQNKATHKIRVMSEANLEKNYCPCCGSKPMQRFANNKPVADLFCPNCHQYELKSNKQKTIGNSVPDGA YRTMLERIRSDTNP  
NFFFLAYKADYSTROLVLPKHPITPDMIIIPRNGIKRNPHEIMCSINLAPLPESGKIPLIDDSRIIEPETVLKRWQSNLFLRNQAEKIDLLAVMKCIDQLTREFTLTSMYEFENKLS  
IQFPQNNHKKIRQLQILRDQNMIEFIRGLYKKNRQIAPNSQVLLSNHDTFTNTYSSAILKTVEVQRNIAAGSSRRKVVGELLATYD

## SEQ ID 1467

TCTTTTCAGAAATGATTCCAAATACGAATTCGCTGCCATATAGGCAATCATAGGCTGACAAATCOGATGATGGTCCACAGCGCGCTTTTTCGCCCGCCATCGGTCATGCTGTGTTG  
AGCAGCAGTCTTCGCTAAATCAGCATGACAAATATGCCGAATACGGTTTATGGGTAATGTCATGGGTTTTCGCGAATACCGGCTTCGCGCAAGAAATGTCGCGTACGACGCGAATAGGTCA  
GCAGGATGAACCTGCGCCATAGGCTGGGAACATGAGTTTTCGCAACTGAGCAGCAGCGGAGGAATCTGCGAGCTTGGAGAAATTTTCGCGGTGACGAGCTCCGCTGACGACGCAAGCT  
CAAAACGCAATTAATGTTGCGATGCCGAACAGCCGATGCAAGCAGTGATGTCGCGATATGACGCAATAAGGGAAGTGGTATTTTCATATCCCGGAATTTTCCGGAATAACCAAA  
CCTGACAGCAGCATCAGTGGCGCAAGGATACAGCAGCACTGCACTCGCGCAGCGGATAAAAAGCTGCGCGCAAAATAAATAACAGCATCATCAAAACATCAGGCTGCCGGAAT  
ACCGAAGCCCATATGATTTTGTCTTGAATGACCGCATCAGCAGTCCGCGCGCTGGAAGCTCAATCGCGCGCCCAAAACCGGCAATTCGCTCTCCAGGGTATCCCGCGCGG  
CCCTGCTGTTGGCAGTGCATGCAATGACCAATCTCGGTAAACCGCGCTCAAAAAGATGAAAACCTGTCGGCAT

## SEQ ID 1468

SPQNDQYELAAHIGNHKADKSDDPHGFFAAPCGHAVFQQSSVNQP\*QYAEYGFMGKCHGFAEYFGKECAADDGIGQDDETCFHGLEHEFFQTEQRQESCELGEVSAVQAFVQQA  
QNGQ\*CCDAEQPVCKQ\*CADMQHKGKVGNIISREFSRENQT\*QHQCGARIQQQLHSAQRIKKAAGKINKQHPNNQAAGIPRAHNDPVLNDRHQCRADVGCRAQNRQRLPRVIPA  
PILLAVPCKCTQSCVNRQRDENCRH

## SEQ ID 1469

TTGGATAATCTGTCTGTTCCTGTTCCCCCAATGCGGTACCTTAATCGCTGCTTGGTGAATTCATTACAGTGTCTGGCAAGCGGTTTGTCCCTATTGGTT

## SEQ ID 1470

LDNLSVAVFPQCAVFKSLLGGIALQVLWQSGLSLLV

## SEQ ID 1471

ATGATTGATTTTGACAAACCGGTGAAGAAGCTGCCATTATCAAAGCTGTTTGAATAATCGTTTCAGACGACCTTGCTCTACAACGAAATCCCTTAACGTCATCGGGAAGATATT  
GGAAACATCCAAACGGCTGTTTGGATA

## SEQ ID 1472

MTDFDKPAREAAIYQSRLLKSPQTTLSSTTKIPLTSCGRYHKNITQAVLI

## SEQ ID 1473

ATGATTTTCGACAGACCCGCTTACTTTCTTTCCAAAGCGGTTTCAAGTGTGCAAAACGGGCAAAATGGTTTCCGTCAATAAGGGCACTGGGATTAATCCAAAGGAATGGCGGAGATTGG  
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CCATAATTTGAACAATATTACTTGGGAAACCAATCTCCCTTAATTTGCTGCGGTTTCTTTACCATTCGACAGAAACAAATCTTATGGGCAAGAAATAAAAAAGCCAAACAT  
ACGTTTCATATGAAATGATGAAGACCAAAATTAAGCAACAGATGAAATGTGTTTGGACATTCGACCTTCAATAAAACCGAAAAACATTCGCAACATCCGACACAAAAACAC  
TCCCTTACTTGAACGCTGCATCTATCGCTTCAATATCGGAGATTAAATTTTGACCTTTTATGGCAGCGGACAAACAGCGGTTCCGCTTAAACATGGTCGGAGATTTCGGG  
TTGCGAATCGAAGAAGATTTTTGAAT

## SEQ ID 1474

MIPADPPYFLSNDGFSQNGQMVSVNKGWDSKGMADLEFYEWLRLCYALLKPNGTIWCGTFPHNYLIGYLMQTVGYHILNITWEXNPFPNLSCRFFTHSTETILWAKNKKAKH  
THYEMKAKQNGKQMKCVWTFAPPNKTERTFGRKHTQKPLERLILSASNIGDLIFDPMGSGTGVAAALKHGRFFCGCELEDFLN

## SEQ ID 1475

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AAGATTACTCGCCGATAATGGCTTATTTATCATCATCGTGATACCTTATTTATTTAGATCAAAATCCAAACAACTCCCGGTTCAAGTAGAGAAATTAACAACTTCGATTTTAA  
AGAAAAATATACAAAGTTAGTTCACTCTTAGGTTGGCGGTTGATATGTTCTATGTTTGAATGATTGTTTACAAAAACCGGAATAT

## SEQ ID 1476

MIIIGIGGARTQTGLRFEERTDLRLFEIIPGYDLRKTDDNAGYEVWFGELKAYCFKKEFYRFLERLEYNINWKDHLKRLLPDNGLPIIRDTLPIIBIKPQQTGSGVDEKLQTCDFK  
RKQYTKLVHSLGNKVGYYVLDWFTKPEY

## SEQ ID 1477

ATGATTGGTTTACAAACCGGAATATTAAGATGTTTATGATTATATTATCAGTGTAACTGCCATTACCAATTTAACACGATTCCCTTAAGGTGGTTTGGACTGCTGATGGTGAACAA  
ATGAA

## SEQ ID 1478

MIGLQNRNIKDVLDYIISVNCHYQFNTIPLRWPLPDGETNB

## SEQ ID 1479

TTGACAGATGCTGCATTACGTTGCGGGAATCCGCGTATTTTGAACAAAGGTGGGCTACTTTATCACAATAGCAGAAAGATGGAAAAACGGCGGGATTGG

## SEQ ID 1480

LTDAAFSVAESAYFQKVGLLYHNSRKMEZNGDW

## SEQ ID 1481

TTGTTCAAAATACCGGATTTCCGCGACACTGAATGCGCATCTGTCAAAGATTATTTGAAAAACGTTGAGTTAGACAAGTCTGCCGACAATGTGATACCATCCAAATATCCGAGG  
GTTTAGGCGGTATTCAGAGTACGGTCTCTTATGC

## SEQ ID 1482

LFRKIRGPRDTECSICQRLFENGRVRQVCRQKYHIQNYRQGLGPIPEYGVLC

## SEQ ID 1483

GTGTCTTATGCTGATGCTGTAAACAATGCCCGTATAGAAAACTAAAAACGGTTGTGCCGACCGTTATGCCGGTTTATGAGCAAGTGTGAGAAATAGGGGCGGTTAATAAAAAACGT  
GGCGT

## SEQ ID 1484

VSYADAVNNARIENLKRLLPTVHPVYEQSVRNKGRVKKRRR

## SEQ ID 1485

TTGCGTAGCCGACTTGGCAACCGGCAAAATCAGCAAGTTCAATAGACCGCTGCTGAATATGCTGCCAAAAACAGGCAAGACCGCGGAATGATCAGGCGGTAGCCGACAAATGC  
CCGACCGCATCAAAACAGCCGAAACCGGCGGTACAGACGGCATAGCCCGACAGCAAGGACGCGCGGCGGCGGCAACCCGAAACATCCCGACCGCGAGGACGGGATTTTTT  
CGCGCGGTGGCAGGGGATTTGGAATTAAGCGGACGGGCTTGAAGGCAAAACGGGCGGGCGCAGAACTGT

## SEQ ID 1486

LRSRLGKRQNVQVHNRRAEYACQNRDRREYQGVAAQMPDRIKPSRNGGTDGIARQQTAQTGAKPETSPTARHGDFLRPLQGGDLDSGTGLKAKRARRTV

## SEQ ID 1487

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CGCATTTGGGGAAACACGGCAACAGACAGATTATCAATCAATTTGAAAGGAACACAGAGTTTGTGAAAAAGATGAAAAACGATAACGCAACCGACAGTTCAATCAAGAAAAATCTTTCA  
CTT

## SEQ ID 1488

MICAPENCITTSFIRPQTNRKPLCHSTCNAIPSSDLGYAHGWTATDRLSNQLERNTEFVKSKNDNANRQFNQKSFIF

## SEQ ID 1489

TGAAATATTGGAACCTTTTAACTGGAAATTTGAAATCCCGTTTCGGGCAAGCTTGACGGATTTCGGGATATGCTGTCCGGCACAA

## SEQ ID 1490

\*NIGTFNVGIVKSPFRASLDGFADHLSGTQ

## SEQ ID 1491

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CGCGCGTTTCCGCAATGCCAATTTTCCGCGCACTTGGCGAGTGGGACGAAACCGGGCTGGCAGATGTCGCGATCCCGAATCAGGACGCGGAGATTTTCAGACGGCTCGAAATCCG

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CACGGCAATACCTCCCGCGCGAAGGCTTATCCCGCGCGTGCAGACTTTACGACGCAAGGCAAAATGTTGCTTAACATCAGCAAGTCCGCGAGGTTGCGCTGCCCGCTTTACGCAC  
AGGGCGACCGCGTGCCTCGGCGCGCGTGTCAACGGCGCAAAATGCAATTTGGAACACGCAACCGCATGTATGACGCTTGCCTTTCCGAAGGATGGGCGCGGACGGGTGAAACACGA  
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## SEQ ID 1492

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HGNTSAGEGPIRAVDFTQQLKLLNLSQVPGCAAIVYAQGDALRRAGVNVNGKCNLEATATLAVSEGADGVKHELQRLGLV

## SEQ ID 1493

ATGCAGGGAITGCACGACATCGGCGCAATCGACAAAAGACTATGCGCGGCTTTGACAAGTCTGCCTGACCGAAATCAAGCCGTTGAGCGCGGGGACATCAAGGCAATCAGGAGAGG  
AGGCATATCGCAAGCCGCTTTCGCCATCTATCTCAACGTGGGAAAAATCACGTTTCGCTTGGAGCGGGCGTTAAAAAGCCGAGCGCGCGCTTGAAGCTGCTGACCATCTCAA  
AAACAAGGCGATCGAAGCCATTCGCG

## SEQ ID 1494

MQGLHDIKAIDKRTMRGFDKSCLEIKPLSGGDIKAIKEKALSQAAFAIYLVNKGHVSAMERGKPKPSGAALKLITIVKNKIEIAIA

## SEQ ID 1495

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TTAATTCGTGAAGTCTTTTATCAGTGATGTTTTGCGGCTGCTCTTGGCAAAGCGGTCATGAAAAACGCGGCTTCCATGCGCTGAAAAATATCAGACTGCGA

## SEQ ID 1496

VYCCBNPAFIFHGICSVKVPFDFACSMVSIVIAKNMAAVFFNSVSSLVMSFSLAKAVMKNARSPLKNRLR

## SEQ ID 1497

ATGACCGCTTTGCCAAGAACGACCGGAAAAACATCACTGATAAAGAACTTACAGAATTAAGAAAAACCGCCCATCATCTTGGCAATGACAGAAACCGACATAGAGCAACGGAAGTCAA  
ACGGCACTTTCAGGAGATACAGCCA

## SEQ ID 1498

MTAPAKNDRENITDKELTELKRTAAIILAMTETDIEQAKSNGTTFTEIQP

## SEQ ID 1499

ATGCGGATATTCAAAAACCAATGGATAGTGAAATTTGCCAAGAACCAAAAAATCAGTGATTCAGAGCTGATAGAGCGGCTAGAGCGGGCAGATAACGGCTGATAGATGAGATTGGCGG  
CGCG

## SEQ ID 1500

MRIFKNQWIVKPAKKHKSIDSELIEAVERADNGLIDADLGA

## SEQ ID 1501

ATGCCGTGAAAAATATCAGACTGCGATAACCCGCGCTTCTGCCCTTGCCTTGCCTTACGCTGCTTAATCACGCGCGCCCAAAATCTGCATCTATCAGCCGCTTATCTGCCCGCTCTA  
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## SEQ ID 1502

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## SEQ ID 1503

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## SEQ ID 1504

LVFEYFHCATVYLVILGIIPKTGNTASRLFIPCNFSYAA

## SEQ ID 1505

TTGGGTTTTCCGTTTTTTTACCCTTGGCAGTGGGAGCGTAGCGGAATGAAAAAGCAAAACCGCACGGAACCGGCTATTTTGAAGCAGGATGGGGTTAAACCGGTTGGTTATATTC  
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## SEQ ID 1506

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## SEQ ID 1507

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TTCATATACTTATTTATCTAATTTTCCCGGTAACAGG

## SEQ ID 1508

VRFGFSFRYAPTAKTVKNRKTPKVVTDSLFFVTAPVTNFLSFSYFSELNLRVGVASPCRITICVCGSPPCDLNLHIYSYTYLSNFSPTVR

## SEQ ID 1509

TTGCGGTATTTTTCGGATACCGTAAAAAATCAGGTTAGTTCAATTAGGGCGGATTGGACGGGATTGCACACTCAGGAAGGGGACGGCAGGATAACAATCAGCTGAAATCCTGTAT

## SEQ ID 1510

LRYPSTVKNQVSSIRADWTGLHSQEGDGRITISLKSIV

## SEQ ID 1511

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## SEQ ID 1512

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## SEQ ID 1513

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GTTCAAACCGGATTGCGCGCATCATGACCGCGAAGCTTACGCGCAGGTTTACGAAAAATTCGACAAATACGCGCACTGGGTTCTGTTTGTGCGCGGTTTCTGCGCGGTTTGGGACTGCC  
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## SEQ ID 1514

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VFTAGISRKVSLRFLIMDGLAALISVPVWYILGEYGAHNDIMLAKMHSLQSGIFIALGLVLAALAWFWRRKRYQLYRAQLSEKRAKRAEKAAKAAQKQ



## SEQ ID 1515

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TACAAGGATTTCAGGCTGATGTTATCTTCCGCTCCCTTCTGACTGTGCAATCCCGTCAATCCGCCCTAAT

## SEQ ID 1516

VAVGCASNLAAGTNTQKRLKILGVFFRLILSDALNQSQIQGPDADCTPAVFPFLTVQSRPIRPN

## SEQ ID 1517

TTGAACCTGCACAGCCTACGCCACTACCCCCCTCAAGATAGCGTGTCTACCAATTTCCACATGTGCGCAITTTGAAAACTGTTATTTCTGCTGCTGAGAACAGGGGCGAGAAGTTCCGTA  
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CAACGGCGGTGAGCGGCTGAGGAAGTTGGCGTTGCGCGCAGAGCCGAATACGCTTTCGCGCTGCGGCTTCCCGATCCGAAGGTGCGGCGCGCATCCGCGCTTTGCGGTGTTGAGCAA  
TAC

## SEQ ID 1518

LNSHSLRPLPPQDSVSTNFTMSAFEKLLFLLLRNRGRFGLAYFGCLLSLYVAEVQTPVCRVGVNIHSHAGCKECCNGRAAEZEVVAGRAEYALRAAASRSEGRAGIRAFVLEQ  
Y

## SEQ ID 1519

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CGCGCAGCGCGCAAGCGGTATTCGGCTTCCCGCAACGCCAATCTCTCAGCCGCTCGACCGCGGTTCGACCAACATTTTCTTTGCAACCTGCATGGCTATGGTGTATTTACACCCA  
CAGCAAAAACAGCGTTTGGACTTCAGCAACATACGACAGCTCAGCAAGCACCCAAACCGGTAAAGCAATACCGAACCTTCTGCCCTGTTCCTCAGCAGCAGAA

## SEQ ID 1520

MEAPKTLIHIINISALAVIVLVLLQHGKADAGATPGSGSAGQVFGSAGNANFLSRSTAVAAATFFATCMANVYIHTHTTKHGLDFSNIRQTQAPKPVSWTEPSAPVPPQQK

## SEQ ID 1521

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## SEQ ID 1522

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## SEQ ID 1523

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CGTTCGAGATTTGCTGTCGCGCTGTTTTCAGACGCGCGCTGTATCGCGCTGTTCGACCGCGACAGCAACATTTGGCGCAGTTTGTATGAGGAGATGCTTTGTATTTGGCGCAACTGGCGA  
AGATTTTGGAGAGCGGTTTGAAGCTTCGAGTCAGCGCGCT

## SEQ ID 1524

MYANMCDMMHALPSSASDKAALYREVLPQIESVVADEADVANLANTAAVLKEAFGNLWVGYPVDTRSDLVLAFFQGLACTRIPFGRGVCGQAWAKGTVVVKDVNAHPDHIACSSLS  
RSEITVPLFSDGRICIIVLDADSEHLAQFDEADALYLGELAKILERRFEASSQA

## SEQ ID 1525

ATGAGCTGCGCGCTTCCCAACGGTCATAAGATGCTCGAGCCGAAAGTCTGCGCGCGCTGGCGCAGGCTTGAAGCTGACGAAAAACGATACGCTTTTGAATCGGCACGGGTTTCGGGT  
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GCGGTATTTGTCGAGCGCAGCGCGGTGACGCGCGCTTTGATTACGCGCAGGCGGATGTGTTGAAGAGAAGGTGCTGTTTCGATATCTTGTGTCGCTTTGAGACGACAGGATGCC  
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## SEQ ID 1526

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## SEQ ID 1527

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CCATCAGCTATCCGACGCTGCATACGCGGATGTTTTCGCGGAGCGCGGTTTGAACCTGTACAACTTCAGGGCGCATCGACGCGTGGCGGTTGAGTTGACGCGCAATGGCG  
CGTAT

## SEQ ID 1528

LGLQAFCLVFFGGFVMDIVQLPSAALKAMMDEGRMFLDVRTEDEAAVCSLPNALHIPNLILPLRQNELPDDVPLVVYCHHGIRSLHTAMYLAEAGFENLYNLGGIDAMAVEVDAEHA  
RY

## SEQ ID 1529

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## SEQ ID 1530

F\*QRMPLAGQAILIQTQDVYVQFNRPLQOCLQKH

## SEQ ID 1531

TTGCTCGCCTTGGCTACCATCTGACTGTCTGCGGCTTCGCTGTTTGTCTGATTTAAATTTAATCCACTATACAATCAATATATTTAAGTCGTTGTAGCCCTCTTGTCTGTCAA  
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## SEQ ID 1532

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## SEQ ID 1533

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## SEQ ID 1534

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 TNRRFFIRTHVQTKHPFPVHPRLQCRRLKLNHIEHKPEKNQAKCRLKPTQTFQASQSEHQKLLSKGWSLSSKCATKVSNSFTSNTFSLRIVKISARCTGLRPTITAIRPSPFNCSP  
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## SEQ ID 1535

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## SEQ ID 1536

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## SEQ ID 1537

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## SEQ ID 1538

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## SEQ ID 1539

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 G

## SEQ ID 1540

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## SEQ ID 1541

TTGGAACGGAAGAGTCTGCTGAAAGGTTTTCAGACGACCTTTTCGCTTCGCGAATTTGTTTTCGCGTATCGGGAATTTTCGCTTTTCGCGCGTGGTTTCGAGGTTGTTTCGCTTAA  
 TAATAACATCTCTTATGATGCAAGGAACCCGACACCG

## SEQ ID 1542

LERKRSSRVQTFPSVSGICFAVSGILRFAANFLQVVCILINILIRMQNRPT

## SEQ ID 1543

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**SEQ ID 1555**

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**SEQ ID 1556**

LSQLGIRLVLIHNGAYFLDRLAAAGRTPHYCRGLRVDTETSLGQAQGFAGTVRSRFEALCGSVSGFARAPSVPLVSGNPLTARPIGVIDGTMEYAGVIRKTDALRFPOLDAGNIVWM  
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**SEQ ID 1557**

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CGCGGATATCTCAACGCGGTACAACTTCACGATACGCGCGCGCAACCGCGCTGCGCGCGCACCGCAGGTTTCGCTACCGCGCGCGCTCAGGAAGGGCTCAACTGG  
ACTATTGCAACCTGTTGCACTTATGCTCTCATATGCAAGCTTCTCACTCTTCATCTCA

**SEQ ID 1558**

MPACFCPHKTRLVWKETQLNVAQGFVVCQKCEGLFKAKHDLASTKEPIFNDLPEAVSDVKLVHRIGTHAISKKQISRDEIADILNGGTTLHDTPPATAAAAAAQAQVSVPPARQEGILNW  
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**SEQ ID 1559**

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TAAA

**SEQ ID 1560**

MPSEPPAASDGIKPTHTERTSCPPVSVRTAKPASGSKPSSTSPKASSAKNAKGLKPTINQARKMLYSTICPKLPRMSNSTASARTPLARNRFPATKSPISSTAVQPCITRRPQPPL  
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**SEQ ID 1561**

ATGACTGATTTCCGCCAAGATTCTCTCAAAATCTCCCTCGCCCAAAATGTTTGAATTCGCGCAATTTACCAACCAAGCCGAGCGCGGTCCGCTTATTTCTCAATGCCGCGCTCTTCA  
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CGTCCGCACTACCGCGCGCATACGCGTAGAA

**SEQ ID 1562**

MTDFRQDFLKFSLAQNVLFKGFETTKAGRRSPYFNAGLFNDGASTLQLAKFYAQSIIESGIRFMDLFGPAYKGIILAAATAMMLAEKGVNVFPAYNRKEADRGEGLVVGAPLKGRVLI  
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**SEQ ID 1563**

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**SEQ ID 1564**

LCVKLIMSAPPEPRRRQHAQCDEARLQAVHFRHQPIDVVRVLAQVNFNGHGNRQGPVHNQKAQIRYPAADAGGNENGSPQTRQETGDKQNPVAVFVEFFLNLRVTFRRHDARN  
RFELEDLPDASGGKHAVARQHAERTDRKHNRIGITHTRNHAARYQGIQFNHABTADDQNEKHRIAVFDKKGFPQKKGHSYSIVGDKKSEQAETPSARNGILSKIMPSESGRGR  
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**SEQ ID 1565**

ATGTTTTCGCTACCGCGTCTCTTTTTCGCGGCGGTTTCTGCTACTTCCGCGCTTCCGCGCTCAAACTCAAGACAACAGTGGCGCGCAAGCGCTTCTTCAAGTGCATCCGCGCGCGCTG  
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AATACCGCGTGGTTTTCGCAAAATCAATCAAAAGCAGCAGCGCAAACTATTGCTGCAACCTCTTCCGCTGCGTATCTATCGATAAAAACGCTGAGGTGCGCATTTTCTCGCTTAA  
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**SEQ ID 1566**

MFVSFSLPGFVLAALAAACKPDNSAAQAASSASAPAAENAAKPQTRGTHMRKEDIGGDFTLFDGSKPFLSLDKGVVILSPGFTHCPDVCPGLIYSDTLKQLGGQAKDVKVVF  
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## SEQ ID 1567

TTTCAAAACAGGTTGATGCACCTTCTCTGAATTTCCGAATAGCTAAACATGCTGCTGCTGCGACAAATTTACACCTGCAAAATCAAGCAA

## SEQ ID 1568

PQNRMLHPPSSNFRIARTCLLVRFHTCKIKQ

## SEQ ID 1569

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GCGGCACT

## SEQ ID 1570

NLSARYLHLHEALGLPMWLKQAAAVLPKNTPTPAQARPTVRAATIRPSQPHNVQTRLETHKALETAHVHTRKPAPEPETPPGLSDGIAPVPAASGITKLAVVSLCPPIEDAVYGL  
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## SEQ ID 1571

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GTCCGCGCTGCTGAATATTGTGTACGCATCTGCCCGAAGGCACGCAACCGCTGCTGCTGAAGTCCGCGCAGCAACCGCGCGCAACGCGCGCTGATACCAACACCGCTTCAGCAT  
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## SEQ ID 1572

MNIRPASPDCAALALDTCNPSAWTORQFESALVSPSEQVFLAEKGRIFAIFVWQLPDESELHLIATAPECRRRGVASALLEYVYHLPEGTQRLILLEVRAGNAAQALYTKHFSI  
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## SEQ ID 1573

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## SEQ ID 1574

LVYSACAALPARTSSRRCPVSGRCAYQYSSRADTPRRHSGAVAIKSSDSSGRFQPTKAAIIPSPSARKTCDGETSADSNWRCVHADGLQTVSSAASAAQSDGEAGRMFMFVPSV  
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## SEQ ID 1575

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## SEQ ID 1576

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## SEQ ID 1577

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## SEQ ID 1578

LKSACHVPSLVQTYLYSEIGLPAVSSCPRAVWRKNVARTVNYRVRTAPFKYCYLSANPLS

## SEQ ID 1579

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TTCATT

## SEQ ID 1580

MPSAPFVFPVQTFALLFQPTKDIHTMDNALTIASGRIFETLPLIAAGIAPTEEPKSRLLIIGTNHENIRLVIVRATDVPTVYRYGAADPGIAGKDVLIHGGTGLYRPLDLEIAKCR  
MNVAVRKGFYDAASQPGCRKLIATKYPEIAASHFAGKGHVVDIIKLYGSMELAPLVGLSDAIVDLVSTGNTLKGANGLEAVEHIVDISSYLVVNKAAALTKYVALLPEIISFGAVAKKHA  
FI

## SEQ ID 1581

CACCTGCAAAATCAAGCAATATTTCAGAAATCGTACCGATCCGGCCAGGCGAGTATGGTAAGTGTGTACCTTATGCCGGACCTGCATGTTGAAACATAAAGGAAAAATCATGAACCGTC  
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CACCOCGCTCCGCAAACTGCCGCACACTGTCTGATGCCGAGCAGGTTTGCCTGACCCAC





CGCGTTTGACAGCCAGGCGCAATACTGCCGCCAGCCGACAGCTTGCGGCCAGCGTCCGACCGTCCAAACCGCGCTGCGACAGCCGCGCAACGCCGCCGAAATCGCGCCGCGACAA  
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TCCAAATAAGCGTCAAAATACGCCGCAAAACCGCTCCAAACCAATAACCGTCCACACAAATATCAAAAAACCAAG

## SEQ ID 1592

VGFVIEAGDVVEIEIGINLRKRAVSEQLHRPDVARSLQVAVGVAHVHMRNRPVAVLRRPFEAFDLALAQARAVPAGKQGFVAVRCLTQRIQIVFGPHAFAGQRLITLAPFAG  
NVYPRPVIYIICIQAVYLAHAQTAAVHQLERVVAHRQVAAVHGQIQHPVQPFRLRQFGYALGLLRFPDVGGRVGAHQPAFDQPGAILPFRQLARQRPVQTLARQPPQRRRLIAPRQ  
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## SEQ ID 1593

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## SEQ ID 1594

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VEFEQRFPDRYFDVGAIEQHAFTVAGGLACGEMKPVVAIYSTFLQRAYDQLVHDIALQNLVPLFAVDRAITGADGPTHAGLYDLSPFLRCVPMNIVAAPSDENECRLISTCYQADAPAAV  
RYPRTGTGAPVSDGMEFTVEIGKIIRREGKTAFAFGSMVATALAVAELNATVADMRFPKPIDELIVRLARSHDIRVITLLENAEDGGAGGANLEVLAKHGIKCPVLLGLVADIVTEH  
GDPKLLDLGLSABAEVRRVREWLPRDAAN

## SEQ ID 1595

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## SEQ ID 1596

VLGVFLRVWKFIPFLVRITAAVPSADTRQNAV

## SEQ ID 1597

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## SEQ ID 1598

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## SEQ ID 1599

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## SEQ ID 1600

MPPEAFQTAFLVSADGTAAVIRTSGINFQTRNGTPSTARPKPPPEPLFPAGFQ

## SEQ ID 1601

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CAGCGACACCGGACTTACCACATCATCAGATATCGAGCTTCCGCGCGCATCGCGCTACACCGCGCTCCGCCAACTGCGCGCACACTGTCTGATGCGCGGACAGGTTTCCCTGACCACT  
GCTGTCTCCTGCTCACTCAGGGCGACACGTCTATGTCGACTGTGCGGTTGCGGTCGCGCAGATGCTTGCCTTATGCGCGCGGCTGACGAGCTTTCGCGCAAAATTCCTCTGACACG  
CGACCGCGCAAAAGTGTGCTCGAAGCGTGCACACAGTGTGCCAAAGCTG

## SEQ ID 1602

VCTLCRTMLKHKGKNEHPSIFGQRRRLPGFRRLFRACARTRLPSSRYAACRRIRLHRRPNCRTLSGCTGLPDPLFVPAHSGRHVVRLCCRAPDACLMRRGARPCRTKFPST  
RRGKSVPRSVQTVCSL

## SEQ ID 1603

ATGGTTGCAAAATAAAAAATCTCAGATTCGACCTTTCGCTTTGAATAACGGGAGCGTGGGTTTATGTCTATTGTCTGACCGACCTGAAAAAGACAAATCTCTACATCGGAA  
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TCCCAAGTCCCAAAATAACAAAGGAGATCCCAATCA

## SEQ ID 1604

IVAKIKFSDSTLSVLNNGERRFVYCLFDLKKDKILYIGKCGNRIFEHENVASRQDPVSGEIIDRLKALSKCKLGRYIISYHLTEVEALAESALIHVKSVLGKLLKNKIAGEBP  
GGISVEELDRRFPSSLPSEINPDGLILAIKHNAPDLDTDELDYLPDNDANLKSRTLGNNVIGKDVASKVKYVIGVHTGLQNAVVSATVDFGFTWTEETKNGRKQTRVRFRTSR  
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**SEQ ID 1605**

TTGAGTGTGTCAACCGGAAGTTTGCAACCGAACCGTCGGTTCGGGTGGCGGGCGGCATCGGGGGAAGTGTGGGCATTCCTCCCGGATTTTTCACATATCGGGCGGACGCGGCAAAATTTTTCGCGTTTGTGTTGCGCGAAGGGGGCGTTATACAAATTTATCAGGCGCACCAA

**SEQ ID 1606**

LSCQPEVCNRTVGSLAASGEVSAFPPIFYISGGRGKFLPFCLREGGVIQNYQAHQ

**SEQ ID 1607**

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**SEQ ID 1608**

MIIVIIYVFLYVSLFEQMFICAVNHATIPNIHIL

**SEQ ID 1609**

GTGATGACGAGTGTTTACGGACACGAAGCAACCGATACCACGCTTCCAGGAAAAGCCACTAAGCTTCAGTTTGAATCGAACCGTACCGCAAACCGACACAGGTGGGCAGGA

**SEQ ID 1610**

VMTSVYGHEATDTTLPGKATKLQFESNRTANRRRWAG

**SEQ ID 1611**

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**SEQ ID 1612**

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ADFAVVHFAAIGIDVLSQSEVDFPHALLGKVGDGFGYVVERAGEFFAARVGDDAEGAVFGTAFNHRHKCRAAFDAGGRQVVEFFDFEGEINDLRQPAGFFVHNHFGQAVQRLRAENHINTRE  
AFDDVFAFLRGDAGNADDEAGVGFPEFTDAPQVGEHPFLCFPAHGTGVEQDDVGVFLGNDLFAAIVPFGKDGQHPFAVVLVHLAABGADKYFFHGLCLSRAAVLAGLHVVMKKFPQTARR  
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**SEQ ID 1613**

ATGAAAAAAGTATTATTATCCGACACCTTCGGCTGCCAGATGAACGAGTACGACAGCGAAAAAATGCTGTCCGTCTTGCCGAAGAACAACGGCGGCATCGAACAGGTACCCAAAGCCGACGAAG  
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SEQ ID 1614

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**SEQ ID 1615**

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**SEQ ID 1616**

VCMKPVVWALLLCACTSNFGDREHOFRLYSGNLNOYSVASPCRTICTVCGFVALS

**SEQ ID 1617**

TTGCGGACCAATTTCATCTATATGAAATCGGAGCGGGCGCATTTGGGAATGGTGGCGGATTACGACGGGGAGGGAGTCGTCCGGGACTACCGCTTTACACATAAAGTGGAAAAGACGAGC  
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**SEQ ID 1618**

LPTNFIYMKSERRHNEWCADYDGEVVRDYRFTHKVEKERSVIRDTVGVIKKEACKSLSOPEK

**SEQ ID 1619**

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SEQ ID 1620

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SEQ ID 1621

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**SEQ ID 1622**

L R I N M N R N E I L F D R A K A I I P G G V N S P V R A F G S V G G V P R F I K K A E G A Y V M D E N G T R Y T I D Y V G S W G P A I V G H A H P E V V E A V R E A A L G G L S F G A P T E G E I A I A E Q I A E I M P S V E R L R L V S S G T E  
 V M T A I R L A R G F T G R D K I I K F E G C Y T H G H S D S L I V K A G S G L L T G P N F S A G V P A D P T K H T L W L E Y N N I A Q L E E F A Q S G D E I A C V I V E P F V G N M N L V R P T E A F V K A R G L T E K H G A V L I Y D E  
 A W T G P R V A L G G A Q S L H G I T P D L T M G K V I G G G M P L A A F G G R K D I M E C I S P L G G V Y Q A G T L S G N P I A V A A G L K T L E I I Q R E G F Y E N L T A L T Q R L A N G I A A A K A H G I E P A A D S V G G H F G L Y P A  
 A H V P R N Y A D M A R S N I D A F K R F P H G M L D R G I A F G P S A Y E A G F V S A A H T P E L I D E T V A V A V E V F K A M A A

**SEQ ID 1623**

SEQ ID 1623  
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SEQ ID 1624

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SEQ ID 1625

SEQ ID 1625

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SEQ ID 1626

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SEQ ID 1627

SEQ ID 1627

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CATTTCCCCCGAACATCTTGAAGATGTCAGTCGAAACCGCGAGATGAGGCGAAAAATTCGCCATATCCGCGCTCGCGCGGATTTTCATGGGACGCTACACCGCGGAAGCCTCGGCGACTACTGC  
GCCGCGCGCAAGCATGTGTTGCCACAGCGCGAACCGCCGCTTTTCTCGCTTTGGGGACATATGATTTCACAAAACGCTCCAGCCTGATTACAGTTTCGGAACAGGGCGCGCAAAAT  
TAGGCGAAACCCGACGCTGCTGGCACAGCGGAAAGCCTGACGCCACGACGCGCGGACAGTTCCTGATGAAA

SEQ ID 1628

SEQ ID 1628  
MKKLINTQSPDQAGLKLALAFETAQNFETERIVADICADVQKRGDAALIEYTNKFPDQTNKSIDDLILTQADLNAAPERLXXXXXXXXTAARRVRESYHORQKMSWSTYDDEGTLGLGOOI  
TFLDRGVYIPFGKAAYPSSVIMNAMPAHVAGVKEIIMVVPPTPKGERNDIVLAAAYVAGVTKVFTVVGGAQAIALAYGTETIPQVDKITGPGNAFVAAAKRRVFGVVGIDMVAGPSEILVI  
ADGTTTADWVAMOLFQAARHDEIAQAAILIGTSQAYLDEVEANDRLIETMPRRDIIEASLGNRGAMILVKDLNACEISNTYISPEHLELSVENPQEAKKIRHAGAIPEGRYTGESLGDYC  
AGPNHVLPTSTRAPFSSPLGTDFQKRSSLIQVSEQAQKLGETASVLARGESLTAHARAAEFRRK

SEQ ID 1629

SEQ ID 1629

TTGGACAACCCGAAAATCATGGGCATCGTGAATCTCAGCCCGGATCTCTTTTCCGACGGCGCGCGTATTCGCAAAACGCCCAACAGCTTTGGCGCATGCCGAACGGCTTTGAAAGAGG  
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CGCGCGCAAAATGACGCTGCTGATGCTGACGATGATGAGGACGCGCGGCGGCGCTTGAAGGTTTGGCGAAGCGTTGGCGCTGAACCGG

SEQ ID 1630

SEQ ID 1630  
LDKPKIMIGVNLTPDSFSDGGAYSQNAQTALHAERLLKEGADILDIGGESTRPGADVFPVPEEEEARVPEVLAEAAAGVPSLSDTRRTVVMKEKALAGGIDIINDVAALTDGEAVELL  
RQADTIGICLNHMRGLPETMQNPYQDVVGEVARYLKTRETCVAAGIAQPRITLDCPGFGGKNLQHNLALMRHLPELMAETGLPLLIGVSRKRMIGELTGEADAAARVHGSVAAALASVA  
RGAOTVRVHDVKATADALKVNEALGVNR

SEQ ID 1631

SEQ ID 1631  
TTGTACGGCAGCGCCGCTTTTGCCATGCGCCCAACAGATGCGGATGGCGCGCAAAAAAGACCGCGCTTACAAAGGACAAGACCCGGCCAAAGTAACGCATTATTTTGACACGGCCGCGCGG  
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CGCGCGCTTATCTTTGGTGTCGCAACAGTCGGACCGCCGCGGATTCGTCCTGATGCTTTGTGCAAAATACGGTGGCGCGGGCTCTTTTTTGAAGCGCGGTTTCGCAAGTGCTACTGTCGCGCA  
TTGGCTCAAAAATCGGTGATTATTTCAGATAATGCGCGATTTCGCGGTATGGGTGCTTATGGAGCAACGCGGAAAAATGGGACATAAGGTAATTTGCTCTCCGCACTTGTTCGCGCACTTGCAGCGC  
CCAACCGGATTGAGAAAGTGTGGCGCAATTAAGCGGATATTCGCAACCGTTTGTCTGATTACGCGCGGATTTGACGATGCCTACTGCTCTATTTTGATTTTAAAT

SEQ ID 1632

SEQ ID 1632  
LYGSRRLPCAQTADADGAQKKTAA YKGQDPKAKVTHYLTRPAGFSDCQRCVCPDEGTGDRRLFRPTARSLEQGHAKARISGKRYRRLSLVSAQVGNRPAPMVCNTVAGVFFFEARFOOCLLPA  
LAOKSVLISDNARFRMGALRGTAASKLGHKVLPPAPCSPENPPIEKVWANKRYLRTVLSDYARFDDALLSYDFDN

SEQ ID 1633

SEQ ID 1633  
ATGGCATACTCTGCGGACTTAAGAAACAAGCTTTAAACCATAGCGGATTACAAAAATCAGGACAAGCGGGCGGGCGCAGACGGTACAAATGGTACGGAAACCGATCCGCCCGCGCTCC  
ATCACCTTAGGGAATCGTTCCTTTGAGCGCGGGCGGGGCAACCGCTACCCGTTTGTGTTAATCCGCTATATTACGGACAATGCAAAACACCGGCCAAACCGCAGCAACGTTTAACCTTG  
TTAAGAAACACGCTTTACCTGCGGATTCGCTTAAAAAACAACAGGCAGCC

SEQ ID 1634

SEQ ID 1634  
MAYSADLRNALNHSGLTKIRTRRAADGTNGTEPIPALHHLRESFPLSGGATPYRFLIRYITDNAKTPAKPQORLTQETRTGCFALKNKQA

**SEQ ID 1635**

GTGCAGGACAAAAACAACCTCTGCTGGCTCGATATGGAATAGCGGGGCTGAATCCCGAAACCGACCGCATTTATCGAAGTCGCGATGATTATTACCGACATCGGATTGTAAAGTGTGTGGCGC  
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AGCCGAAGTCGAACAGAACTGCTGGACTTTATGTCGGAATGGATACCCGGACGCGCCACACCGGATGTGGCGGACTCCATCCACCAAGACCGGGCTTTATGGTCAAATATATGCCGAA  
CTGGAAAACTGACTTCCATACCGCAACTCGACGTTTCCACGCTGCCAACGCTGGAAGCTCGGCCATTGCCAAAGCGCTGCTCAAAACGGGTTCCGACAGGCTTGGAGC  
ACATTTCGAGAGCATCGAAGAAATGCGCCACTACCGCGAATCTTCTGATTTCCGCCCCGAAAGCCGAAGCGCAA

**SEQ ID 1636**

VQDKNLCLNDMEITGLNPETDRIIEVAMITIDSDINVLQASEVYAIHQSDDLLNDMEWATATRGRTGLTQRVRESSSTAEVEQKLLDFMSEWTPGRATPMCGNSIHQDRRFVVKYMPK  
LENYFHYRNLDVSTLKEIAKRWNPPIAKSVVKGSHKALDILESTEEMRHRYEHFLISAPKAEAQ

**SEQ ID 1637**

TTGCCCGCCGCTGTGAACCGATTTTCGATATTTCCAAGAAAGCCGTTATGCCCTACCAACAATCACCCTCAACGTTCAACGATGCCGTGCCGGAACGCCCTGCCGAGCGCGTATGGAAC  
ACGGTGCATCTTCCGCCGCCATCGAAGATGCCGTGCCGCGGACGCAAAACGAACAGCGGATTTTCGCCGGAACCCGGTATGCCACCGGAACAAATCTGGCAGCAGAGCAAAAGTCATGCCCT  
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AGGTTCCGCGCTCGCGCTGGATATTGACGCAACAGGCGCTCCGCTCCGCGAGGGACAACCGCGAACAAGCATCGCTGATCGATCTCTCTCGCCGACAGTCTGCCTCAAGGGCAATTC  
GACGTAGTTTGTCCCAACATCTCTCGTAACCTCTTCGATATCTCGGCGAATGCTTCGAGCCCGCACACCAACAGGGCGGACGCAATCGTGTGTTCCGGTTTGTGTTGATGAACAGGCGCAAG  
AATCTCGCGCGCATTTACAGCAATGGTTCGATCTCGACCCGCGGAAACTGACGAAGGCTGGGCGCGCTTGAGCGCGTAAAAAGC

**SEQ ID 1638**

LEPRLKPITSPFRKVPMPYQYITVNVNDAVERLADALMEHGALSAAIEDACAGTONEQAI FGEPGMPTBQIWQCKSVIALFGHEDEAAAVIDAABQCGKLDAYTGETTENQDWRMLTQ  
SQDFPIRISDRMLWTPSWHEAPEGC AVNRLRDPGLAFTGSGHPTTRLCLKMLDTQLKNGESVLDYCGSGILTIAALKLAGSAVGVDIDEQAVRSGRDNAEQNVDAQFFLPDSLPGQGF  
DVVVANTIANPLERMLGEMLAARTKOGGRIVL SGLLDBQAEELGGIYSOWFDLPDAETDEGMARLSGVKR

**SEQ ID 1639**

ATGCGCGGCAGATTCAAAGGCGGGCGAGACATGTGGGACAACATGCCGTCTGCCGCCCGGAATAGCGGTGCCGTCCGAAGCGCACAAAGACGGTTTCAGACGGCATATAATCTGTTTTTATTATTC  
GGGAGGAGTTTCAGATGGCAGCAGACAGTTTGGCGGGCAGGACGGTTTGAAATCGGTTTGGAACAAACCGAAAATCATGGGCATCG

**SEQ ID 1640**

MPADSKAAOTLGOHAVCRPNSGAVRSAODGFRRHIICTFLFREEFRWHDTFGGQDGLKSVWTRKSWAS

**SEQ ID 1641**

ATGCTGAAAAAAGTTTAAATCGCAACCGGGGCGAAATCGCCTTGC CGGTACTCCGTGCTGCCGCGAAATGGGCAATGCGCACCGTTGCCGTGCATTCCGAAACCGACAAAGGCAGCCTGC  
ACGTCAAACCTCGCCGACGAATTCGTGTGCATTCGTCTCGCGCTTTTCGGCAAAAGTTATCTGAACATTTCCCGCCATCATTTGCCCGCCGCCGAAGTAACCTGCGCGGACGCTGTCCACCCGGG  
CTACGGCTTCTCTGCGCAAAACGCCGATTTTCGCCGCAACAGGTCGAACAGTCGCGCTTTACCTTTCATCGGCCCGAAACCCGACACCATCCGCTGATGGGGGACAAAGTCTCCGCCAAACAC  
GCGATGATAGCGCGAGCGCTGCCCTTGCCTCCCGCTCTGCAGCGCGATTCGCCGACGATGATGCCTGAAATCTCTCAAATTCGCGCAAAAGTCGGTATTCCCGTGATTATCAAAGCATCG  
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CTCCGCTGCACCGCCCGCGCCACGCTCGAAATCCAAGTCTTCCGACGAAACCGCGCTCTATCTTGC CGAGCGCGACTGTTCGCTGCAACGCCGCCACCGAAAGTCATCGAGGAA  
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CAAAACAGAAAGACATCAAAATCGAAGGCCACGCTTCGAGTCCGCGCATCAATGCCGAGAGACCGGTACAACCTTCATCCCGAGCCGGGCGCGGATGGAAGAGTGCACCTGCCCGCGGCTTC  
GGCATCCGCGTGGACGCGACCATCTACCAAGGCTACCGCATCCCGCGCTACTACGACAGCCTGATCGGCAAAATCTGCGTATCAACGCGCAAAACGCGTGAACAGGCATGGCGAAATGGCGCG  
TCGCATCTGCGCGAGCTGGCGGTAAACGCGCATCAAAACGCAATACGCGTTCGACCGCGACTCTGTCGCGGATGCGGGTTTCAAGAGCGGAGTGAGCATTCATTACCTGGAGCATGGCT  
GGAAGCGCGCAAAACCAACAGGACAAA

**SEQ ID 1642**

MLKKVLIANRGEIALRVLRACREMG\*LATVAVHSETDKSLHVKLADESVCI GPAASAQSVLNTPAI IAAAEVTCADAVHPGYGFLAENADFAEQVBQSGFTTIGPKPDTIRLMGDKVSAKH  
AMIAAGVPCVPGSDGALPDDDAEILKIADKVGYPVLIKASGGGGGRGMRVVEKKEDLLQSVEMTKARAGAAGPNPMVYMERYLQRPRHVKIQVLADEHGNNAVYLAERDCSLQRKHQVIEE  
APAPFIDEKARKKIGKACTDACKRIGYRGAGTFEFLYEDGEFFIEMNTRVQVEHPVTETLTGVDIVQEQRLIASGLPLQYKQDKIKIEGHAFECRINAEDPFYNFIPSPGPITSCHLPGGF  
GIRVDSHYOGYRIPPYDLSLGKICVHGKTRQOAMAKMRVALAELAVTGIKTNTPLRLDLFADAGFOEGGVSIHYLEHWLEARKTKQDK

**SEQ ID 1643**

ATGCGATTTCGCCAAATTAATAAACTGATGTGATTGGTTGAAGAATCGGGTATCGCCGAATCGAAGTAACCGAAGCGGAGGAAAAAGTCCGCATACCCGTACCATTCGAGCTCGGGCAG  
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TCGCCCTATGGTCGGCAGCTTACGCCGCCCGGCCGAATCGCCCGCATTTGTGCGAAGTCGGTCAACAGGTCAAAGCCGGCGACACGCTGTGCATCATCGAAGCGATGAAGCTGATG  
AACGAAATCGAAGCCGAAAAATTCGGCAGGTCAAAGAAATTCGGTCGAAAAAGGTAACGCCGTCGAATTCGGCGAACCGCTCTTCATCATCGGA

SEQ ID 1644

MDLRKLRKLLDLVEESSIAEIEVTEGEEKVRITRTTIAAAAAAPVYAAPVPAAPAVTPPAAPVAASAPAAAPAAARDLSDAQKSPMVGTFYRAPGPNAAAPVEVGQOVKAGDTLCIEANKLM  
NEIEAEKSGTVREILLVENGTPVVEGPEPLFIIG

**SEQ ID 1645**

GTGCGCAAAATCAAACTTCTCGCACAATTCCCCCAAAAACCGCGGTTTTTGTATATTTTACTGGACAATTTACGCACAACCTTCGGGAAAAATGAACACAATTTCCAGGTCTGTTTCCACCCACA  
GGAAACCGGTATCCGGAACACCAATTCCGCCCGGTTTGCGCGGTTGCGCAAGCGCGGTGTTTTCTGAAAAACCAACGCAACAACCCCGGGAACACCGGCAGCCCTTTAAAGGAACAGAAATG  
GATTTGCGCAAAAT

## SEQ ID 1646

VRKIKLPAHFPOKPPFFDILLDIYROLRENEHNFTTVVSHRKTVSEHHSARFAPLPOAGCFLKNQRRNPPEHROPLKEQKWICAN

SEQ ID 1647

ATGTGCAGGAAGTTTGATTTGCGCACAAAGATGCCCCGAGTCAAGAGTGTTTATTCTAATCTGTTGGTTTTTCGGGCAAGATGCGTCTGAAAAAGGGCTAAAGTCCGTA

**SEQ ID 1648**

MCRKFDFAHKMPRVKSVYSNLLVFRAKMPSEKGLKCV

**SEQ ID 1649**

GTGCGTATATCGCGGCTTGCCTCAACGAGAGTGTAATAATGGATATTTTCAGATTTTGACTTTACCTTGCCCGAACACCTGATGCGCCAGCATCCGCCCGAGGTGCGCGGCAGCAGCCGC  
TTTGTGTTACCGCGCTTCCGATATGCCCTGCAAGACCGGGTGTTTGGCGATTGTCGAGGCGAGCGAAGTTTGGTATTCAACAACACCAAGTCATGAAGCGCGCGTGT  
TGGCGAGAAAGACAGCGCGCGGAGGATCGAAGCCCTGATTGAGCGTGTGTGGACAACATACCGCATTTGGCGCAGCATCCGTTCTGTCGAAGTCCCGAACGCCGTATGGGGCTGTGT  
GAAGGCGGGTATCCGTGCGCTGATGGTCCGGCGTGAGGCCGAACGTCTCGCTCGCTTTTGAAGGCGGTCAACCGTTTACGAATTTTGGAAACAGACGGACACCTGCCCTGCCGCTT

ATATCTGAACGTGCGCCGATGTCGGGACGACGACAGCCGTTATCAAACTGTTATGCCAAATATCAGGGCGCGGTGCGCCGCGCGAGCGGCGGGCTGCATTTTACGGAAGAACTTTTGCGCCG  
TCTGAAGAACAAGGCGCGGTAACTCGAGAACTAACCTGACGTCGCGTGGCGGGGACATGCCAACCCGTCGCGCTGCATTAATACTCGAAGAACACAAATGCACGCGGAATGGTTTGAAGTG  
CCGTCTGAACCGCTGCGCCGCTTGCGAGCGGCAAGAGCCCGGGGGAACAAGCTCTGGCGCGTCGCGACGACTTCATCATCGCGCCCTCGAGTCTGCGCGCGCGTACGCGGATATTTGAAG  
ACGCGACACGGCGACACGGATATTTCATCACCAAGGCCGCTACCGGTTTAAAGTGTGTCGACAGCGCTGGTAACTCAATTTTCATCTCGCGAAATCGACGCTGATGTGTCGCGCGCTTTTC  
GGGTATGGGTCATATCCGCGCGCTGTACCGTCATGCGATTGAACGTGAATACCGGTTCTCTACGCTACGAGATGCGATGGTTTGGGGCGGAACGAAGGGGGCGGGCTT

**SEQ ID 1650**

VRIMACPNSVKMIDISDFDTLPEHLIAQHPPVEGRSSRLVALSDMPLQDRVFGDLPDYVEAGDVLVFMNTKVMKARLPQKDSGGRREALTERVLDNHTALAHIRSSKSPKPGSLV  
EGGIRAVMVGREGELPCLRFEGGTQVYELLEQNGHLPLPPYIERAADDDSRVQTVYAKYQGAAPTAGLHFTTELLRLKDKGAVTAETVLHVAGTGFQFVRVDKIEHKHSEMFV  
PSETVAEAEAKARGNKAWAVGTTSMRALESAAARTGYLKDGQGDITFITPGYRFNVDRDLVTFHLPKSTLLMLVGAFSGMGRHIAVRYHAIEREYRFFSYGDAMVLGRNEGGL

**SEQ ID 1651**

TTGACCTTTAAGCACCTAATTTGGGGGGTGGATTATCCAACTGCGGGACATCCATAAAAATACCGCCCGAACACGGTTCAGACGGCATCTGCCTTGCAACGGACAGCAGCAGTT

**SEQ ID 1652**

UTFKHPNLGRWLIQLPDHKNTARTTVQASALQRTAAV

SEQ ID 1653

ATGCCCAAACGTAACGACCTAAATCCATCCTTTATCATCGGCGCCGCCCTATCGTTATCGGTGAGCGCTGCGAATTTGACATATTGCGGCGCACAGCGCTGCAAGGCTTTGCGGTGAAGAAG  
GCTATAAACTCATCTCGTGAATATCAACCCCGCCACGATCATGACGACCCCGAAATGCGCGGATGTTACTCTACATCTGAGCGGATATTGTGGCAGAGCGGTGAGAGAATATTATCGCCAAAGGA  
GCGGCCGATGCGATTCTGCCACGATGGCGGCTGACAGCCGCGCTGAACGTGTGCGCTGGATTGGCGCGTACACGGCGTCTGGCGGAAATATAATGTCGAGTTAATCGGCGCAACGAAGAC  
GCGATCGACAAGCGGAGGACCGCGGCCGTTTAAAGAGCGTGAAGAAAATCGGCTCTCTTTCGCCGAATCTTTTGTGCGCACACCATGAACCAAGCGCTTGGCGGGCGCAAGAACG  
TCGCGTTTTCGACGCGATTCGTCTGCTPTTACAGAGGCGGTGTGGCGGGCGGCACTTGCCTACAAATAAGGATAGATTTTTGGCGGATTGTGCGAAGCTTTCGATGCGGTGCGCTACGCT  
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CATACGGCGGACTCGATTACGTTTGGCGGGCGCAACCGCTGACGGAACAAGGAATACCAAAATCATGCGCAACGCTTCGTGTGGCGGATTTGGCGGAAATCGGGCGTGGACAGCGGCGGCTCG  
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CCGCGTTTGTGCGGTTTCAATTCGCGCGACGGAAGACAAGAGCGAATTCGCGCGGAACGTGCGCAACCCCGGCGCGGAACGTAATGCTGTTTGTGGCAGACGCGTTCCGCGCGGGCTTCACGCC  
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SEQ ID 1654

NPKR2DLKSLIIIGAGPIVIGQACEFDYSGAQACKALREEGYKVLVNSNPATIMTDEPMADVTYIEPIWQTVKEIKAKERPDAILPHTGGGTALNCALDLARNGVLAKYNVELIGATED  
 ATRKAEODRGRFKEAMEKILGSCPSPKSFVCHTMNEALAAQEQVGPFTLIRSPFTMGSSGGQIAYNKDEFLAICERGFDASPTHELLIEQSVLWGWEYEMVDRKADNCIIICSTENFDPHGV  
 HTGDSITVAPQATLTKKEYQIMRNALASLEIRGVDTGSSNVQFAVNPENGEMIVEMNPRSVRSALASKATGPPILAKVAALIKTEQSVLDELANDITGGRTTPKSPESIDYVYTKIPRA  
 FPEKPAADRLRITQMKSGVEVMAAGRTIQLQVKALRGLETLGCGPNRSPDEKATIRRELNPAGPERMLFVADAFKAGTTPPEETHEICALDPWFLAQITLDMKEKSPESDQGLVLDYAL  
 RRLKRGKFSKRLAQLLNVSEKEVREHRYALKLHPVYKRVDTCAAEFATETAYLYSTYEECESRPSDRKKVMILGGGPNRIGQGIEFDYCCVHAALALRESGFETIMVNCNPETVSTDFD  
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 QIQKYMREAQVQSDSPVLLDFFLANATEVDDVDCVSDGKDVVIGTGMQHVQAGIHSGDSGCSLPPYSISEEIQDETRRQTKAMAYALGVTGMLNMQFAVDGVVFLVFNPRASRTVPFV  
 SKATGVPLAKVGARCMAGISLKEQGVKEVVEVDNDFYAVKEAVFPFIIKPGVDITILGPMRETSGEVGVGASGAGEYTKAQLAGERALNTPGKIFLSVREKGERVIRKAKNFQALGYGICAT  
 RGTAPVYITHEGLIVQALNKVPEGRPHIGDALKNGELIALVNTVSTSDPSVDSHIIROSALQORVPOYTTTAGEAMSEGAKSRYDLGVYSVQVELHGRKLKRNH

## SEQ ID 1655

TGCGCCGAACACTTTCAAAGCTTCGCAAGGGGTTCAAAGACCTTTTCACTGCGGCCCTTCAATACCACCGATAACCAFTTGC GCGCGCAACAGCCAGTTTCGGGAATATTCACGCT  
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AAAACGTGTCGGCAGGCACGCGCACGCGCAGCGCGCTTTCGACAAATTCGCCACACTTATATATGTGCGCCCTTCTTAGGACGCAATATATAGGCGGTATCCCATCGGTAACACCGTAGGA  
TTGGACATATCCAAGCTGACATTTTAGGCAACCGGCTATGGTCGGGCAA

**SEQ ID 1656**

CAEHFQTFRRNGFKDLFTCPFPFTTDNHLRAQQPVFGNIPRFSNRHIGQGVVMLQICTCTDRGKCRPDGILYHVSVELVRPNKGVGGISRELLIQTFDDILIFIKONGCRARLKQLQFLRGFP  
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SEQ ID 1657

ATGTTT TAGT GATATCTACTTGAACCCAAAAAACTATTTTGGCTATAGAAAAAGATGGCTTTTAAGGCATTTTGGGATAATGGCGGACAATGCCTATCTAGACTTAAAAGTAGTAGATGGAA  
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ATAACCATTAGATCCATATACAGGGAATGATTTAATATGGCATGTGCAAAATCGATCCAAATGATGGGGTGGCCAAATCTTGGAAACTTATTAATCATATGGGAAAAGTTACAGCAAAAGTATC  
CTAATATTATTAATTTTCGTATAGAAAAAATGATTTTCACTAAA

## SEQ ID 1658

MFSDIYILPNKPYFIEKRLPFKAFWDAGGQCYLDLKVVDGKIALCGQLINYNTSTVNAABEVYRSIIDYILISNEILIVRTKPSFKNIFSTNEKZYKEIEKINKFLYKMDWYLPFND  
ITLDPYTGNDLIHWDIDPNDGGAQPLETYQSWELQKYPNITTFYDKNDLILTK

## SEQ ID 1659

TTGCCACCAITFCGGAGAATGCCCTCTCCCGACGCCCTCCCGACGGGGAGGGAGTGGTTTCGGCAGATTTTCGGTTGCCGTTGGTTTGAAAAATAACTTAAATTTGCAACCGTTGATTT  
CAGGTCGTCTGAAAAAGAAATGCCGAAATATCAACAGCGGGAATTTTCAGGCAGCTTTATCGCAAGCAGGTGGAACAAACGCCGCGAGCATTTTTCAGACGACCTT

## SEQ ID 1660

LPPFGECPLPSPFPGREWVSADFSVAGGLKNNINLQPLISRLAKNARNINSNGNFSGLYRKAGGTNAASIFSDDL

## SEQ ID 1661

TTGTTGCCCTCTCTCCAGCTCTCTCCACGGGGAGAGAGGACGGGTGGCTGTGGGGTTGAGGTTTGCTGCAAGGAAAAACAGGTTATTCAGGTTGCTTTTTGCTTTTCAGACGACCTTT  
TTAAACGCTTAATTCAGTTAATTTTACCTTATTATTTTCAAAATCTAATCAAAATCAACCGTTTGCTACCGTCTGGCTGCTTTTCCAAATCTGCAATACGGCAGGATTTCCGCCAGTA  
CATCGTTTGTCTGCTGCAAAATTTCTGATTCAAAAACGACGACGGTAAAGCCCAAGCTGTGAGATATACCGTCCGCGGTTGGTATACGGCTTGTTCGGCTGCTGCCCGCGTC  
TGCTTCGACANTCAGCTTGGCGGTTCACGCACATAAAATCAACAATATAATTTCCCATCGCTGCTGTGCGCGAAATTTATAGCCGTTTCAGACGGCTGCCCGCAGGTGTGCCCAATTTT  
GCTTCGCGCTGCTCATTTCTTGACGCATGGCTTTGGCGCTTGGCGCAGGCGGGGTTTTGGCGGTCAA

## SEQ ID 1662

LLPSLQLSPTGREDSAVGEVCCCKENRFLRLFCPSDDLFRRLIQLILPYFQNLKINRLLPCWLLPQLQYADPQYIVCLLQNFVLPKTHGKAQAVEIYRPRVVVYGLFRVLPV  
CFDNLQGRYAHKINNIIPIRLLSAEFLAVQTACPQVLPQCFRLAHLTHGFGALAGGVFGQ

## SEQ ID 1663

ATGAACCCGCGGAGAACTATTGACCGCCGAAAAACCCGCCCTGCGCCAAACGCCCAAGCCATCGCTCAAGAAATGAGCGAGGCGGAAGCAAATTTGGCAACACCTGCGGGCAGGC  
GTCTGAACGGCTATAAATTCGCCCGACAGCAGCGGATGGGGAATTATATGTTGATTTTATGTCGTAACGCCCAAGCTGATTCGGAAGCAGACGGCGGGCAGCAGCGGAACAGCGGT  
ATACGACCCAGCGCGGAGCGGTATATCTACAGCTTGGGCTTTACCGTCTGCGTTTTTGGAATCAGAAATTTTCAGCAGACAAACGATGACTGGCGGAAATCTGCGGTATTGCG  
GAATTTGAAAAGCAGCAGCAGCG

## SEQ ID 1664

MNPPEKLLTAENPALRQRAKAMRQEMSEAEKLVHQLRAGRLNGYKFRQQPMGNYIVDFMCTVTKLIVEADGGQHAEQAVYDHARTVYLSLGFVTLRFWNHEILQQTNDVLAEILRVLQ  
ELEKQPAR

## SEQ ID 1665

ATGCTCTGACCGATACGCCCACTGGAAACGCTTTACAGGAATTATCCGCACACGGCATCAAACTTTAAGCGGCATCGTAGCGGCACAGGCGCAATGGGCAAAATCCAATCGGTTT  
ACCTGCGCGATCCGATGCGCAACCTGCTGGAATCAGCAGTTAT

## SEQ ID 1666

MPADRYAPLETVLQELSAHGKPLSGIVARTGAMGKIQSVYLRDPGNLLEISSY

## SEQ ID 1667

ATGAAAATTAGCGCACTCGACCATCTAGTACTGACTGTTGCCGACATGACCGAACCATCGCGTTTTACACACAAGTTTTGGGCATGGAAGAAGTTTCATTGGCAACACCGTAAGCTT  
TGTGTTTGGCAGTCAGAAAATCAACCTACACGGGCGCGTGGGAAATTCAGCTTAACGCGCAACACGCCGCTGCGGCACAGCGGATTTATGCTGCTGACCGATACGCCCACTGGAA  
ACGGTTTTACAGGAATTATCCGCACACGGCATCAAACTT

## SEQ ID 1668

MKISALDHLVLTADIDRTAFYPTQVLGMEVSPGNRKRALLFGSQKINLHGRGAEIQPNAQHAACGTADLCLLTDTPHNKRFRYNYPTASNL

## SEQ ID 1669

ATGGTCGAGTGGCTAATTTTCATTTCCAGCTTTCTTTTTTCAGACGGCAGCAGCATACTGTTGCCGCTCTGAAATCATTATGCTTTGTTTTGCAGCCTTCATATTGCCAATGAATTTGCGA  
ACAAA

## SEQ ID 1670

MVECANFHFQLSFDGSSILLPSENHYACFAAFILPMNLNKH

## SEQ ID 1671

ATGCCCCCTGCCGAAGTCCCTTCAGACGGCATTTGTCAAGAAATTTTATTAACAAACAGGATTCCTCATGAACACCCCCGCCCTCCTGCTCTGCTGACGGCAGCGTATTCACGGCACAT  
CAATCGGTTACGAAGGTTCCGCTTCGCCGGAAGTCTGTTCAATCTTCGATGACCGGCTATCAGGAATCTTGACCGACCGCTCTCTGCAACAAATCGTTACCTTCACTTACCCCCA  
CATCGGCAATACCGGCACCAACGCCGAAGATGAAGAAAGCCGACGGTTTACGCCGACGGCTGATTCGCCGACCTGCGGCTTTGCAACAGCAGCTTCGGCGCTCCGAAAGCCTGCMC  
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AAACCGGTGTTCTGTTTCAAGGACACCCGAAGCCAGCCCGGTCGCAAGATGTCGGCTATTTGTTGCAACAATTCATTTGCAATATGAAGGCTGCAAAACAGCA

## SEQ ID 1672

MPPAEVSDGIVKNPIKIRIPIMNTPALLVLADGSVFHGTSGYEGSASGEVVFNTSMTCYQELIDPSTYCKQIVTLATYPHIGNGTNAEDESRSVYAAGLIIRDLPLHSSPRAESLH  
DYLVRNETVALADIDTRRLTMLREKAGGAILTGADATVEKAQELIAAPGSMVGDLAKEVSCETETVETWEGENELGKGFVTPDKQPYHVVAIDFGVKTNILRLMASRCRLTVVPAQT  
SAEDVLALNPDGVFLSNPGDPEPCTYALAEVQKLMESGKPIFGICLGHQLISLAIGAKTLKMRFSHHGANHPVQDLDSGKVITTSQNHGFAVDADTLPANARITHKSLFDMLQGIETD  
KPVFCQGHPEASPGPDQVGYLFDKPIGNMKAQA

## SEQ ID 1673

TTGGACATATCCAAGCTGACATTTGACGCAACGCCATGGTCGCAAAACGGAGCATTCGGCAAGTTTGACAACGATTCAAAAGGTTTAGATCAGTTTTCGACCGGTTGAAAAGCTTGG  
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**SEQ ID 1675**

**SEQ ID 1676**

**SEQ ID 1677**

**SEQ ID 1678**

**SEQ ID 1679**

**SEQ ID 1680**

SEQ ID 1681

**SEQ ID 1682**

SEQ ID 1683

SEQ ID 1684

SEQ ID 1685

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## SEQ ID 1686

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YLPYPYKGVSGPDTAELNKRGNVWVHTITRAGLAGVYVYTGVI CRDTGQCPQLVYKTRFSFDNTGLAKNTGRDLRHTPEPSRENSPIYKLSYDYNLWVSFNLGSEGTAKDGRSSNKLVSFDE  
NNSNSNQNLVYTTBGRHISLGDWQRSTAMAYTYLNKHLHLLDKQRIENIAPGKTVDLGTLRPRVETKTNNWGNLLSFMATWKIEDKGNITVRLGLPEVKAGRCTNTAHPNPNKAPSPALT  
APALWFGVPVQNGKQVQMYASVSTYPGSSSRIFLQELKTRTDPARPGHSLAALDTQNIKSREPNNRSQTIVRLPGGVYKINSKNGRVRVAGINGNDGKNDTPGIYKDLVTPPEADWSN  
ILLPWTARYGNDIDFKTFNPFNSKTKNGKKQYSQKYRIRTKEDNDKPRDLGDIVNSPIVAVGGYLATANDGMVHLFKRNGTDQRGYELKLSYIPGTMERKDIENSDSLAKELRAFAP  
KGYVGDYRGVDDGFPVLRITDDQDKQKHPFMFGAMGLGGRGAYALDLSKIDGNYPAAPLFDVKNNGNKNRVKVELGYTVGTPQIGKTQNGKYAFLASGYAAKNIGSGDNKTALYVYD  
LENGSGSLIKRIBVQGGKGLSSPTLVKDLDGTVDIAYAGRGAICTALI

## SEQ ID 1687

TTGAAACCCCGCGCTCGGACATCCGTCCTTCGGACGGCAGGATCAGGCTTTGTCGGGAGGGGTGCAAGCCCTCCGAATCAGGGCGGCGCTTATGTCCGCGCTCGGTGTGGAAACA  
TATTTTATCCCTTAAATCTTGCTTCGCGGATACCGTCGCGGCGAGGCGCGCAAAACGGCGGATTCGCAAAACCGCGGATCCGCGCGCGCGGATTCGCGGTGCAAGCCCGCTT  
CGCGCGGCTGCAAAAGGGGATGTTCGCAAGGTAAACGCGCCCTC

## SEQ ID 1688

LKPRRSIDIRPSGRDQALSGRGASPSSESRRLMCRPACWNIFYPLNLASRDIVGGRRRAANGIRQ7ARSRRRIAGCKAPPARLPKGDVVRKGNAPL

## SEQ ID 1689

GTGCAATGTATAGGGTTGCGCATCTTCTCCTTCGCGCTTATCCATGGTACAGCGGTTTTTGGCAATCCGCAACCGTTTGCCCGGCGCGCATTCGCGCTCGCGGCAATGGCGGGCC  
GGGAGCGCGCATTTTCAAGTTGCGGCAACCTTTCCCAACAACCTTAACCGCC

## SEQ ID 1690

VQCIGLPHHSPCALIHGTAVFGNPQFPARPAIAACAMAGRGGGIFQVAATFPNNLTA

## SEQ ID 1691

TTGTGGGAAAGGTTGCGCAACTTGGAGAAATGCGCGCTCCCGCGCCCTCCCGACGGGGAGGAGCGGATTCGCGGAGATTTTCGGTTGCGGCGATTTGAAAGGCAACTTAAATTTG  
CAGCTGTGTGTTCAGGTCGTCTGAAAAATAAAAGCAGCGCTGCACAACCTGTPTTTCCTTCAGCAAACTCAACCCCAACAGCCGACCGTCTCTCCCTGTGGGAGAGAGCTGGAGAG  
AGGGCAACAAGCCCAAGGCTGTATTTAGGCGTTAAGTTGTGGGAAAGGTTGCGCAACTTGGAAAAATGCGCGCTCCCGCGCGCGCATTCGCGCGCAGGCGGCAATGGCGGGCGGG  
CAACCGTTGCGGATTCGCAAAACCGCTGTACCATGA

## SEQ ID 1692

LLGKVAATWRMPPRPSPTGEGADCGRFPGRFRERQLKFAAVVSGRLKNKQPAQPVFLAANLNFNSRPVLSPCGRELERGQQAARLVFRRLSCWERLPQLGKRLPGPLPRRRQWRAG  
QFVADCKPLVHG

## SEQ ID 1693

ATGTATAGGGTTGCGCATCTTCTCCTTCGCGCTTATCCATGGTACAGCGGTTTTTGGCAATCCGCAACCGTTTGCCCGGCGCGCATTCGCGCTCGCGGCAATGGCGGGCGGGGA  
GGCGGCAATTTTCAAGTTGCGGCAACCTTTCCCAACAACCTTAACCGCTTAATACAGCCCTTGGCGCTTGTTCGCCCTCTCTCCAGCTCTCTCCACAGGGAGAGAGCGGTCGGCTGT  
GGGGTTGAGGTTTGTGCAAGGAAACAGGTTGTGAGGCTGCTTTTATTTTTCAGACGACCTGAAACAACAGCTGCAAAATTTAAGTTGCTTTTCAATCGCTGCAACCGGAAATCTG  
CCGCAATCCGCTCCCTCCCGCTGGGGAGGCGCGGGAGGCGGCAATTCCAAGTTGCGGCAACCTTTCCCAACAACCTCAACCGCCCAATACAGGCTTTTCGGCTTGTTCGCCCTCTCTC  
CAGCCCTCTCCACGGGAGAGAGGAGCGGGAGGCTGTGGAAAT

## SEQ ID 1694

MYRVAASFLRAYFWQSFWSATVCPARHCLRGNGPGRHFPSCGNLSQILNRLNTSLAACPLSSSLPQBERTGRLLGLRFAARKTGACGCTLPFRRPETTAANLSCLSNRLQPKNL  
PQSAPSPVGEGRGGILQVAATFPNNSTAPIQAFRLVALSPALSHGERGRGGCM

## SEQ ID 1695

TTGGGGCGGTTGAGTTGTGGGAAAGGTTGCGCAACTTGGAGAAATGCCGCTCCCGCGCCCTCCCGCAACGGGGAGGAGCGGATTCGCGGAGATTTTCGGTTGCGGCGATTTGAAAG  
GCAACTTAAATTTGCGAGCTGTGTTCAGGTCGT

## SEQ ID 1696

LGRLSCWERLPQLGSECLPGPPRGRERIAADFSVAGDLKGNLNLQLLPQVV

## SEQ ID 1697

TTGGGAAAGGTTGCGCAACTTGGAGAAATGCCCTCTCCCGCGCCCTCCCGACGGGGAGGAGTGGGTTTCGCGAGATTTTCGGTTGCGGCGATTTGAAAGGCAACTTAGATTGCGAG  
CTGTTGTTCAGGTCGTCTGAAAGCAAAAGCAGCTGCACAACCTGAT

## SEQ ID 1698

LKVAATWRMPPRPSPTGEGVGFGRFPGRFRERQLRFAAVVSGRLKSKQPAQPD

## SEQ ID 1699

TTGCGAACAGAGGCACATCATGAATATACAAAACATCCGCACCTCTCGACACCGTCGCGGTTCCGAATACGGCACGCACGCTCGGCGGCGAAAGCCGCTCCGCTCGGTGCGACAGC  
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ACCACGCGCAGGACATCGCGCTGATAGACGCGCGCAAGGCTGTGGATATGTTCCGCAAGGTCAACATTCGATTTTGGGCGATTGGAAGAACATGTCGCTCCATATCTGCTCAACTCGG  
GGCACAGCGAAGCACTGTTGCGCACGGACGGCGGCAAGATTGCGCGCACGCTCAACGTCGCCCTGCTCGGACAGCTTCCCTAAGCTGCGCGTACCGGAAGCCATGGACGGCGGCAC  
ACCGCGCGACTGTTGCGAGAACACCCCGCATCGCGCGAATCTACACCGATGCGCGATTCCAAAATCGCCTGGGCAATGCGGACAAAGGCAAGACPTCAGCAGCGCGGTTCCCTAAAAATT  
GTCGTCGA

## SEQ ID 1700

LRTEAHIMNIQNIITLLDVAVPNTARTLGGEKAVRSVGQRSDGIIHALHFGFVFAHIAAALADAVQETLMPETGGAHILGIDTEIGTHKVRPGVTTIKGVKNIIVASGKGVGKSTTT  
ANLAAAMARMGARVGLDADLYGPSQPTMLGVHDKPDQKNQKLI PVESSDGIQVMSIGFLVDTGQAVVWRGPMVSQALQQLIPQSENDEVDYFLIDLPGGTGDIQLTSQRI PVTGSVIV  
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VVE

## SEQ ID 1701

TTGTGCGAACTTTTACAGGTATGCGCGGATTTGAAATCCGTTGCCAAATATCCCGTGCAACAGCAGTCTGCAATTAAAGCTGTAAAAATTGCT

## SEQ ID 1702

LCELLHGMRRIVKIRQNTIPCKQQAIFVKIA



## SEQ ID 1703

TTGGTGTGTTTGTCTGGTGTCTGCTGTTTGGATTGGGTACGCAAGCCGACGAACCTGCCGGGGCGGAGGGCGGCTTTGACCTGCTGTGCGGGCAGCGGCTGACTTTGGACAGTTTA  
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TTCGGGACGCGGTCGGAAGTGGCGCATATATGCAAAACCGGGCTTGGGCTTTCCGACTGTCAAGCATGAGGACGGGGTTTGGCAAGGCTTGGCGGATTGCCGCAACGCTGCCGTG  
GTTTGGTCAAAAATGGGAAATGGTCCGCTATACGACGGGAATCAGCAGTTATTTGGGGTTGCGCGCAGCAATTTTTCAGCGGATTTTTCGGT

## SEQ ID 1704

LVFLVLSFLDVRKPFDEPAGAAGRPLTLLSGRLTLGQFSRDRTVLVYFWGSMGVCRYQSPILIDLAADGVFVGVAVRSGSASEVAAYMAKRLGLFPTVSEDEGLARSRIAATPAV  
VLVKNKGVRYTTGISSTWGLRARIQADFFG

## SEQ ID 1705

TTGATTCTCTACATAGCGGAAAGTTTGACAAAAACAAAGTTAACCGAAAAATCCGCTGAAAAATTCGTCCGCGCAAGCCCAATACTGC

## SEQ ID 1706

LILYIAESLTKTKVNRKNPEKFRASPHNC

## SEQ ID 1707

TTGGTAGGCATTGTTTAAGTCTCCAAGTTATCGAAAAATCAAACTTTCAAACCGTGGGAAAGCCTGTGGCGGTAATTTTGTATGCAACCGTTATA

## SEQ ID 1708

LGRHCLSLQVTEWTFKPSGKPVGVIFDATVI

## SEQ ID 1709

ATGCCGTCTCTACGCTTATCCGCGGCTCTACCGATAAACCAACGGAATCCCTATGACCAAGACACAACCTCCACCTGAACAACTTCTGACTCTGCCCAAGAACGAGGTTCCGTGCCCA  
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GCTGCCGCTGCGCGAGCGTTACCGTCAACCGCAATACCTGGGAAACCAATACCGCTTCCATCAACCTCGACGCGAGCGGCAAAAGCAGGCTGGATACCGGCTTCCCTTCTCGAAC  
ACATGATCGACAAATCGCCGCCACCGCATGATTGACATCGACATCAGCTGCAAGGCGACTGACATCGAGAACACACCGCGAAGACATCGGCATCACACTCGGACAAAGCAAT  
CCGGCAGGCACTCGGCGACAAAAGGATCGCGCTTACGGACATTCCTACGTCGCCGCTGACGAGAACCCCTCAGCGCGCTGCTATCGACTTTCCGCGCGCCCGGACTCGTGTACAA  
ATCGAATTTACCGCACACTTAATCGGACGTTTCGATGTCGATTGTTTGAAGAAATTTTCCACGCGATCGTCAACACAGCATGATGACCTGACATCGACAACTCAGCGGCAAAAGC  
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## SEQ ID 1710

NPSTLSAGSTDKPNIPIPIKTQLHLNFLTALQEAGSLPKLAKLCYRTPFVALYKLQRLKQAEQPDARGIRPSIMAKLEKHTGPKGWLDRKHRETVPETAAESTGTAETRIAETAS  
AAGCRSVTVNRNICTQITVSVINLDGSGKRLDTGVFFLEHMIDQIARHGMIDIDISCKGDLHIDHFTAEDIGITLQQAIRQALGDKKGIIRRYGHSYVPLDEALSRVIDLSGRPLVYN  
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## SEQ ID 1711

AAGTAGTATCTCGTATGCTCTTCGCCAAACAGCAGCAGCAGCGGCGAGATTGGGAATTGAAAGAAAAGGTGTGTGCAAAACCGCGTGTTCGACGATTGGACGATTTCATCTTTGCCA  
ACGGGACGCTTTTATTTTAAAGAAATAACGGAACCGCGGCTTTCCGACGCTGTTCGAGGATTGAAGGCTCAT

## SEQ ID 1712

K\*YLVMLFAKQHDHAGRLGIERKRCVQNGVFDLDDFIPANGQVFI\*RINGTAAFGSLQLGLTAH

## SEQ ID 1713

TTGGCGGGCGCTCTCTGTGTGTCAGGAGGAAATATGATTATTGTCTAGCAGCGCTGCCCGGAGCGGACATTGCCGGCTGTGCGCTTCATCCGACGAGAGGCTGCGGAAACACA  
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AGGAAATCTGTACGGTTGGCAAGCGCGCAGCGCGTGGGAAATCGTCCGAACCTGTTTGAAGGCGGGCGGA

## SEQ ID 1714

LGGPSLVSGNMIVMSRRAEADIAGVVAFIRSRGLREHISHGDERTVIGAIGDDRVLVSVREVQTLPEVEKAVRILDTWTKTVSRNRAEDSRVAAGVAPGGGTIVRAAEPVSNAD  
VFLDPPTTANLYDVLADGGRGRCRLAEQAAAHGAGKPVLRVVRNVRHVEAALNAGADILYLGGLMSDLAVLNEAGSLNIPVLVCKDKHSAEDWLNAAEYVVSRRNRHLILGESGV  
LGHTKHPYRLDVESTVVRQISHLFVIANITGLWSRDMPEIILYLAKAAGACGIVGTCFEKAGG

## SEQ ID 1715

ATGACCAATTCAGGCCATTCTGAATCAGGCGAATATTACCGATCAGCAATGCGGATTATCCGCTCTTTGGCGGAAACGGCAATTGGATTTCAGGATTGGCGAATCAGGCGTGCA  
TTTTCGCGCCAGCCTGACCGGTATCCTGACCGGCTTGAAGGCGGGGTTGGTGTGCGCGTGAACCTTCCAACGACCAACGGCGCTTTATCTGAAGCTGACTTCCGAGGCGGAGAA  
GCTGTATGAGGAAATCGCGCAAGAGTGGACGAGCGGTACGACGCTATCGAGGAAGTGTGGCGCGGAGAAATGCTGCTTAAAGACCTGTGCGCAGAACTTCCCAAAATCAGGAGT  
CGTTGAACTCG

## SEQ ID 1716

HTQFRPILNQANTIDQWRIRILLAENGLDFQDLANQACILRPSLTGILTRLEKAGLVRLKPSNDQRRVYLKLTSEGEKLYEIEIGBEVDERYDAIEEVLGREKMLLLKDLIAELAKIED  
ALNS

## SEQ ID 1717

ATGTGACGAGTCTCTGATTCAAAAGCGCTCGGTCCGACGTTTCCGCGCATACGCGCTATTACGAGTTCAACGCTATCCTCGATTTCGCAAGTTCTGCCAACAGGCTTTTAAAGCAGCAGC  
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TGAAGGTTTTCAGGCGGACGACCAACCCCGCTTTTCAAGGCGGGTCAGGATACCGGTACGAGTGGGCGCAAAATGCACGCGCTGATTTCGCAAAATCTGAAAATCCAATGTCGCGCTTTTC  
CGCCAAAGACGGGATAATCCGCTATGCTGATCGGTAATATTCGCTGATTGAGATAGGCTGAATGGGTGATCAGGCTTCCCTTGCCTGTATCAGACGATATGATAGACGATGCT  
TT

## SEQ ID 1718

MCSSSDSKSRSDVSAHYGLRVQRILDFGKFCQQVFKQHFLLAQHFLDSVVTLVHFFADFLIQLLALGSQLQINAPLVVGRFQADDQPRFFKAGQDTGAGAQNARLIRQILKIQCAVF  
RQRTDNPLLIQIRLILQNRPELGHQGPCLYQTDIDRRHF

## SEQ ID 1719

TTGAAAGTTTCTGCAAAATCCGCCATTTTCCCTTTTAAACCGTCCCTTATATAAGAATGCTGCACACAGGCNTCCCCCATGTGCAGCAGTTTC

## SEQ ID 1720

LKSLQIRHFSPLNRPYKNAHKAAPHVQF

## SEQ ID 1721

ATGGCGGATTTCAGAAAACCTTTTCAAACCTTCCTTCCTGATGCGATGGCATCTCTGCGCGCAGCGGTTTCATGTCATCAGCAGACGGTGCGCGAGGGCGTTACGGCATTACAAATGACGG  
CGGTTGCGCGGTTACCGAGCAGCGCGGACCGTGTATGCTGTCATAAACCGGAGTGCGCGAATCATTCGATCTCTGCGAAAACCGCAGCGCTTCGATCAATATGCTGCGCGAGCAACA  
TCAGGATGTTGCCGAACATTTTCCGGGCTGACCGGCTGTCGCGCGAAGAGCGGTTTGCTTACCATATTTGGCATCGCGGCAAAACGGGACCACTTGAATAGAAAGCGCGTTGCGGCAC  
CTGCAOCCGCAATGTTGTCGCGCAACATGAAATCGGCACGATTTTGTGTTTACGTCAGGCTCGACGAAATCAAAAACGCGGGTGCAACGCCCGCGCTGCTGTATTTCAGACGGCAGT  
TTAGGCTTTAGAC

## SEQ ID 1722

MADLQKTFQTSFRDAMASCAAGVHVITTDGAAGRYGITMTAVAPVTEPPVWMLCINRSARIIPILSEWSLCLNMLADEHQDVAEHFAGLTGLSPEERFAYHIWHRGKTQGLEIGALAH  
LHGHIKHEIGTHFVYVRLDRKNCCKRPALLYFRQFRPLD

## SEQ ID 1723

ATGAAAGCGATGATACTGGCGGCGAGGACGCGCGAGCGTATGCGCCCTTTGACCGCACCACTCCGAAGCCGCTGCTCGATGTGGCGGGTAAGCCTTAATCGGTGGCAGCTTGTCCGCTC  
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AGGCGGTTTGAAGACGCGAGCGGATCGCGCAGGCAATGCGGCTGTTGGGTGGGACCGCTTTTGGTGGCCAAACGCGACGCTGCTGACCGACATCGATTTCACCGCGCGCTTCAGACG  
GCATGCTCCCTGCCCGGCGACATTTCCGCACATTTGTGCTGTTGGGAAATCCCGCGCAACCCGACGCGGATTTTCCCTGCTGCGCGACGCGCGCTGCGGCGGGAAGTATCCGCGG  
GCAACGCGATGACATTCAGCGGCTGGGTATTTACCGTCTGAAATGTTTACGGAATCGAAGCGGCGAGTGTGGCAAACTCGCGCCGCTATGCTGAACGAAATGCGGCAAAACCGCGT  
GAGCGGTGAGAATACGCGGCTGTTGGCTGGATGTCGCGCAGGATGCTCGCTGTAAGGAACGCGCAAGCCCTTGCAGCGCTTGAAG

## SEQ ID 1724

MKAMILAAGRGMRPLTDTTPKFLLDVAGKPLIGWHLCRLKQAGTFEIVINHAWLGRQIENALDGSAYGVNIAYSPEAGGLETAGGIAQALPLGGQPLVANGDVLTDIDTAAFPQT  
ASSLPGHISAHMLVGNPPHNPDDGDFSLPDGSRVPEVSGNGLTFSGVGIYRPEMPDGIAGSVAKLAPVLLNEMRQNRVSGQKHTGLWLDVGTVCRLKEAQAALAAWK

## SEQ ID 1725

TTGACCGCGCTTTTCGCCAAAATGGGCTTGCAGGGCATAGATTTCGGATTTCCGCCACCTTTATCCGCACTTGGTCATCTCGCGCGCTTGGTATTGTTTGGACCTACACCGGCAAAATGGC  
AGGGCGTAAACCGCTTCACGGGGCGCAACCGGAGCTTTCGCTTTGTCGCGACTCGCCACCGCGCATCTGGCTCGCTACTTCAAGCCCTGCAACTGGGCAAGCCCGCAAGTCGC  
GCCGTCGACAAATTACGCTGCTTGTGTCGCTGATGGCGGTGATTTCTTAGACGAAACCGCGCAACGCGAGGATGGATAGACTTGGGGCTGTTACGCGCGCGTGT

## SEQ ID 1726

LTAVFAKMLQIGDISDFATFIRTLVILAAALVLFITTTGKMGVNGFTGRNRTFLVLSGLATGASWLAIFYKALQLGKAPQVAPVDKFSVLVLVALMAVIFLDERPNTQEWIDLGLVTAAC

## SEQ ID 1727

TTGGGCATTGGCATCGGCAGGCTTCGCTCATTCACCGCGCTTTTCGCCAAAATGGGCTTGCAGGGCATAGATTTCGGATTTCCGCCACCTTTATCCGCACTTGGTCATCTCGCGCGCTTG  
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CCCTGCAACTGGGCAAGCCCGCAAGTCGCGCCGCTCGACAAATTCAGCTGCTGCTTGTGTCGCGCTGATGGCGGTGATTTCTTAGACGAAACCGCGCAACGCGAGGATGGATAGACTT  
GGGCTGCTTACCGCGCGCTGTTGACGTTGGCACTGAAACGT

## SEQ ID 1728

LGIGIGRLRLIDRRFRQNLGHRFGRFHLPHLGHPRRLGIVFDLHRQMAGRKRLHGAQPDVSGFVTRHRRILARLLQSPATGQSPASRRRIQIPGLGRADGGDFLRRTPHAGMDRL  
GAGYGGVLFALAKR

## SEQ ID 1729

TTGGCAAAACCGCGCTCAATGAGCGAAGCGCTGCGGATGCCAATGCCCAAAACAGCTATGCGTTCCTGCCCATGTTTCTCCTTGGATTGTGAACATATGAACGGTATTTTGTGCTG  
CGTCAAAATTTCACTCGCGGTTTGGTGC

## SEQ ID 1730

LAKTAVNEAKPADANAQNSYALLPMFSPWIVNMMNGIFVAASKISLRVWC

## SEQ ID 1731

TTGTTGCTGCGTCAAAATTTCACTGCGGTTTGGTGCAGATAACGTTATAATATGCTGATATTTTTCATCCACCTGTTTGTGCGC

## SEQ ID 1732

LLLRQKFBGPGADNVIICLILFSIHLFVA

## SEQ ID 1733

ATGAGCTTCAAAACCGATGCGGAAACCGCCCAATCTCTCAACATGCGCGCGATTTGGCGAAATTTGCCGCCAAGCTGGGTTTGAACGTTGACAACATGAGGCTTACGGTCAATACAAAGCCA  
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CGCATTCGCCATATCGGCAAGACTCTGTGATGCTTTGCGCGAGCGCTTCTTTGGGTCGGGTGTTGCGGTGAAAGCGCGCGCGGCAAGCGGCTTACCGCAACATATCTACCAAGGTAACGATGACATCAACCGG  
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GGGCATCAAGAGCAAAATCGTGGGATTGCCAAAAAGTGTACGGCGCGAAGATGCGATTTCAGCGCGGAGCGCTGCGGAAATCGCTCGCTGGAAGAACTGGGCTTGGCAAAATG  
CGATGTCGATGCGGAAACCAATATTCATTGAGCGCAACCGCAAACTCTTGGCTGCGCGGAGGCTTCCGATCGCGCTACCGGATCACTGTTTCCGCGCGCGCGGCTTCATCG  
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## SEQ ID 1734

MSFKTDAETAQSSMRPIGELAAKLGLNVDNIEPYGHYKAKINPAEAFKLPQKQGRILIVTAINPTPAGEGRITVTIIGLADALRHIGKDSVIALREPSLGPVFGVKGGAAGGGYQVLPME  
DNLHPTGDFHAIGAANNLLAAMLNDHNYIQNELNIDPKRVLMRRVVDMDNRQRLNIIDMGKPKVDGVMRPGDFITVASEVMAVFLAKDISDLKRFENILVAYAKDGPVYAKDLKAH  
GAMAALLKDAIKPLVQTEBTPAFVHGGPPANLAHGCNSVATRLAKHLADYAVTEAGFGADLGARKPCDIKRLAGLKPDAVVVATVRLKYNNGVERANLEENLEALAKGLPMLK  
HISNLKRVFLPVVVALNRPVSDSDEALAMIEKACAEHGVESLTVWVGKGGAGADLARKVVAINDQPNPFGPAYDVELGIKDKIRAJAKQVYGAEDVFSAEASAEIASLEKLGIDRM  
PICMAKTQYSLSDNAKLGCPGFRILAVRGITVSAGAGTIVALCGNMKMPGLPKVPAEEKIDVDEHGVHILF

## SEQ ID 1735

ATGAGTTTGAANTGCGGCACTGTCGGTTTGGCCAACTCGGCAATCCACCTTTTAAACGCGCTGACCCCAATCGGCGATCGAAGCGGCAAACTATCCCTTCTGCACCATCGAACCCCAAG  
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CAAAGCGCAAGGCTTGGCGCAACCGGTTCTTGCACATCCGTGAAACCGATGCCATCGTCAACGTCGTGCGCTGCTTTCGACGACGACAACATGTCACCGTTTCCGCGCAAGTCGATCCG  
ATTGCCGACATCGAACCATCGGCAACCGAATTGGCGCTTGGCGACTTGGCAAGTGTGAAAAAGCCATCGTCCGCAAGAAAAACGCGCGCGATCAGCGCAAGACGCGCAAAACTAG

TCGATTGTGCAAAAACCTGCTGCGCATCTGGACGAAGGCAAAACCCGTGCGTTCCTTCGGTTTGGACGCGGAAGAACGCGCGCTGCTGAAGCGCGTGTCTCTGCTGACGCGCAAAACCTGC  
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GAAATCGCGCAATTTGAAGACGCGTGAAAGAAGCCGAATTTCTTGGCGAAATGGCGCTTGAAGAACCGGGCTTGAACACGCTCATCTGCGCGCGGTGTACGACCTTTTGGGACGTCAAAACCTACT  
TCACCGCGCGGCGTGAAGAAGATCTCCGCGCTGGACAGCAATACAAAGGCGACACGGCGCGAGCGCGCGGTGATCATACGAGTTTGAACGCGGCTCTATCGCGCGCGCAAGTGAATGTGCT  
CTACGATGATTTTGTCTGCTGCTGCGCGCAAGCGCAAGCAAGCAAGCGGCAAAATGCGCGTGAAGGCAAGGAATACGTGCTGCAGGACGGCGACGTGATGCACTTTTGTGTTAAGCTG

**SEQ ID 1736**

MSLKCGIVGLGVNPGVKSTLFNALTQSGIRANYPFTCTIEPNVGIVEVPDPRAELAKTIVNPKMQPAIVEKVDIAGLVAGASKGEGGLGNRFLANTRETDATVNVVRCFDDNNTVHSVGVKVDI  
LADIEFTIGTELALADLASVEKATVREEKRASGDKDAQKLVDLCKKLLPHLDGEGKPVRSFGLDAEERALLKPLFLITAKPAMYVGNVAEDGFENNPHLDRLKELAAKENAPVVAACAHES  
ETAELEDGEKAEPFLAENGLEEPGLNRLIRAGYDLLGLQTYFTAGVKEVRANTTHKGDTPAQAGVIHTDFERGFIRAQVLTDDFVSLGGEAKAKEAGKMRVGEKGYVVDGVDVHFLFNV

SEQ ID 1737

TTGCGCGAAATGCGCGTCTGAAGCCGGTTTGTGGTGTTCGACGTTCCCATACCGCGGAATGCAGCGCATCAAAATAAAATCCGCGCGCATTTCCGATTGTGCCCTCCCGGATTCCTGC  
AAAACAAATGCTGCCCTGCCGTTCAGCGGAAGCCGTCGGTATTCCGAATATCCCGAACCCCGATACAAATGACCTTTAGACGGCATTTGCACAGCCCGCGCGTTCAGGTAAAAAC  
ATTA

SEQ ID 1738

LPMPSEAGFGGFRRSHTAGMOPHONKIPPAFFICPPRFLOKLPALPLREAVRYSEYPEPRYKHTFQTAFAPAAFOVETL

**SEQ ID 1739**

ATGAGCCAAAGCCTTACCTTACCCTACCGCCCGGACATCGACACATTGCGCGCCGCCGCGCTTGTTCGCTCATCGTGTTCCATATCGAAAAGGATTGGCTGCCGGGGCGGGTTCTCGGTGTGCGTATATTCTTTGTGATTTTCAGGCTTTTGTGATGACGGCGATCCCTCTTCGCGAAATGTCCGGGGGGCGGTTTCTTCTTCAAGACATTTTATATCCGCCCGATCAAAACGGATTTTCCGCCGCAFTTTTCGCCGTATTTGGCGCGCAACGCTGGCAGCGCGCTTCTTTTATTATCAACAAAGATGATTTCTTCTTTTGTGGAAATCCGCGCTGACCCGCTTTGGGTTTCGCCCTCCAACTGTATTTTGTCAAGGGGAAGGATATTTCGATCCCGCGCAGGAAGAAAGCCCTCTGTGTCACATTTGGTCTTTCGCGTGCAAGAACAAATTTACTTTGTCTTTCGATATGTCTGTGCTGTGCGCCGCGCAAAAGCGTCTGCGGTACAGTTTCGGCTCTCTGCGCGCATTTGCGGCTTAAGCGCTTTCGCGCTTCTTTATGCTTTCCGCGCTGCTAGATAAATATTACCTGCGCCACCTTGGCGCGCTGCGAAATGCTGTGTCGGATCGCTGCGCGCGTGGGATCGGTTACCGGTACCGGCAACAGCGGAATCCCGCGTGGGAAACGGTATGCGCGCGTGGCGCATTTGTTTTCGCGTGCATACTGTTCGCCCTGCCGTGTTTGGCTATTTCGGAACAAACCGCTATTTTCCCGGCCCCCGCGCTTTGATTCCCTGTCTGCGCTGTTGCGCGCGTGATTTATTTCACCATTTACGAACACCCGCTTAAAAAATTTTTCCAATGGGAARTCACCGTGTCCGCGCGTTTGATTTCCATTATTCGCTTTATCTGTGGCAATGCGCGGATATTGCGCTTTATGCGCTATATTCGCGCCGGACAACTGCGCGCTTATTTCGCGCGCGCGCAGCATCGTCTTGACCTTGGCGGTTTTCCTGTATTTCTTATCATTCGATCGAAAGCCGTTTAAAAATGGAAAGGCTCGCTTCGCACAACTCCGPTTATAGGATTTATGCGCTTGCCCTTTGCGCCGCGGCTCGTTTTCGCGTAGGCTGAGGCTGTTTATGGGTTTATGGGCAATACGAGACCGTTTGGGGCTGACCGGTTCCAACGCTTCGTCACCAATGCAATACCGAGAACCAATGCTCTGTTGGGGGATACGGAAAAACCGCGGAAGCTGCTGGTTTGTGGCGGACTCCACGCGCACCATTACAAACATTTCTGCGATGCCGTGGGCAAAAAAGAAAAATGGTCCGCCCATATGGTTTCCGCGACGCTGCGCTATGTGGAAGGCTACGCGTCCCGTGTGTTTCCAAAATCGGGCGCTGCCGCGCGGTTTACCGCTATGCGCAAGAACACCTGCCCCGGTATCGGAAAGTGTTTGGCGGATGCGCTGGGGCAGCCAGATGCCGAAAAACGCGCGCTCCCTGCGCTACGATCCCGGCTTTTTCCTCAAAATTCGACCGTATGCTGCACAAACTCTCATCGGAAAAACAAAGCCGTTTACCTGATGGCGGCAACTTGGCTTCGCTTACAACTGTCAGCGCGCTATTTATGCTTGTCTTACGCATACCCGGTTGCCGCCAAACACTGCGCCGACGACGAAAGCACCTTGAAGGCCAATGCCCGCATCAGGGAATGGCAGGCCAAATCCCCCAAGCTCTATATTATGTGCGCGCATATATCTCCCGCGATTTCCAAATCGCGCGGATTTGCCGGTTTACTCGGACAAAGACACCATCAACCTTTACGCGCGGCACA

**SEQ ID 1740**

MSQALPYRPDIOTDLRAAAVLSVIVFHIKEQWLPGGFLGVDIFFVVISGFLMTAILLRENSGGRFLKTFYIRRIKRILPAPFAVLAATLAGGFFLTKDDFFLLMWSALTALGFPASNLYFAR  
GKDYFDPAQBEKPLLHIWISLVEEQFYVFPFILLLVARKSLRWQPGFLAALCALSLAASPMSALDKYLLPHLRACEMLVGSLTAVRMRYRQQRNPVAGKRYAAVAGALFSACILSACLFA  
YSEQTAYFPGPAAALIPCCLAAALITYFNHYEHLKPKFFQWKITVAAGLISYSYLWLNWPHLAPMYRITGPNLPPYSPAAAIVTLTAFSLISYHCIEKPFKKWKGSPAQSVLWITYALPMLVLG  
AGSFFAMRLPFMAQYDRGLGTRNSTRNSCHNNNGKQCLWGDTEKQPELLVLGSDSHADHYKTFDDAVGKKKEWSATMVSADACATVEGYASRVQNWAAACRAVYRIABEHLPRYPYKVLVAMRWG  
SOMPENRSRLAYDAGFPQKFDRLMLHLSEKQAVIYLMADNLASSYNVQRATYILSSRIPGCRQTLRPDDESTLKANARIELAAKYPNVYITIDAAAYTPADFGYIGGLPVYSCKDHIHPYGGT  
ELAKRPFSEKQORFLDTRHNN

SEQ ID 1741

ATGAGCGGTATTCACCAAGACTCGTCGAATCGCGCGGCGCTTATCGCGCAAAACCCGACATCGAAGCTTTAGACGCTTTTGCTGAACGAACAAAAATCGCCCTTTACTCGGGTTTCGACCCGACAG  
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CAAAGCCGCCGAACCGACGCTTGAAATTCGCGCGAAACCGTTCGCCGCTGGGTAGGAAGCATACGCAGCCAAATTAACCCCTTTCTTGAGCTTTGAAGCGGAAACCGCCCGCATTTATGGCGAAC  
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TTGGCAGGCTCCCAACAAAGAAAGTCGCGCAATTTGTCAATGCCAAAGCGGTTCTGCTCAACGGCAACCGCTGGAAGCCACCAACCCGACCGCGGCAAGCCCGCGCATGCTTATC  
TGTGTGATAGGCAATCAAAACGTTTCCGCGGATACACCATCTCCCGCGCGGGCAACGCAACCACGCGCTTTTGGTTTGGAAA

SEQ ID 1742

MSVIGDLQSRGLIAQTTDIEALDALLNEQKALYCGFDPDTADSLHIGHLPLVLAARRFPQAGHTPIALVGGATGMIQDPSFKAAERSLNSAETVAGWGSIRSQUTPPLSFEGGNAITMAN  
NADWFGSNGNCLDPLRIDIGKHPFSVNAIMNKESVKQRIDRDGAGISFTFEPAYSLLQGYDFAELNKRRAVLEIGGSDQWGNITAGIDLTRRLNQQKQVFGPLPLPLVTKSDGTFKFKTEGGAVVL  
NAKTSPPQYQYQWLKQVADVVVKFLKYPTPLSIEEIGVVEAKDKASGSKPEAQRIIAEEMTRLIHGEALAAAQRISSELSFAEDQSRLTESDFEQALDGLPAFEVSDGINAVRALVKTG  
IAASNKEAFGEVNAKAVILNKGKPARANNENHAAERPDADVLLIGYKRFQKYPITLRGRKNHALLVWK

SEQ ID 1743

TTGGAAATAATCCGATTGCCGCAGAAATGCCGCTCTGAAGCTTTTCAGACGGCATTTTTATCAAAATCAAAAACCCCTGCGCGTCTCGATATGTCGTCATTTCCATGCAGCGGGGAATTCAAACCTGTGCCACGGAACATTATCGGGCAAAACGGTTTCTTCAGTTCTACGTTCTAGATTCCCGCCTGCGCGGGAA

SEQ ID 1744

LEIIRLPOKCRKLSDGIFIKCTPCACRYVVISMOAGIOTCPHGNSGKTVSSVLSRFRPPARE

SEQ ID 1745

ATGAGATTATTAATTCGGT-TTCCACAATAACGCTGTGAAATATGCGGTGGCGGTGCTGACGATGCTGCTTTTGGCGGCAGTCGGGCTGCAGCTTCCGTATAATCGCACTTCACGCCCGAA  
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CGAACCCGACGGCGCGCGGTTCGCGCTTCGCGTCAAGAAACCAAAATCGGATTGAGCTTGGAAAAAACCCTGTGCTCGGATCGGATACAGGTTGAAAAAATGGGTGGTTTCTCGGGTTCGGGATAC  
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AGCGCGCATCGATACCGAATCTTCTCCGACAGCTCTATGTTACAGCAACCGCTATACCAATCTGGATACGAGGAATTTCTGAGATGTCCTTATCCGCAACGCGCTCCATCCGA  
AAACAAACCGCTTCCCTGAAATACCGGTACCGTGGAACCGCTCATACCGTCGATTACCGGAGGCTGACCGCGCATCAATTCGCGCAAGAGAAACAGAAATCTCCGAAGA  
CACCTGCTGGAACAATGGCAGTGGCTCAAACTAAAGAACCG

**SEQ ID 1746**

MDLLSVFHKYRLKYAVAVLTMLLAAVGLHASVYRTFTPENIRSLQSQIAHTRKISPDADIRRRLLPRPTVILKNLITTEPDGGRVAVSVKTKIGLSWKNLWSDRIQVEKWVVSADL  
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FNAGGADAAGLGRADTSFRNLHLTAQIPALALKWNSIKTGTVNGTTFAGGEYARWDGSPKLDKANLHSGIANIGNAEISGSKTFLRLQTNFSLGSLVWSRDLGAPRLHISTLQDITVD  
RLPQFRPI SRLGSLSI PNQWNAELNGTFFDRQPVAAKPKYTRBGAHLEAAALQKINLAPYLDFFRQNGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDMDMETYLHADKDHIALSR  
PFGSLYGGHTGGISIANTRPATYRLQNASNTIQIPLLQDLPGFHSPSGNDVIDL/FASGENRKLQIRSLQSSLSLNSGNAHWGIDHDSILKNGLSGKISGSTPPYRFTLNSEISDGI  
SRHIDTFLPSDSLYVTSNGYTNLDTQELSEDVLRNAVHPKPKPIPLKITGTVDKPSITVDYGRLTGGINSRKEKQKILEDTLEQWQWLPKPEP

**SEQ ID 1747**

ATGCTTCCAACTGTTTACAGCGGCTTTTACACAATTCGCGCATTTTTCATCATTTCCCGACACACCGCAATCTCGAAACCGCTCATTCGCGCGAGCGGGAATCTAGATCTGTCAG  
TGCAGAACTTATCGGGCAAAACCGTTTCTTGAGATT

**SEQ ID 1748**

MLPTVSDGIFYYTIPAIPIPHSRQHRNLETRHSRAGNLDLSVQELIGQNGFLRP

**SEQ ID 1749**

TTGGAGTCGATGAATCGGTGGGCTTACGTCGCCATTCCTCATCAATCAACATTTCTACCGTTTTCATCGAATCCATCGAATCCGCGCTTCGCAATCTGACCTATGCAACCGAACCG  
TCATTCACCGGAATGGGAATC

**SEQ ID 1750**

LESMMKASVRHSQSNISTVFIESBSAPFNLTLNRTVIPTEVGI

**SEQ ID 1751**

ATGCGCTGCAACCTTCAGACGGCATTTTGTGACCTCGCGTTTACGGGCGCGGGCGGGCGCAGTAAATACCGAACCGCTCATTCGCGACACACCGTAATCTCGAAACCGCTCAT  
CCGCGCAGCGGAAATCCGACCGCGCGCGGGAATCTATCGGAAATGACTGAAACCGCGCTTAGATTCCCACTCCGCTGGGAA

**SEQ ID 1752**

MPSEPSDGI FDPAPVYGRGAGAVKYPNRHSRQHRNLETRHSRAGNPDPRRGNLSEMTETPRPRPPLPWE

**SEQ ID 1753**

GTGACGGCGGATTAGCTTACCGCGCGCAACGCATTACCCAGGATTATCGGGAACCAACCGGTGCAAAAAAGGCAAAATAGCACGGTAAGCGATTATTTACAGAAATCCGTAACGATT  
CCATCCACCCAGGCTGTCGCTCGGCTACGACTTCGGCGGCTGGAGGATAGCGGCAGATTATCGCGCTTACAGAAAGTGGAAACACAGTAAATATTCCTCAACAAAAAGGTGAACGA  
AAACAGGGCGAAAGATAAACGTCAGCAATATCTGAAGCGGAAATCAGGAAACCGGTACGTTCCACCGCTTCTTCTCTCGGCTTGTCCGCGTTACGATTTCAACTCAACGAC  
AAATTCAAACCTATATCGGATGCGCGTGGCTACGGGACGCTCAGACATCAGGTTTCGTTTCGTTGAACAGAAACACGACTGTTACCACTTACCTACAGAGTGGTAAGCAAGTCTTA  
TCGTACGAGGTTTCAGCTTCAAACTTCCCATCAGCAAGCGCGCAGCAGCGCGCTTGGGCTTCGGGCGGATGGGCGGCGTGGGCGATAGACGTCGCGCGCGGCTGACCTTGGACCGCG  
CTACCGCTACCACTATTGGGACCGCTTGGAAACACCGCTTCAAAACCGCAAGCGCTCGTTGGGCGTGGCTACCGCTTC

**SEQ ID 1754**

VQADLAYAERIETHDPEPTGARKGKISTVSDYPRNIRTHSIHPRVSVGYDFGWRLAADYARYRWKNSKYSVNTKKNENKGEKINVTQYLKAENQENGTFHVVSSLGLSAVYDFKLD  
KFPEYIGMRVGYGVHVRHQVRSVEQETTTVTLQSGKPSIVRGSTLKLPHHSRSSLRGLFGAMAGVGDVAPGLTLDAGYRYHYWGRLENTRFKTHEASLVGRYRP

**SEQ ID 1755**

GTGTTTCAACACATAGCACCGCGCTGCTGCGCTTTTGTGCGTTTGGCGGCTTCGCGCGCGGAAATTTGCTACTTTTCCCGCTCGGCGGGGCGGACCGCGCGCACACTGTCTATA  
AACCGCAATACCGTTTACAA

**SEQ ID 1756**

VFQHLAPRLRLRVFVRLARSAGNLPFPASGGGRNGRHTVYKPYRLQ

**SEQ ID 1757**

TTGTGCGTTTGGCGGCTTCGCGCGGGGAAATTTGCCTACTTTTCCCGCTTCGGCGGGGCGGAAACCGCGGCGCACACTGTCTATAAACCGCAATACCGTTTACAATGACCGCTGTTTCAAC  
ACACTCCCGAACCAACATGTTTCAACACACCGGACGGCAGATCAAGCACCGCGCTATGTTGCTGCTC

**SEQ ID 1758**

LCVWRVRRREICLLFPFRAGGTGTLNINRNTVYNDRLFHHTPERMNVSTHGTAAHQAPPYVSS

**SEQ ID 1759**

ATGTCCGAGTGGCGGGTTTCAACCGAAAGGAAATACAATGAAATCAGGCCGGGCGGCACAAACCGCGCGGACTTTCGCGACGGGCGCGGTAACCATAGGCAATTTTCGACGGCGTAC  
ACCTCGGACACAAACACATCTTCAAAAACTCCGCTCGAAGCGGACGCGCGGATTCGCCGCTCGTGCCGCTGTTTTCGAAACCCCAACCAAGAAATTTTTCGCACTCCGTACCGGCA  
AACCCCGCGCTGCGTATCAGCCCCCTGCGTACCAACTGGAATTTGCTGGAAGGACGGGTTCGCTCGATGCGCGCTGGGTTTTCGCTTCGATCGGAAATTTTCCGAAATATCCGCGCA  
GCAITTTATCGACCGCTGCTGCTCAAACTTGAATACGCGCTATTGCTGCTGCGGATGATTTCGCTTCGCGGCGGGCGGGAAGGCTGTTTGAACCTTTTGGGCAACAGCGCGATA  
TGCAGACCGAGCGGACCGCTTCTGCTATTGTCGAAGACATCCGACACAGTACCGCGCTCCGCGCAAGCGCTTTCAGACGGCAACCTTTCGCTATCGGAAATTTTGGGCGGAGCTA  
CGTTTGGGGGGCAGGTTGTGACGGCAGAAACTCGGGCGCACTTAAACCGCGCGGACCGCAACATCCGACTCCCGCGGCAACGTTATGCACTCGGCGGCGGTTGCTGCTGCGAGCG  
GACGGCGCATTCGGCACCGCGCGCGCTGCGGCTTCAATCCACCGCTTGTATGCGCGCTGTTCTCAAAAGCTGGAAGTCCAPTTCGCTTCGACTTTCAAGCGGATTGTTACGGAC  
AACCGTTGAACGTCGCTTCTGTCACAACTGCGGACGAGGAAAGTTTACCGGTATGGAAGAACTGAAAGCGGGAATGAAGCGGATATGAAGCGGCAAGTGTG

**SEQ ID 1760**

MSEWRGNRKGNWKIRPGRHNPDPFHGAATVIGNFDGVHLGHKHLQLKLEADARGLPVAVVFPQKEFFALRTGKTPPCRI SPLRTKLELLEBGTCDVDAWVLRFRDNFSELSAQ  
AFIDRLRLQTLNRYLLVGNDFRFGAGREGCFELLAQQPDMQTFERTPSVIVEDIRTSSTAVRQALSDGNLAYAKKLLGHDYVLGGVVHGRKLGRTLNAPTANIRLPGHRYALGCVFVVEA  
DGAFGTRRGVASFNFPTVDGGCSQKLEVLHFDQGLDYQLNVRFLHKLREDEKFDGMEIRKRIEADMEAAKCM



## SEQ ID 1761

ATGTCGCGAGAACATACACACAAATCGGCTGGGTAGGCTTAGGGCAATGGGTCTGCCTATGGTAACGGCGCTCTTGGACGGCGCATCGAAGTCGGGTATACAAACCGCTCGCCCGACA  
AACTGCCCGCATCTCCGCCAAAGGAGCAAAAGTTACGGCAGCACCGCCGAACCTCGTCCGCGCTGCCCGCTCATTTTCCGTATGGTTTCGACTATGCCGCGCTGTGGACATCTGAA  
CGGATCTCCGCGACGAGTATGGCGGCAAAATCATCGTCAACATGAGCACCACTCCCGGACGAAACCTCGCGCTCAAGGCACTTGTGCAAGCGCGGCGGACAGTTTGGCGAAGCACCC  
GTTCCGGATCGTGGACCGCGCCACCAACGGCACATGCTGATTCTGTTCGGCGGCGAGCAAGCGCTTTAAACCGCTGCAAAAAATATTTTCCCTTGTTCGGCAAAAAACCTTCCATT  
TCGGCGATGTTCGCAAAAGGCTTCGGCGCGAAACTCGTCTTGAACCTGCTCTTAGGCATTTTCGGCGAAGCGTACAGCGAAGCGATGCTGATGGCGCGCAGTTCCGCATCGATACCGACAC  
CATGCTCGAAGCCATCGGCGCTCGGCAATGGAATCGCTATGTTTCAACAAAAAATCACTATGGCGAAACCGTGAAGTTCCCGCTGCTTTCGACTCAAAACGCTTCCAAAGACCTT  
AACCTCGCGCTCAAGAGCTTGAACAGCGAGGCAACACCTGCGCGCGCTGAAACCGTGTCTGCCAGCTACCGCAAGCAGTTGAAGCGCGCTACGGCGAAGCAGGAGCTTTCGCGCTT  
ACCTGAAATGGCAGAACAC

## SEQ ID 1762

MSAETTTQIGWGLGQMLPMVTRLDDGGIEVGVYNNRSPDKTAPISAKGARVYGSTAELVRACPVIFIMVSDYAAVCDILNGVRDLGAKIIVNMSTISPTENLAVKALVEAGGQFAEAP  
VSGSVGPNATNGTLLILPGGSEAVLNPLQKIPSLVGKKTFFHGDVKGSGAKLVNLSLIGIFGEATSEAMLMARQFIDTDTTIVEATGGSAMDSMFQTKKSLWANREFPPAFALKHASKDL  
NLAVKELDQAGNTLPAVETVAASYRKAVEAGYGEQDVSVVLKLAH

## SEQ ID 1763

GGCTTACGCTTGAAGAACAGCCTGTCCAGCGACCATGCTCCGCGCGCGCTGCCGCGATATAGAGAAATAGCAAGCAGAACAGCACTCGCGACTCGCGCGCTTGGCAATCGGGAACAAA  
GCAATTCGCGAAGCGTGGCCATAAAATAGGCAACCGCCATCTGCCGCGACAAAACAAACGCGCGAGGCGCGCAACAGCGCCAAACACCAAGCAATTCGCAAAATAC  
CGCAAGCAGCAGCAACCGCGCGGCGAACCCTTTCATGGGGAAGCGAAGATTTTCGACGTACCGTGCAACAAAAACAGGTAGGCGGTACGATACGCAAAACAGAAAGCAA  
AACAGGTTGGATACGTTGACGCAATCGGACAT

## SEQ ID 1764

GFTLEKQVQRPSCAARCRDIEKYAEQHCGLAAGVNRQSLSGSVRHKIGNRHLAGQNKRRARKQAQHQQAADNF\*WIGKQQQPAGRTAHFNGEGEDFRRTVQKQVGGYDTQNRQ  
NRLDTVAIGH

## SEQ ID 1765

TTGGCTACAAATCAGCCTTTTAACTGTTTCAGACGGCATAGGGGTTCCCGCTGTGAAATACTGTTTGAAGGCAATGCCGCTGAAACCGAAATATTTAACAATAGAGAT

## SEQ ID 1766

LGYNQPPNCSGIGVSRCEILFEGQCRLLPKYCNRD

## SEQ ID 1767

TTGATACACCAGTCCGCGCGCGCAGACACGGCTGGCTCGCAGGCGAGTCCAAAGCGTGGTCTGCTCAAAATGACGGCAAAACGCTTTGCTTTCGATACCTGCCAAGCGGAATCGCGCGCA  
AGCGCGAGCGTGTTTTAAACGGATAGGCAACGTCATTCGACGGCGATACTTTGTCTTTGTATTCACCTTCGCTTCGCGCAGCGAAGAGCGCAATTCAGCAGAAATGAACCGGTTTCG  
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AAAGTCTTTTTCGACGGCAATCTGTTTCGCGCGCATATTCGCGGCACAATTCGCGGAAACGGGCTTTAGGCAATCTTTGCCGTGCAAGTTTTCACCACTACTTCGATGGCAGGCGG  
TGGCAGTCCCAACCGGTACATAAGGCGCGCTCAAAACCGGCTTGGGTTTGTCTCGGATAAATATGCTTTTAAAGAAATTTATTGACGGCATGACCGATATGGATGTTCGCGCTTGGCATACG  
CGCGCGCTTCGTGCAAGATGAATTTTCGACGCGCTTTGGCGATTTTCGCGCAGTTTTCGTAACGTTTTCGCTCGTACCACTTTTCAGCCAGCGAGGCTCGCGCTTGGCAAGATTGCGCGG  
CATCGGAAACGGGCTTTCGACGAGGTTGACGCGTTTACTGTAATCGGTCATTTTAACTCTATTCGTAACAATTTTCGCTTCAGACGGCATTTGCCCTCAACAGTATTTCAACAAG  
GAAACCGCTATGCCGTC

## SEQ ID 1768

LHHRVRAGRHGLARRQSPRRGRPNDRKRFADTQACGCGKRDGVFKRIGNVNRRTYFVFHFRFRQRRRAIQAEKLRFRAPVZLAGVDFAEHTHIGFGFBIHQVRIVPVQAHAQAD  
KVFFLFGNLFPGIIPAAQFAETGRFRIHFAVQFPHHFQDAVAVPTRYLRVKTGLGFAADNNVKNFIDGMDMDVAVGIRRAVVFQNEPRTAFQDPAFLVTLVLPAPQPRRLALGKIAA  
HRKRAFEQVDGFTTVIGHFLISIVTIFRFQTALEPLKQYFTTGNPYAV

## SEQ ID 1769

ATGACGGAATTACAGTAAACCGTCAACCTGCTCGAAAGCCCGCTTCCGATGCGCGGCAATCTTGCAAGCGCGAGCCTGGGTGGCTGAAAGCTGGTACGAGCAAAACGTTACCAAAAC  
TGCAGCAATCGCAAGGCGCTCGCAAAATTCATCTGCAAGCAGCGCGCGCTATGCCAAGCGGACATCCATATCGGTATGCCGCTCAATAAAATCTTAAAGACATTTATATCCGAG  
CAAAACCAAGCGGTTTTCGACGCGCTTATGATACCGGTTGGGACTGCCACGGCTGCCCATCGAAGTATGTTGGAAAAATGCAAGCGCAAGATATGCCATAAGCGCGCTTTCGCGGAA  
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ACTCTGCGCTGCGAGCGCGCGGTGCTGCGCGCGCGGACGCTGGTATCAATTAATCGATACGCCCAAGGCAAAATGGTCTGGCGAAGATTTGGCGGAAGCGCTTTGAAACGCTACG  
GCTTTTCAGACGGCATGCCATCTTTCGCCAAACACCGCGGCAAGCTGGAAGCTGCACA

## SEQ ID 1770

MTDYSRTVNILLESPPHNRGNLAKREPAWLKSWYEQKRYQKLREIAKGRPKFILLHDPPPYANGDIHGHAVNKLKLDIIIRSKTQAGFDAPYVPGNDCHGLPIEVNVEKLHGKMDPKARFRE  
LCREYAAEQIARQKDFIRLGLVLDNDNPLYTMDPKTEADTVRMLGEIYKSGVLYRGAKVPQCLDCGSSLAEAEVEYKDKVSPADIVATPKFNVVALAAAFGLAGIEGKAPAVITWTTFFW  
TLPASQAVSAGADVQQLIDTFPKGLVLAKDLAEGALKRRYGFSDGLAILAETTGDKLENCT

## SEQ ID 1771

ATGAATCATCGTTCCTCGAAGCGGATATTCCTATGCTCAACGGCGAACACGTTACCACCGATGCCGCTACCGGCTTGGTGATATCGCGCTCGCGCAGGTTTGAAGACTACCGGCTCT  
GCAATAAATACGGCATCGAGCTTTACAACCTGTCAACCGCGAAGGCAAAATACATTAAGCGAAACCGCTCGTGTGCGCAGGATGAGCGTTTGGAGGCGAATCCCGTATCTCTGCAATGCC  
GGAAGAAACCGGCAACCTCTTGGCAAGCAGCAAAATCGAACACAGCTACGCCCCACTGTGCGGCCCAAAACCGCGCTGATTACCGAGCGACAGGTCAGTGGTTTGTTCGGCATGGACAAA  
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AGGCAATCGAGGCTTGGTTCTTCCCTCGATAAAGCGAATTTAAGCGCGGAAGATTGCGAACATTACGACAACTCCCGGATACCATGAGCTATGTTGACTCAGGCTCGACGCTATTAT  
TCCGTTGTAAGAAACACGGAAGAAATGGAATGCGCGCTGACTTGTACTCGAAGCGAGCAACACACCGCGCTGGTTCCAATCTCTATGCTGACCGGTTGCGCTCATCTCATGGGAC  
CGGACCGGTATAACAGCTGCTGACCCACGTTTCTGTTGACCAAAACCGCGCAAAATGTCGAAATTCATCGGCAACGCTTCGCGCGCGCAGAAATCTATAACGAATTCGGCGCGGA  
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CGCGCGCGCAGCGCGCAACCGCGGTATACCATACCGCGAGCTGCTGTTCTTGTATTCGACCGGATTTTGTGCTTACCGCGCGAAGAGCGTGGGACATCATCGCGCGCGGCGAAGAA  
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GCTGCTTAAAGCAGAGTGAAAGTCGCTGATGAATTCGCTTTCGCGCAAGCGGAGCGCGGCAAAATGCGAAGCGCTGCTGCGATTACACCGCGATGTGGCGCGGTTGCGAGTTAT  
GAAACCGCTGCGCAACGCTGTGCGGAGAAATGTGCGGCGGAGGCGAAGCGCGCATTAACGCT

**SEQ ID 1772**

MNHFFLERIDIMPLNGEHVTTDAGTGLVHTAPAGHLEDYAVCNKYGIELYNFVNABGKYISETPRVAGMSVWEANPVLQWPEETGNLLASSKIEHSYAHCHNKHPTPLIYRATGQWFGVGNDR  
AGSDGKTLRDKAIKAVDDTEFFPPNPGRARLESMEIGRPDWVVSQRQYWGPTMTFFVHKETGELHPNSAEILLEKVAQRIIEKGIEMAWSLDKSELLSAEDCEHYDKLPOTMDVWFDPSGSTHY  
SVVKQRELEWPAADLYLEGSDOHRGWQSSMLTGCASSMGRAPYKQLTHGFFVVDQNGRKMKSIGNVVAPOEYNEFGADILRLMAASTDYSGELAIKSKILLKRVTESYRRIRNTLSFLP  
ANLSDFNPIEDAVQOADMVEIDRYALVLARRIQERLAGGYIPRYAFHFAVKDIVSFCSEDLGAFYILDILKRLYTTKADSRARRSAQATLYHITRSLVLLIAPILCTFGBEAWDIIIGGEE  
DSVLFTNPIEDAVQOADMVEIDRYALVLARRIQERLAGGYIPRYAFHFAVKDIVSFCSEDLGAFYILDILKRLYTTKADSRARRSAQATLYHITRSLVLLIAPILCTFGBEAWDIIIGGEE  
ETVCKRCAENVGGEGETRHYA

**SEQ ID 1773**

GTGGGAATGACGGTTCGGTTGTCTACGGCCCGCTGATTCCCGACACCGGATCGCGTCTGAACCTTCTCAGACGGCATTTTTCATGCGCTCGCCGTTTACAGGCGCGGGCGGGCGGCAGTAAAT  
ACCGGAACCGTCATCCCGACAACACCGTAACTCTCGAAAACCGTCATTTCGCGCAGGCGGGAATCTAGATCTGTGATGTCAGGAACCTTATCGGCAAAAACGGTTCTCTGAGATTT

**SEQ ID 1774**

.VGMTVRLLRPADSPTTTPMPSEPSDGI~~F~~DALAVYRRGAGAVKYPNRHPRQHRNLETRHSRAGGNLDLSVQELIGQNGFLRF

**SEQ ID 1775**

ATGCGCTGTGAACCTTCAGACGGCATTTTGTATGACCTGCCGTTTACAGCGCGGGGCGGGCGCGGGGAATACCGGAACGTCATTCCCGACAATACGCAATCTCGAAACCGTCATT  
CCCGCGCAGGCGAAATCCGACCTGTCCGACGGAACTTATCGGA

**SEQ ID 1776**

NPSEPSDGIFDAPAVYRRGAGAGKYPNRHSRQYRNLETRHSRAGGNPDL SARKLIG

**SEQ ID 1777**

[illegible]

**SEQ ID 1778**

MNPARKKPSLLFSSLLFSSLLFSSAAQAASEGNGRGPYQADLAYAAERITHDYPEPTAPGKNKISTVSDFRNIRTHSIHPRVSVGYDFGGWRIAADYARYKKNNDNKYSVDIKELNKN  
 QNKRLKTENQENGSTFHAVSSLGLSAVYDFKLNDFKFPYIGARVAYGHVRHSIDSTKKITGTLTAYPSDADAAVTVYPDGHQKNFTYQKSNSSRRLFGGAMAGVGDVAPGLTLDAGYRYH  
 NWGRLENTFRFKTHASLGMRYRF

**SEQ ID 1779**

ATGAATCGTCATTCCCGCGCAGGCGGGAATCCGGTCCGTTCCGGTTTCAGTTATTTCCGATAAAATTCCTGCTGCTTTTTATTTCCTAGATTCCCACTTCCGTGGGAA

**SEQ ID 1780**

ENRHSRAGGNPVRSVSVIDKFLLLFISRFPLPW

**SEQ ID 1781**

TTGATGGAATGGCGGGCGGAAGCACACCCTACGGCCCGCGGGATTTCGGCTCGCGGGGAATGACGGGGTTTCAGGTGCTGTTTCAGGTTCCTGTTTAAAGTTCTCTGTTTCGGTTGC  
TATTTTATAGAAATGACGAAATTTTAGATTGCAAGAACTTATCCCTCCGCGCTATTCCACGGAAGTGGGAATCTAGAARTAAAAAGCAGCAGGAANTTATCGGAAATAAC

**SEQ ID 1782**

LMEMAGRSTPYGPPDFRLRGNDGVSGCCFRFLFLSFCGLLFYRND EILDCKNLSPPPSFPRKWESRNKKQOEFIGNN

SEQ ID 1783

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GCTCTAAAGCGCTGCAACCCGGCTGTACATCTTACCTACCTGCGCGCTGCGCGCGTATGTGACATATCGCGCAACGGGTATGTACAGCTCTGATTTTGGTCGAGCTTAAAGAGGGCTCGCGAA  
AGTGGGATAAAGAGTTCTACATCTGTCCAAGGCGACTTCTACACCAAAAGGCAAAAAGGCGCGCAAGGCCGTGCAACCGTTGATATGGACAAAGCGGTTCGCGCAACAGCCCTGAATACGTGTGTA  
TTCAACGGCCACGTAGGCGCTATCGCGCGCGGATACGCGCTTGAAGGCCAAGACGCGCAAAACCGTGCGTATGTACGTCTGGTAACGGCGGCGGAACCTGTGTCTTCTTCCACGTCATCG  
GCGAAATCTTGACAAAGTTTATGTTGAAGCGGCAAACTGATTAACGAAACGTCACAAAGCACCATCTGTGCTCGCGCGGCTTGCATCATCTGTGCAATTCAAAGTCGACATCCGCGGCAA  
CTCACATTTGGTCGACCACTCCATCTTCCGCGCATCTCAACAAAGCGCGTGTGGGCGGCTTGAAGATGAGAGGTCGCGAAACCCCTGCAATCATGACTCAAAATTTGAGTGATACCGCTTAC  
CGGACGAGCGGCGCGGCTTCTGCGCCCTGCGTCTTCCGCAACGGCGGCTGCTCTCTGCGCCGCGAGCTCTGTCATTCGAAAAAGCGGTTTAT

SEQ ID 1784

MKRQALAAAMTASLFALAACCGGEPAAQAPAEETPAASAEAASSAAQATAETPAGELPVIDAVTTTHAPEVPPAIDRYPKVRVKMETVEKTMKMDGGEYEVRYWTFDGDVPGRMIRVREGDTVE  
 VEFSSNNPSSVTPHNVDFHAATQGGGAAATFTAPGRSTSTFSFKALQPLGYTHCAVAPVGMHLIANGMYGLILVEPKGLPKVDKEFYIVQGDFFYTKKGKAQGLQFPDMDKAVAEQPEYV  
 FNGHVGALAGDNALKAKAGETVRMYVGNNGGPNLVSSPHVIGEIFDKVYVEGGKLINEVQSTIVPAGGSAIVEFKVDIPGNYYTLVDHSIFRAPNKGALGQLKVEGANPEIMTQKLSDTAY  
 AGSGAASAPAAASAPAAASAPAAASASEKSVY

**SEQ ID 1785**

ATGCTTGACATCTTCAATTAACTTCCGGGACCGGGCAGGCGTTACACCTTATACGTCCACTTTCGTGTGGCAAGAGTCTCGTGTTTTTAATAAACAAGTCGACGCCACCTATTCTCT  
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ATCCTGCCACCCTGTGTGGTTTGGCGTACGGTTCGATTCAAACTGAAGCTTATGGCTTTTCTTGAAGCGTGTATCGGTGCTCTCGTCCGTAAACACTCGTCACTACTCTCTCGGT  
GTTAAGAAAACCGGATTTCCTTAAGCTTCCACCTACCGGCTTAAACAAGCTATTCACAAGCTTGCCAACCTAACTTCTCCGTCCCCACATCGCATTTGAATCAAGTACAGGAATAT

## SEQ ID 1786

HLAHLQLTFRRHAGVTPYTSFVFLARVLVFLINKSQPPILCDPPGLTEQVLNLRGHTFSRSYGINLPSSFSRVLSSALEPSSCPPVSVCGTVRFKILKLGFSWKRIGICGFVSVNTRHHFFG  
VKKTRICLSLPTGINKLFOOLANLTFSVPTSHINOVOREY

SEQ ID 1787

ATGTCGGGTTTGACGAAACTCGAAGCCCCGCATACGGCTGCATCGCGGTCAAACCGCCGCCGGGGCGGGACGACGTGTCTTCTGTTGTGCGCAAGACGCGGAAGGCAGAATCTTGGGCT  
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GCGTTACCGGTTGCGGACCTTGCGCCACCGCGAAACAGGGCGCCGGCGAGGCGTAATGATTGGGGCTTTGCTGAAAAATTGGAAGCCCGCTGCTTATTGTCGCGCAATCGCGTCTTCT  
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CGTGGCGAACTCAACGCGCGGTGACGACGGCGGTTAAGCGCGCGCGATTGGTGGCGCCCTGCCGAACTGCCGACCTTGAAGGGAACACGGGCGCGGACGTGCTGCCGTGGGC  
CCTGAAGGCGCGCGGTATGTATAACGACTGCAGGCGCGGACCGGCGCGCTGGTACGGCGGTGGGCGCGGATTGAGTTGTCAA

## SEQ ID 1788

NSGLTKLEAPAYGCIKPRGGGHVFFVVGKDAEGRILGLGNQNMVSIIPDPADIDGYFWPSKILGGKAVPSSPABGRYRLSDVAATAKQAGAGEA\*MIGALLKNWPKLLILSAIAFF  
AVSWQLDRAAQYRRGYGAAYSEVSERLKAAVEHAHARKSSAAYQAQKAAREEKERVYVQTKIIEKPVYRNACFDADGVRELNAAVDDGG\*AAARRFGAALPETAAP\*REHGRGRAVVG  
PEGGRYV\*RLQGAARRAGTGVGRGLSQ

## SEQ ID 1789

ATGTCTACCGTTTTCATCGAATCCATCGAATCCGCTTTTCGACACCCCGCCCTACGCAACCGAACCGTCATCCACGGAAGTGGGAATCTAGGACGCGGGTTTGGGCAACCGTTTTC  
TCCGA

## SEQ ID 1790

NSTVFIESIESAPSTPRPYATEPSPFRKWSKTRGLGNRFIR

## SEQ ID 1791

GTGCTTCGGCCCGCCATTTCATCAATCAACATGCTACCGTTTTCATCGAATCCATCGAATCCGCTTTTCGACACCCCGCCCTACGCAACCGAACCGTCATCCACGGAAGTGGGA  
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CAGTGGTCGAAGTGGCGGTGCTGCTGCTGTTTTCAGTATCGGGAACCGCTCAACGTCATCCCTTCGTTTTCGATCTGACGCTGCTGTAACAATCCGGCGCGGCACTTCAAGCTTCTTGGCG  
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TATCGCGGTGCTGCGGCAATGTCATGCTGCTGATACACGCTCATGCTGCTGATCTTATGTTTATTGGCAAAATTTGGTTTATCCCGCTTTAATATTGCCGACAGCTTTATC  
TGGTCCGTGCGGTGTTGGCGGTGCTGACAATATCTCCATCGCAAGATAGCAAAAAACG

## SEQ ID 1792

VLRPAISINPTCLPSSNPNPPFRPPGTPQNRHSHSGSNLGRVWATVLSKPKFGRVRIACAGHTGFKITAFVSGTGKGGFRVEMHSFIRLLKNMSSSVSSKTRYWVLALAAIVLD  
QWSKAVLSSFPQYERVVNIPSPFDLTLVYNPGAAPFLADQGGWQKYFFVLAVAVSAYLVRAILRDEFAALGKIGAAIIGGASGNVIDRLIHGHVVDPLFPWQNWFPYFAPNIADSPFI  
CVGAVLAVLDNIVHRKDSKKT

## SEQ ID 1793

ATGAACGGAACCAACATCATCTTCCCAATCCGCGCGGCTTTCGCGCGGTGTGGATCGGGCAATCAGTATTGTCGAACGTGCTTTGGAAGAATTCGCGCGCGCGGTTCATGTCGCCACG  
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## SEQ ID 1794

MNGKTIILANPRGFCAGVDRAISIVERALEEFAPVYVRHEVVHNFVVDNLRKGAFFIEDLAEPVPGATLVYSAHGVSKAVQJEAERGFVRVDFATCLVTKVHKVBARLDAQDCKEIH  
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## SEQ ID 1795

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ACGTGCGTTGCAAGTAGGACGCGTTGCTCCACCATATACGATGATTCGCGCGATGCCGCCACTTCGCGCAGCGGTTGCTGTTGGACGAATTTGGCGGAACCGCGGTTACGCGCGGATGATGCTTTG  
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AGCCGCGCGGATTCGCAAGGATGATGTTTTCGCTTCAAGTTTTCGATTCGCTGTCAGACGCAATTCAGTTTTCGCTATCTTTCGATGCAAGATGATGTCAGACCGCGCAAC  
ACCGCAGCAGCAGATAGAGTGTGCGCAATATTAAAGCGGGA

## SEQ ID 1796

VLPKHPMALTASTFAQIGFALAAQLGQDEHDAFFRAPPPAHGFMPSAYGQYFPHQHPGRGRACRYADFAPAFKPRALQVGRVHHIRIDSARCRHFAQAVAVGRIGRTDHNHDV  
ALFRQLFDGGLPVGRRIADVFLVRIADIGETRVQRGDDVFGFIDRERGLADIGFVGVSDFFPCHISDRFDQKHFAKCLPHRAFDLGLVPLMFDHDFTLVLIQSGDFLMHFRQASRIK  
YPETALRRFLHLRLRYAVCRINQCRARRHFRQVFDKRAFFAQVHVDFVDDFAHINRRAEFFQSTFDNTDQPIHTGAEARIKDDGFSVHKFCIPCSGDIHVFLSLRWTLISSTAN  
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## SEQ ID 1797

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CATCACCGCATCGTTTCAACCTGTTTTCGCTTTTGAAGAACCGGCAATCCCGGTTGACGACCTTATGCGCTACCGTAATTCGCTATGCGCGGCGAGCCTATTTCGGGCTGCTC  
AAAGTGGTTCGCGCAAGCCACTGAGGCGATGTTTGAACCTGTTGAAAGCGCGCAACAGGCTAAGTGCGCCGCTGCGCGC

## SEQ ID 1798

MSTFFRQTAQAMTAKHIGRPLSELQVIDWQPIBQYLIHQTRYLRDRRGRPAHPLSSMFAVLPGQWHSLSDFEHSILITRIGFNLFCRFDEPGIPGCTFLCRYRKFYARAAYFGLL  
KVGAQSHLKAMCLNLKRAANRLSAPAAA

## SEQ ID 1799

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CATTTGTTGTCGCGATACGCGGCAAGCCTGCATATGGCGGCAACGCGCGCGCGAGTCGCGGTTGCCACCGCGCACATTCGCGGCAACAGCTCTTGGCGCACCGCATCTCGC  
CGTATTGGACGCTTTCGCGAATGCCCGGTTCCTGCGACGATTTAGCC

## SEQ ID 1800

MTTPKLIIFDWDGTLADTTQPIIDTMRSPAEBCGFPPEAERVSLIGYSLPEIRALLLEMPSEAAVADIARTYSAHYLNPNRNMFLFPDAPPCLDKLKAQGFRLAVATGKGRAGLDNAI  
SQATGGYWLATACAGGYEYKPSPEMVFLCGBGLDPKRALVVGDTAHLHMAANAAGAAVGVATGARSREQLLGAPHLAVLDGLSELPGFLARHYA

## SEQ ID 1801

ATGAACCGACTCGACCAACTTGGAAATCCGTATCAACCTGATTGCAATGTCTTTGACAAATGGATCGGCGAGCAGGATTGAATTACAACCTCTTTACCGTACTTTATACCTGGCAACCG  
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CAGCGCGCAACGGTTGCTGCTGCTGACGCAAAAGGCAAGTCCATGCCGCACCTTTAACAGAAAACCGCGAGGAATTCAGCGCAAGAGTATTTCCACATTCGCGCAGCAAGCGCACAAAC  
CGGCTGTTTCCGATTGGATGCACTGGCGAAGTATGAAAAACAATCTCGGAAAAATAAAAA

## SEQ ID 1802

MNRLDQLGIRINLICNVFDKNWIGQDNLWNLFTVLYTLATEGSRQKHIGBESLPRKQTVSGVCKTLAQGLIEWQEBQDRRERLLSLTEKGVHAAPITENAQEFSDKVPSTPGDKRTT  
RLFADLDALEAVMEKTTISENKK

## SEQ ID 1803

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## SEQ ID 1804

MKYKDLRDFIAMLBOQKGLKRVAVHPVSPHLEMTIADRVLRABGPALLFENFVKPDGTRYDYPVLANLFGTPEVAMGMGADSVSKLREIGQTLAYLKEPEPPKIKDAPSKFLPLKDIWS  
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EYQFAGLLRGSRTLEVKICGSLQVPARAEIVLEGVHPNETALEGPGYDHTGYNEQGHFPVPTVERITMRENF IYHSTYTGKFPDEPAVLGVALNEVFPVLLQKQFSEITDFYLFPEGC  
SYRMVAVSMKKQYAGHAKRVMTCWSFLRQFMYTKFIIVDDDDVNRDWNKEVINAVTTRMDPVRDVTVLVENTPIDYLDPASPVSLGGKMLDATSKNPGETDREWGRVVKIDPAVTVKID  
GIWGLGL

## SEQ ID 1805

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## SEQ ID 1806

LGFGCRRKGFFAKASCRNLRLQTAFLPRAGCGNOSGVMSCKKTGQFGQTVQYQEMKAKELFARMCAGGNADCRACVCREHQVVRRIADNQCLFKVESQFAESEYHFGRGFGVFPFRAG  
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## SEQ ID 1807

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ACCGCGCTCTCCCGCTCGCGC

## SEQ ID 1808

LCFIKIEPLSFQMGQFMSVFRINMTAATVLAALSPFVAQQTADLETWHIKGQSYNALATEKNGDYSSLKAAIWMTASIPASPPAA

## SEQ ID 1809

ATGGATGACCGCTCAATACCGCGTCTCCCGCTGCCGCTGAAAGACAAAAACGCGCGCAACCGCAACACCGCTTACGCGCGATTGGGCAACCGGTGATGGAAGCGCT

## SEQ ID 1810

MDDRLLFRVSPCRLLKDKNAEPEQPOHPLRRIGQTRDGR

## SEQ ID 1811

TTGGGCAACCGGTGATGGAAGCGTTGAGACCGAAATCAGCGGTGCGATTACACCGAAATGGCAATCCATGCAAGTTACAGCTATTCGACAGCCAAATCAAAACCGCGCAATCCAC  
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TGCAGGGATGATGACGCGGTTATGCCAGTTCGATGCGATGGCGGCAATACCGCTTACGCGCAAGCTGAAGCTGCAAAATCAATGCGGACAACTTCAACCGCATTTACTACGCGCG  
GTCGCGCGCAGAACCTTTAATCTCCCGGTTGAGGCGCAGCGCTGACGCGCAACCTGCGTTACAGTTT

## SEQ ID 1812

LGRVMEGVETETSGAITPKWQIHAGYSYLSHQIKTANPRDDGIFLLVPKHSANLWTTYQVTPGLTVGGGVNAMSGITSSAGMHAGGYATFDAMAYRFTPKLKLQINADNIFNRHYAR  
VGGTNTFNPISERSITANLRYSF

## SEQ ID 1813

ATGCGCTCACAACCGGATGATGCGATTGCGAAGGAAAAACAGACCGAACCGGACGCGAGACCGCTTTGCGCGTTGCGGTTTACCGCTTCCCGCGAGTCTGACCCACAAGCGCAACATCATGA  
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GTCTGAAGGCTATCCCGTCTCTTTGCTCTGACGCGGCAAGCCTTTTCCCGCGCTGTACACATCATGCACTGCG

## SEQ ID 1814

MRSQPEYGLAKENRPNRQADRFAGSVLPLAASLTHKPNIMKPIPTDTQPAILPOAFETELKSTCGRIYRIQTATLGEHQSEGYFVFLVLDGEAFFPRCTTSCSR

## SEQ ID 1815

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TGAAACCGCGCTATTTCGGACACTCGTTCGGCGCAGTGTTCGGACTCTATTCCTGCTTTCCACCGCTGTTTCAGACGGCATTGGCTGATATCCCCCTGATTTGGTGGCAACACGCGCG  
ATACTCGACTTTATCCGCTTGAAACCGCGCTGGACGGCATCGATGCTGCTCAACATCGCGCAGCTCGAGCGGAGCAGCGGTTGCAAAACGCGGAGAACGCGCATGGCAGGCGCAGG  
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## SEQ ID 1816

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## SEQ ID 1817

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## SEQ ID 1818

MAKSHVSHLENTQAKLHHSNRSLTEAGEBYRQCSYALDILDAAQKAAGTEKPGQLLRVTMPLNFASSQICNLWAEYRERYPEVALELILNDRHVDLIAEGVDLALRVSTLSPS  
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## SEQ ID 1819

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CACCACCTGCGCGACGCGCGCATCCGCTTCAATTTGCTGATGCCAACGAAAAAGCGTGGCGAGGCTTCAAGTGCCTCCGAATGGAAGGTTACACGAGTTCGCGATTGTTGCGG  
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## SEQ ID 1820

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## SEQ ID 1821

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## SEQ ID 1822

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## SEQ ID 1823

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## SEQ ID 1824

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## SEQ ID 1825

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## SEQ ID 1826

LTLMLHLKRGLPDTPAIGIKTKSKTCLNVKSI

## SEQ ID 1827

ATGCCGCCATCCGTCCAAAGAAATCCTGCCCAACGGCAGGCTGCAAAATCCTGTTCGCCGACGAATCCGCAITGACGCTGATGCACATCTCTCAAACGCGGACTGCCGATACACCGGCAAT  
GGCATCAAAACGAAATCAAAACCTGTGTAACGTAAAATCTATTAACTGCTTGCCTCGCTCCGAA

## SEQ ID 1828

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## SEQ ID 1829

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## SEQ ID 1830

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## SEQ ID 1831

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## SEQ ID 1832

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## SEQ ID 1833

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## SEQ ID 1834

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## SEQ ID 1835

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## SEQ ID 1836

NIYCFY\*YNFSTQENMDTLFSLKVFQVVQ

## SEQ ID 1837

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## SEQ ID 1838

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## SEQ ID 1839

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## SEQ ID 1840

VVLSSPTVFRHRPANPLPSVPSVAHRSVPCPPSKSSECTPRRSRCSIPTTGRGVRPKAARPKGLRLYASGSYPSAISKRAPSNSMTSPFRILAVLRISVPLENTSPSAINAFACPL  
SASPANFKRSHKAMYSLSR

## SEQ ID 1841

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## SEQ ID 1842

MQRKSRVAVIPAQARIQTLIYWKCLR/LTAISNFRIPAFEGMAI

## SEQ ID 1843

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TAATCTACTA

## SEQ ID 1844

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## SEQ ID 1845

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VEVAARACQOSEAVCKRVRVEAVVFAA VAADF DARAAEVFKFKQVALGCCROIITTHMGNHRHRAA V DGGDAVCCRPPVAYRAGFAVAQVFGERLLL VFDVSVFDEELGDVGAADHF  
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## SEQ ID 1857

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## SEQ ID 1858

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## SEQ ID 1859

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## SEQ ID 1860

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## SEQ ID 1861

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 TATCTGCGCTTTTACACAAATTTCAAACCGCGCCACGAAATGAAACCGGCGATTACCGCTGGGCGCAGTCAACGGCGCAACGCGCTTTTGTGGGAGAAAGTTCTCTCGGATG  
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 ATTGAAGACGCGGTGATTGTGAACACTGCGCGCACCGTCGATCAGACTGCTGCTTTCGTCACATCAGCGCGCGCGCACCTGTCGGGCAACACGCGTATCGCGGAGAA  
 AGCGGATAGGACGCGCGCGTGCAGCGCGCACGACAAACGTCGCGCAGCGGGTTACCGCGGTGCGAGGCGGTTATCGTATGCGACATCCCGGACGCGATGACGCTGCGCGCAAC  
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## SEQ ID 1862

LKDWQMSKAVKRLFDIIASAGLIVLSPVFLVLIYLIRKNLGSFVPPFIRIRPGDKPKPMVKFRSMRDLSDGILPLDSERLITDFGKKLRATSLDELPELNVNLKGMESLVGPRPLMQ  
 YLPLYNKFNRRHEMKPGITGWAQVNGRNALSWDEKFSQVWYTDNFSFWLDMKILFLVFKVKLIEGISAQGEATMPPFAGNRKLAVIGAGGHGKVARELAALGTYGEIVFLDDRQGS  
 VNGFPVIGTLLLENSLSPQFDITVAVGNRRIRQITENAAALGPKLPVLIHPDVTSPSAIIQGSVVMKAVVQAGSVLKDGVIVNTAATVDHCLLDAPVHISPGAHLSGNTRIGEE  
 SRIGTGACSRQTTVSGSVTAGAVIVCDIPDGMTVAGNPAKPLTGRNPKTGA

## SEQ ID 1863

ATGAACATTACCATAGCCGCCCCCTACTGCTGCTGCCCTCCGAACCGCATTTCAACCGCTTTTGGTATCTGGCAGAACTATTGTGCAATCGCAGCGGTGTTGCTGATTACCAGCACT  
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 GACCAAGCATACCGCTTCGTTCAACATTTTGAAGAAATGGTTGGAAGAACTGCGCTCCGGGCGAAGCAAGCGTCTGCTATTCGCGCTATTCGCGCTGATGTCACCAACCTGCTGTTGGGCAAA  
 CACAAAGCGCGTTTGGTTACAAATGATTGTGATGTCAGGACGATGTCGCGGAGTCTTCTCTCTGCTGCTGCTGTTTTTGAAGAAATCCCGCACAACTACTGCTTTGCTTCAC  
 GCGCAACCGGCTTACGCTACGCGGACGCGTGTGCTGCGGTATCGCAGACCTATCTGACGCGCGCAAGAAAGCAATCCGAAAGTACCGCGCGGAGTGTATATCGGTGCGGATTT  
 TCGCGCATCGCCCCCCCCCGGATTCGCTCCAAACCGTCCGCTTTTCTACTTTGGGACCGCTCAGTTACAATATGACGTTGGAAGCGTGTGCAAGGCGTTCGCAAGCTGTGTGAC  
 GACGGGGAAGCGTGAATTCGACATTTATGGCGCGCGCGCGGATTTGGACAGGCTCAACAAATATGCTGCGACGCGCATCAAGTTTACGGCTTACCTTACCGCGAAATGATGTGCG  
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 GAAATCGTCCGCGCTTACGCGACGACATTTCTATCGGAAATCGTCAACTGATTGAAGATGGCAATGAG

## SEQ ID 1864

MNITIAAPYCSLSEPHFNRFWYLAELLSQSHDVLITSNFKHYDKSFRFPEDAKAASQGRILKVMLEESGYSKNVSLGRVTSHHRFVKHFEKMLENCRPGEQDVVYSAYPLIATNLLIGK  
 HKARLGYKLVDDVQVWPEFSVVPFLKIPHNLLPFASRANRAYRYADALVAVSQTYLDRAKEANPNVPGEVVYIGADFAAIAPPPRFRSKTVRFFYLTGLSYNDVEIVCKGRVRLID



DGENVELHIMGGGPDRLRKQYACDGKIFYGYTPYAEHMSVAKGCDIAVNAHSHYAEQSTNKLSDYNALQKPILNSQVHDEVAEVLTLPLHENYRSGDVGFPQAARDILKRKNDPFQSD  
 ETVRRFRHDISYRKIVNLIERIANE

**SEQ ID 1865**

ATGGGCGGCATPATCTGGCAGGCTGCATCTCTGGCCACCAGGAAAAATTTGCACAAACTGTTTCATTATTTTGAAAAACAAGGTTTCCCAATTATGAAATCATCTTGACTACTTCTATGTCCG  
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CATGTGCGAAACCTTATGCTCCGACGACGAAATCTACCGCACCAACCATGGCTGCGTACGAAATG

**SEQ ID 1866**

MGGISGRLLHPAPPEKPAQTVSLFEKTRFPINKILLTSMGLGGTETATVRLGRLLKRRHGHDIILASDGPVFGVEAQASGIENQVPDVFYRGGLAGLYKSTFAYARMLRREQPDIDCQAR  
VVPACALAAKIVSPKTKIICHSHGLDAATYPTAKLPDKLGAYITIGNCKHEREKILRHGFPAGRIAYAYNTPPEFHFRTEKECAVLGTLRLDVTVAHVLMDLTKKRVGRNTPVRLNHA  
GIGEEENDNLKAQAKRLGIEDKVFLLGGVRDLTCGYFKEVDILVNTPHCVGDHGAGVGNLLEAGLYDTPVWTYNMAGISEMVTGQTGYCIPPGDDEAFIEAVDTLKHPELRSQHGKALHK  
HVETLCSDDIYRTHAAAYEH

**SEQ ID 1867**

TTGCTATATAATAACGCCGATAAAAAACGGCCCGTTTCAGACCGCCGCCCGCCCGGAAAAGCGCAACCCGGACTGCCGCACCCCGCCGGCAGCCCGACGGCC

**SEQ ID 1868**

LLYNNADKKRPVOTAAARPEKRNPDCTPPAAATA

**SEQ ID 1869**

ATGTGGAAAATGTTGAAACACATAGCCAAAACCCACCGCAAGCGATTGATTGGCACATTTTCCCGGTGCGACTGGAACAACTTTTGATGCTGGGGTATCCGGTGTTTGCGCGCTGGGCGA  
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ATTATTCGGGTGCGGACATCTCTGTGATGTTTGCCATGAGTTTGGACGATGTGCGCGGATTCGTCGGAACAATATCCAAATTGAAAGACATCGGACACCGGATAGAGTGGTCGGAACGGA  
ACATCAAAGGCGCAACT

**SEQ ID 1870**

MWKMLKHIAIKTRHKRLIGTFSPVGLNLLMLGYPPGGAINAVIAGRVQALLYALVVFLLWLVLVGAARRIADTRTFTTRITYTEIAVPVLEQRQRPVPSAVTARVALSREFVSPFEEHL  
 IAATSVSVISFGACIMLLVLEFVWGVSAVGILALFWLLPRFAAISENLYPRANSLERDNEFIRKGDERQLYRHYGLVSRLRVLISNREAFGYLCVGAAMGILPGFAFVMMTLKGYGSAGH  
 IYSGVTYLMFAMSLIDVPRLEVOYSNLKDIGORIEMSERNIKAGT

SEQ ID 1871

TTGGTGTTTCGGGCGGCGTGATTCAAATGTAATTGGTATCCTGCTCGTTAAATTGATGATGTTGGCGGTTTCGGCAGCAGCCTGTTTTCGGGGCAGACGGTGATTGAAAAAATTCGCGGGC  
TGACACAGCCCGACCTGCCTGAAAAAGCCGTGCGCTATACCGCCCGGTAACGCAGGTTTGGTGCCTATTCCTTTATTGCCAACGGGACGCTTGCCGCTTTGTGGCCCGGTTGGGGCGATA  
TGATTGGTGGGCGGTTTATACAGGCGTGATTGCTATGTATTGATGGGGATGCTGTTTTCGCGGCGAATGGCTTTACCGCAAATCTTGTGTGAAAGTC

SEQ ID 1872

LVEGRRDSMYWYPVLVNLMMIAVFGSSLPAGOTVIEKLARLOOPLPEKAVRYTRRVTVQVHCVFFIANGTLAALLARLGRYDHWAVYTGVLAYVLEHGMIPAGEWLYRKLVLKV

SEQ ID 1873

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SEQ ID 1874

MDYKEILIGYAGSISAVLAVIILPLLWYPIPPADDIGRIVLMQTAAGLTVSVLCGLGDAQVREYYAAADKDTLFTKTLFPLPPLFSAIAAALLSRPSLPSIILFSLDDAAAGIGLVLPFL  
SPLPRFLRLLVLVRMEGRALAFSSAQVLKLAAILLLPLTVGLLHPFANTSVLTAVYALANLAAAFLLPQNCRCLKAVRRAPFSPAVLHRGLRYGIPLALSSLATWGLASADRLFLKKYAG  
LEQLGVYSMGI SPFGAALLQSIFSTWTFPIYFRAEENATPARLSATAESAAALLASALCLTGIFSPLASLLPENYAARVFTVVSCHLPPLFTYLTISGIGLVVRKTRPIALATLGA  
LAANLILLGLAVPSGGTRGAAVACAASFWLFFVFKTSSCHLHPLKRLPLVYHLLTFLCLASSAAYTCFCTPANYPFLFAGWAAVYLAGCILHRKNLHKLPHYLKKGFPFL

SEQ ID 1875

ATGTTTTCGGACACAAATATATCATGATGAAAAAGCCCTCCGACTTGC CGCTTTGGGGCGTTTTCACATTCACCAACCCGCGCGTGGGTGCTTATCGCACCGGACGCCAAATG  
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 CGGACGCACACCGCCCTGCGCGGAAGCCCTGCTGCGTTTCCGCGTAACACGCGTGTGCGCCCATGCGCGACCCCAACCCGCGGTTCAGGCAAAGGGCTTGTCTGCTCAAAGCAGCG  
 GGCATCAAGACGGAATCGGCACTPACTTGAAAACAAGACACGCGAAGCTCAACCCGGGATTTTTATTCGCGCATCGAACCGCGCGCCCTTTGTGCGCCTCAAAATGCGCGGTTCGCTGGAGC  
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 TCGCGCTCTTTTCGGCAAGAGTTTTCGCGCAAACTCATGTTCCGAGCAGGCTCGCAACTCATCCGCTATTTTGGCGAAAATTTGGCGGACGAAATCGTCTGTACCGTTGCCCAAAAT

CCTCGCGCGCGCAAGACCTGTTTCCCTGCCGAAAACCGTGCCTCCCTTCCGACACCGCTTTCAGCGAAATCTCGGACACGACATCAAAACCGTGTTCGGG  
AAAAACGGCAACGCTTT

**SEQ ID 1876**

MFSDWIMSMENALRIALGRFSTSPNPRVGCIVAHGSQIVGQGHVHAGEPHAEVHALRQAGEMAAGATFVTLBPCSHYGRTPPCAEALLRSGVTRVVAAMRDPNPPVAGKGLVLLKAA  
GIKTECGLEENKARILNRGLSRIERRRPFVRLKCAVSLDGKTAISDSSFWITGEBEARADVQVLAESCAVLIGITVLADNRLNVRAPPTLRQPARIVLDSRLRLPNSHLVFDGQSP  
TYIATLERDEKILRPYREHAHRIIMPSETADGKIDLHILMRLLADESGPEILNVEAGSELTSAPLAENLADETVLYRSPKILGGGKDLPSLPENRAALSAPPIAMTPVSSEILGHDIKTIVFR  
KNGMAP

**SEQ ID 1877**

ATGCCCGTTTTCGCCCAACCCCGACACCCGCTTGTGATTCGCGCTGATGGAAGAACGCAACGCGTGCCTCCGCGCGCGCGCAATGCCCGGCTGCGGCAACGCTTCGGCACGCTCGAA  
ACCGCGCAACTCAAAATGCCCGCTCATCGGTCCGGACAAGAACGCTTCGCCCTTCAATGCACAACGCTCCGCAACGCTGACCGCGCGCGCGGAAATCCGCGCTGACACCGCAAC  
AGATCGACGAAACCGTCCGCTGACGGAACACAGGCTCTACACTTCGGGTGACGCGACATATCCATCCGAACTTGTGAAATCGTGTGAGGAGCTGTTCGGGCAAAACACGGAAGC  
CGCGTCCGTTTTCGCCCGCTGCACAAACGCTTCGACACCGCGGAACATTTCCGCTCGTGGCTGCGCAAGCGCGCAAAACCTGATTCCCAACCCATAGTATACGATACGATATCCATATGTT  
TTCGGACACAAATATATCCA

**SEQ ID 1878**

MPVLRPRPHRCRFPAPDGRTPRRPFPMPRLRQTLRHARNRRITQNNARRHRSQETALQCTTPQRPDRRRPKIRPDTTRDRNRPPDGTQALHFGSARHILIRTCRNRAGGAVRAKHGS  
RRPFRPAPQTLRQGTFRVLVAGARRQNLIPPTHDTVSLCFRTQIYP

**SEQ ID 1879**

GTGCCGAAGAAGGCTGGAATCGCCCGCGCGCGCGCTATCGGTTTTCAGCTTCAGACGGCATCAGGAAGAAACACCATGAAATGCCCGCTTTCGCCCAACCCCGACACCGGCTTGTG  
ATTCGCGCTTGTGGAAGAACGCAACGCTGCGCGCGCGCGCAATGCCCGGCTTTCGCGCAACGCTTCGGCACGCTCGAAACCGCGCAACTCAAAATGCCCGCTCATCGGTCCGGA  
CAAGAAACGTTTCGCGCTTCAATGCACAACGCTCCGCAACGCTGACCGCGCGCGCGGAAATCGCGCTGACACCGCAACAGATCGACGAAACCGTCCGCTGACGGAACACAGGCTC  
TACACTTCGGGTGACGCGACATATCTCATCCGAACCTTGTGAAATCGTGTGAGGAGCTGTTCGGGCAAAACACGGAAGCGCGCTCCGTTTCGCGCGCTGCACAAACGCTTCGACA  
GCCCGAACATTTCCGCTCGTGGCTGCGCAAGCGCGCAAAAC

**SEQ ID 1880**

VPKAKWSPAPPAYRFDVQTASGRNIMKCFCAHPDTRVDSRLMEERNVARRRRQCPGCGKRPQTLTAELKMPAVIGPDKRSFPFAQRLRNDLTAARKSALTPEQIDETVRLFEHRL  
YTSQRDISSELVEIVLEELFGQNTFAAVRFAALHRFDSPEHFAWLAQGGKT

**SEQ ID 1881**

TTGCGACCATCTGAATCATTTGGACAAACTATGTGTCAACTGCTGGCATGAATGCAATACGCGCAACCATATTTATGTTTTCCTTTGAAGGCTTCGCGCGAGGGCGGCATTACCGACC  
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GGAAACGCTTCGCGCCATCCGCAAGGCTTCGCAAGGCTCAAACTCGCTGCGCAACCAATCCCTTTATGCGGAAATGTGGGCGGCTACTGGCTGTTTCCCAACACGCGGCTTTG  
GTCGATTTTTCGCGCAACGGAAGGAAATTTTCACCCCGTGGCGCAACCAATCCCTTTATGCGGAAATGTGGGCGGCTACTGGCTGTTTCCCAACACGCGGCTTTGCGCGCGCTTCGCGACG  
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CGTCCGCAAGCGCGCTTCGCGCAAGGCGCGCTGCTGACGACGATGTAATGTCGATTTTTCGCGAAGTAACACCGCGGACGACGCGCTGCGCTTATCTCCACCGTCCGCGTACTGCG  
GATGAATCGTGGTCCCAACTTCCGCTGAACGAACTGCTCATGTTCCGCGAAGCAACATCGTCCGCGACGACGCTCCGCAAAATCCCGCTTATATAGTCCGCAAGGCGCTGGAATCG  
CCGCGCGCGCGGCTATCGGTT

**SEQ ID 1882**

LRPSEFQGTMCQLLGMNCTPTDINFSPFEGFRRRGGITDHDGFGIGFEGKGVRLFHDDKPSANSVPADLVRAQIKSENVAHIRKASQGTSLANTHPPMREMGGYWLFAHNGHL  
VDFFPQGEFFHPVGTTFDSERAFCHILNRLRTRFAARPDDDTLFDALAGLTHEIRKFGLFNMLSDGISLFAHASTLLHYTVRQAPPKARLLDDDMVDFEVITPDDRVAISTLPLTR  
DESWSQLAVNELVMFRGNIVRHRPENPVYMSAEEGLEIARAAGVSFV

**SEQ ID 1883**

TTGAAATTCAGATTCCCGCTGCGCGGAATGACGGCTCAAAAGTTACGGAACGAAAACACCGAAACCGGACAAGTCGATTCCCGCTGCGCGGAATGACGGAATCTTAAGTTTCC  
GCTTTGTTTCTGTTTTCGCGGAA

**SEQ ID 1884**

LKFIIPACAGMTAQKLRNEKQPKPKDSRLRNDGILSPRLCLFSRE

**SEQ ID 1885**

TGTTCCTCCATTTATCCCGGCAAAACAGAAAACAGAGCAAACTTAAGATTCCGTCATTCGCGCGAGCGGGAATCCGACTTGTCCGCTTCGCTGTTTTCGTTCCGTAACCTTTG  
AGCGCTCATTCGCGCGAGCGGGAATCTGGAATTTCAATGCTCAAGAATTTATCGGAAAAACCAAAACCTTCGCGCTAATTCGCGGAAAGTGGGAATC

**SEQ ID 1886**

LFPIIPAKTENKGNLFRHRSRAGNPCTCPVSVVFRSVTFEPSFPRRRRESGLSMPQEFIGKNQNSAVIPAKVGI

**SEQ ID 1887**

GTGCTTCAGCACTTAGGGAATCGTTCCTTTGAGCGGGCGGGGCAACGCGGTACCGGTTTGTGTTAATCCGCAACAGCAACCTGTGCGCGCTATTACCGGAAAGCGGGAATCCAGT  
CGGTTCAGTTTCGCTCATTTCCGATAAATCTCTGCTGCTTTTCATTTCTAGATTCCCACTTTCGCGGGAATACGCGGGAAGGTTTGTGTTTTCGATAAATCTTCAGGCAAT

**SEQ ID 1888**

VLQHLRESFPLSRGATPYRFLIRNSNFAVITAKAGIQSVQFRSFPINSCCFSLDSHFRNGYGRVLFVSDKFLRH

**SEQ ID 1889**

ATGCCGCTCGAAACCGCGCTCCCTTTATGCGGACACGCGCGCGCGCACACGCTGCTGTTTCCGCCAAAACCTCCGCAATCCGCGACAACGCGCGCTTATGCGCGCGCTTGCAGAG  
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AACCAAGCAACTGCGCGCTGCGCGCTCAGGCAACCTGCGCGGATTCGCGCGCGCTTCAACCTTCCCGCGCGGAGGAGATGTTTTCGCGCGGCTGACGCAATTCGATGCGCGCAATC  
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**SEQ ID 1890**

MPSETALPLYADTRAHTLVWFRQNLIRIDNAALCAVAAGSPVIGIWDIAETDNPRRAAFYRQSAEALQGLARRGIPLYTAASPAVLVRLAVRLNIRAVIADESHTPADKLADNALMH  
ELDKHGLIALTFVNDRSVFGKTDLTDPNGTAHTDFNRYREVWLDLP SKQPPAGSDFLAATYRQPPFNLPAPPALSDGIFLPQNGGFTAAWRQWRRLLEQAASYSVLKDFPSRKNTSLMGA

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NQNWRLLAASRFTCPDIAAASYRTDPDGTFLKRHIPELAHLSADTVHTPWRFACSVDTGYPARPVAV

## SEQ ID 1891

ATGAAACCCGGTITTTTTCGGACATATTTTTCACCGTATTAAGCATTCCTATCCCGCTTTGTGGTATAGTGGATTAAATTTAAACCGGTACGGCGTTGCCCTGCGCTTACCTATTT  
GTACTGTCTCGCGCTTCCCGCCTTGTCC

## SEQ ID 1892

HKPGFFGHIFLTVLSIATPALHYSGLMLNRYGVASPCRTICTVCGFAALS

## SEQ ID 1893

TTGCAGGGATTATTCGGAATAACGACAACCTGTCCCGCGTCATTTCCGCGCAGATGAAATTTGGAAATTCAAATACAGGAATTTATCCGGAATATAGCGGATTAAACAAAATCAGGA  
CAAGCGCGGAGCGCAGGCGAGTACAAATGGTACGGAACCGGTTCGCTTGTCTTACGACCT

## SEQ ID 1894

LQGLIRNDNL SAVISAQMEIKFKITGTIPEYSGLTIRRRRRRQYKHYGTGSPGASAP

## SEQ ID 1895

ATGTGTTGCCCGCGGGTTGACGCACGATGATGACTTCCATCATCATCTCCCGGAAAGCGCGCATCCGGTTATCCATATTCAGGGATTATATCCGGA

## SEQ ID 1896

ECRAGLTHDDDFSPSFAKAGIRLFHIAGTTYPE

## SEQ ID 1897

ATGAAACACCTGACCGTACACACCGCTTCGCACAGCTACCCCATCTTTATCGGCAACGGGCTGCTCCGCGAGGCGGAGCGTCTCAAACCGCATTTGGGCAACCGCGCCCATCATCA  
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CAACCTCATCTTTGACGGCGTATGCAAAACCGCGCGAAGCTAAACACCGCTGATTGCGCTGGGCGGCGCGGTATCGGCGACATGGTCCGGCTTTGCGCGCGCCACCTTACGAGCGCGC  
GCGCGCTTCAATCAATACCGACACGCTGTGAGTCAGTCCGACTCATCGTGGCGGAAAAACCGCATCAACCAACCGCTCGGCAAAATATGATCGGCGCGTTTATCCAGCGCGAG  
CGGTGCTTGCAGATTGGACACGCTGCACACCTGCCCGCGCGGAACTGTCGCGCGGTATGGCGGAAGTCATCAAAATACGCGCGCTCGGCGACATCGGCTTTTGAATGGCTGGAACA  
GCATATGCCGAACCTGATGCCACTGCAACCGCGCGCCCTCACCAAGCGGTGTACCGCTGCTGCCAAATGAAGCGAGACATCGTCCCGCAAGACGAAACCGAAGCGGATACGCGCATGG  
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GCAAAACCTCCCGCGAGATACCGCGCGCTCGCGCGCTGCTCGAAGCGCGGAGTCCGCTCCGACCGCGCGGTGTTCCTTTGAAAAATGGCTGCGACATATGAGCCAGCAAAAA  
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## SEQ ID 1898

MKTLFVHTPSHSYPIFIGNLLPQAGSLLKPHLGKRAAIITNETVAPLYLGTLPALDAAGVSHPSIILPDGEAHKNWTLNLIPDGLMQRNRAERTLLIALGGGVI GDMVFAAATYQRG  
APFIQIPTLLSQVDSVSGKTAINHPLGNMIGAFYQPAVLADLTHTLPAELSAEMAIVIKYALGDI GF FEWLEQHPMELALERAPLTQAVYRCQMKRADIQAQDETEQGIRAH  
LNLGHTFGHVAEMGYVWMLHGEAVALAARLSQGLKRTSAADTARLAALLEAAGLPSAPPVFAFEKWLAEHSHDKKVS GGIMRPIGLNRLGEAVITKITTDTILRLTLQPYL

## SEQ ID 1899

GTGATGAAAACTTTAACCGCAAACTCATCTCATCGGAGTATGGGCGCGGCAAACTACGCTGGGCGCGCAAAATGGCGCAGCGCTGGATTACCGTTTTTACGACAGCGATCACGAAA  
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CACCGCGCGCGCGCGGTGTTAAAGAAGAAAAACCGCGCTTATCCGCAAAAGCGGACGCTGTTATCTGCAACCGCGCGCGGAAACCGCTGCTGCAACCGCAGCGCTCGGACAAACAGC  
CGCGCTTGTGCAAGTTGCGGATCTTTGGCGAAATGCGCGAACTCTACGCGCGCAACCGCGCGCTTACCGCAAAACCGCGACTTTACCGTAGAATCGGCAAACTGCGCGGAAACCG  
TGCAAAACCTGCTCAAACCTTATCCCA

## SEQ ID 1900

VKNFNGKLLILGLMAGKTTLGRQMAQRLDYRFDSDHEIAAAAGVPIPTIFEMEGEQFRSRETAILKLLIVLPHIVLSTGGGAVLKEENRALIRKSGTVVYLHAPPETLLERTRCDNS  
RPLQVADPLAKRLRELYAARDPVYRQTADFTVESANCRETVQTLRLRLR

## SEQ ID 1901

ATGTTTGAACCGCGCGCTTTCGCGGCGGAGGTTTCGGCTTGTGGGTACGCGGGATTTTATACGAAATCGGCGGCGCGGTAGCTTTTGAAAAATACCGCAACATCCCGAAT  
TTTCTGATTTTAAAGAAAA

## SEQ ID 1902

MFDPFAFRGGRVRACRVTAGFYTKSAGRRYVWKNNPITPNFSDPKEK

## SEQ ID 1903

TTGTTAATCCGCTATAGTATTGATAAATATTTATCTCAATATATTCAATGGATAATTGTTTACCTAAGCAAGATAATTGCCCTTTCTGACAAAT

## SEQ ID 1904

LLIRYSIDKHIIIFNFIHIVLSKDNCLPLTH

## SEQ ID 1905

ATGAGGCAAGAAATTTATCGGAAAAAACCGAAGTTTAAAGACCTAGATTCCCGCTGCTCGGGAATGACGGGTGTTTCGGGTGCTGTTTTTGTGGAATGACGAGGCTTTGGATTGCG  
AGGATTATCCCTTCCCGCTCATTTCCCAAAAGTGGAAATAGAAATGAAAGCAACAGAAATTTATCGGAAATGACCGAAAC

## SEQ ID 1906

MRQEFIGKPKFKLDLSRLGNDGVFRVAVFCNDLDCRDLSPSPQKWSRNEKQEFIGNDRN

## SEQ ID 1907

GTGCGGACGTGTTTCGGATTTCGCGCTGCGCGGAATGACGATTTCGGTATTACTGACGATTTCATCGGCGGTAGGGTGGGCTTACGCGCACTAATTTACCGCATCAAGGTTTTGGGGAA  
TAGGGCTAATCGCGGTTTTGCTTTTGGCGAAGTTGGTGGAAATCGCGCGGTGAAGCACACCTACAGTCCACCTACAACCATCTTACGATCCGCTTACGATTTATCTTCCG  
CTGCCGATATCGCGCATTTCCGCAACGCGGGAATC

## SEQ ID 1908

VRTCSDFLRGNDSGITDSSGRRVGFSLISPHQGFVIGVTRFRFLAKLVIGIGLKHFTLQSTLQPLIRIRLTHLSFACRYAVIPAQAGI

## SEQ ID 1909

TTGAGCGCTCATTTCCCGGAAATCGGAAATCCAGTCCGTTTCAGTTTCGGTATTTCCGATAAATTCCTGTGCTTTTCATTTCTAGATTCCCACTTTTGTGGAA

## SEQ ID 1910

LSRHSREIGNFVRVSVIDKFLLLFISRFPLLHE

## SEQ ID 1911

ATGACGGCTCAAAAGTTACGAGACGAAAAACAACCGAAACCGGACAAGTTGGATTCCCGCTGCGCGGGAATGACGGCATTTCCGTCGCGCAAAAGCATAAAGAAAGGCATATGCTG

## SEQ ID 1912

MTAQKLRDEKQPKPKLDSRLRGNDGISVAARSIKGHNL

## SEQ ID 1913

ATGTTTTACAGCATATGCCCTTTCTTATGCTTTTTCGCCGACCGAAATGCCGTCAITCCCGCGCAGCGGGAATCCAACTTGTCGGTTTCGGTTGTTTTTCCTCTCGTAACCTT

## SEQ ID 1914

MFYSICPFMFLPAATEMPSFRRRESNLSGFGCFSSRN

## SEQ ID 1915

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TTTCGACCAAAAGCTTGAATACGAGGCTATGTTGAAAAACGCGCGCACTTTGATTGTCGCGGTATTATGAAGAAAAACAGGCAATACCGTGAACAAAGTCCCGCTGTGGGCGACAT  
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## SEQ ID 1916

MNTKLIKII SGLFVATAAQTASAGNITDIKVSLSNPKQIKVVSFDEIVNPTGFTVSSPARIALDFBQGTGISMDDQVLEADPLLSKISAAQNSSRRLVILNLNKPQYNTFEVRGNKVM  
IFINESDDTVSAPARPAVKAAPAAKQAAAPFESVSVSAPFSPAKQAAASAKQTNIDFRKDGKNAGII ELAALGFAGQPDISQGHDI IYTLKNIHTLPALQSLDVADEFKTPVQK  
VTLKRLMNDTQLIITTTGNWELWNKSAAPGYFTFQVLPKQNLSESGVNNAPKFTTGRKISLDPQDVEIRTILQILAKESGMNIVASDSVSGMPLSLKVDVWDALDVLVQARNLDMRQ  
GNTVNIAPRDELLAKDAFLQAEKDIADIGALYSQNFQLYKNVEEFSILRLDNADPTGNRNTLVSGRGSVLIDPATWILIVTDTRSVIEFKRILIDELDVPAQVMI EARIVEAADGFS  
RDLGVKFGATGRKRLKNETSAFGWGVNSGFGGDKWEAQTKINLPVAAAANSISLVRAISSGALNLSASBSLSKTKTLANPRVLQNRKEAKIESGYEIPFTVTASGGGNSNTFELK  
AVLGLVTVPNTIPDQGIIMTVKINKDSPAQCSAGNNTILCISTKSLNTQAMVENGGLIVGGIYEENGNMTLTKVPLLDIPVIGNLFTKRGKTRRELLIFTFRIIDTAGNSLRY

## SEQ ID 1917

ATGAACACTATGCCCTTACTCATCAGCTTCTTGCTCTCTCCGCGTGTCCCAAAATCTCGAAGACCTAAACGAATGGATGGCACAACCGCGAGCGCAAGCCAAAGCAGAAATCATACCTT  
TCAAGCACTTACCTGCCGCTTGCCTGATACAGCCCGCGCAGCTTACAGGCGCAAGCAGCTTCACTTCCGCGCATGGAACCGGCCAAAAAGGGGAAAAATGCCCGGACACCA  
GCGTATTAAAGAAACGCTGGAATAATCAGTTTGGAAAAATAGCGTTATGTGCGGCAATTTGAAAGTCCGACAGAAAGTCTCCGCTTCAATCGAGGCTGAAGTTATGTCTACACTGTGCGT  
GTCGCGCACTATTTGGGACAAAACTACGCTAGAAATCGAAGCATTACCGACGACGATCATCTGAACGAGCTGATAGAAGACAGCAGCGCACTGGGTTCCCGTAAAGCAGAACTGC  
TGTGAATTTCTCCGACAAAAACCGCAACAGCGGACGCTCCGCGAAGCAAAAT

## SEQ ID 1918

MKHYALLISFLASACQNSSEDLNEWMAQTRREAKAEIIPFQAPTLPAVPVYSPQLTGPNAFDPRMETAKKGENAPDTKRIKETLEKPSLENMRYVIGLKSQKVSQFIEABGYVYTVG  
VGNVLQNYGRISITDDSIILNELIEDSTGNWVSRKAELLNNSDKNTBQAAAPAAEDN

## SEQ ID 1919

ATGGCTTCTAAATCATCTAAACCAACTTGGATCTCAACAACTTCACTGCTCAACCTTCTGCCAGGCTTTTATCGCCTGCTGCTGCTTCCCGCGCTGCTGGGGCTCGGTTATGCCG  
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TGCCTCAATCCGCTTACCTTCGATATCATGTTGAACAGCTCCGACAGATCGAAGAAATTCCTTGGTTCAAGAGCTTCACTAGGCGGCTTCGAGCAACGCTCTGCGCTTGGAGC  
GTTATGCCCAACCTTCCGCTAGATGACGCTCCCATCAAAAAATTACCCTATTCATTTCCTTACCGGAAATTACGACAGATCAGCAATTTACCGCGATGTCCGCGAGTCTCTCCGAA  
TCATTACCTTGAAGTCTGAAATCGCCCAATCTCCGAAACCGCGGCAATCTGACGCGCAAGAGCAGTATCTGAACTCAGCGCATTTGCCACCCTTACCAAGCAAAATCCGTAGA  
AGAGCTTCCGCGCAAGCGGCACAAAATGCCGAGCAAAA

## SEQ ID 1920

MASKSKTNLDLNLHLNLPLRFLIALLVAAVLGLYAGLFKQSMESLEBEYAKETELKNTYKQKSIDAASLNNLRDELASIRSTPDMILKQLPTDAEIPNLVQELHQAGSSNGLRLDS  
VMPQPPVDDGPIKPLYSISITGNYEQISQPTRDVGSLRIITLESILKIAQSPENGGNPDGKSSILNLSAIAATYQAKSVBELAAEAQNAEQK

## SEQ ID 1921

ATGGTTTGGCAGCCCGCAAGCTGCAGGCTGAAGATTTCGCAATGTCCGACCGTCAACGACGTGCTACAGGCGGTTTGAAGATTACAGCCCGC

## SEQ ID 1922

MVVAARKLQAEDEFNRVTRVNDVVQAVLKIQAG

## SEQ ID 1923

ATGAACAAATTTAATCAAAATCAACCTCTCTCCCTACAGGGAAGAGATGAACAAACGCAACAGCAGCAGTTTAAACGCTGATGTACGGGCGCGTCTGACGGGCGTTGCCCGCTTGGG  
CAACCTTACCTGTTTATGCACAATATGATCAATAACAGTTCGGAAGAAACACGCTGCTGGAATCTCCATCGCACACTTGGATACCGAGCTGTGCGAAATCAAAAGCTCAACAGGAAAA  
AGATGCCCTTCTGATTAAAGAAAAACAAATCGAGGAGCTCCAGATCAAAACGCTTCAAGCCGCAAAATCTCGACAGCTGAAATGAGGCGCTCCCGGGAAGCACTTACCTAACCTCGCTG  
GATGCCGTTACCGCGGACTCTTTATCGGCTCAGCGGAGGACATCCAGCGACAACCGGCTTGGCGCCATGATGAGGCGGATGCCAATACCGGCATATTAAGCAACCCGAAATTTGTAAGCA  
TCAAGAAAAACAAATTCGATCAAGAATTTACCTTTCAGGCAACATTACAACCTATCGTAAAGCGCGCGAATCCAAGAGAAATCCGCTTCCGGAACGCAAGGAGGCAAC

## SEQ ID 1924

MNLIKINLLPYREEMNKRKQKQKTLMYGAVLTGVAATAATYLFIDNMINKQSEKNTLLEISIAHLDTLSEIKLQKQKDAFLIKKNIIEELQIKRLQAAKILDSLEAVPGSYLTL  
DAVTADSYRLSGRTSSDNVAMRAMPNTGIFKQPELLSIKNNHQEFTLQATLQPIVKAESKENPASNAQEAN

## SEQ ID 1925

ATGGCTTGTGTTAAAGCTTGAAGAAACCTTAAAAACAGATGCAAGCTCCCTAAAAATCTTCGGGACTCAATAACCGCGCGGCAATCGGCATCGATATCGACAGCACTTCCATCAAA  
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GAAAGGATGAAATCGAACCCCTGATTGACGCAATCAACGACCGGATGAAATTTATCGCGCTTGATGTGGCAATTTTCGGAACAATCAACGCTTACGCTGTGGATAAACCAATTTTGC



CCCCGAGCTTGC CGAAGAAAAAGTGGCCATTTTCGGCGTATATGCCGCACAGACCTACGCCCTGGTATCCAAAGACGGA AAAATCCTATACAAACAGGAAACCTCCGTACGGCAGGAACAG  
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TTACCCAGAAATACAAAAGGGTGTTCAGCTTTTATTACACCACGCAGACCGCAGACGATATGACCGACATCAAGCATATCTCTGTGACGGGGGAAGCGGTGCGCCAGAAAGGCATCGCCCA  
AACCCTGCGCTCGCAAAACCAATGCGGATGTACAATGCGTCCATCCCGCGGTTTATTTCGACACGACCTCAAAACAGACGAACAACAATTCGAACCTGTGATGCGCGACACTGACCAAGGCG  
TTGGTTTGGCGCGTACGGGATTA

**SEQ ID 1926**

MRLFKSLNPKKTKDAKLPKKSSGLNNAAGIDIDQHSIKMVQLSGRSLNQIQLEKYVIAPKLNIIQGNKVQNYDQLVTYTLQOAYAKLGTSCKNIVASVPPQNLAITBQLTYTTAKDAELDL  
QGFVSSSI SEASSISLEEANYDYQVLSQSAVGEAVLSVASRKDEIEPLIDAFNAAGMKLSALVDPIGQYNAYALWINHFAPELADEKVAIPGVIAAQTALVLIQDGKILYKQETSVEEQ  
LNQLIQRTYQVTAKEABEINSPOKPSDYQESVANYFNQIITQRIQRVLQFYTTQTADDMTDIKHIIILTGEAVRQKGLAQTVASQTNADVQCCHPARYTANDLKTDEQOFELDAPTLTKA  
FGLAVRGL

**SEQ ID 1927**

GTGAGTAACCGTTTCGGTATCCGTAATGGATTCCTTGTTCTTTGCACATTGAAACCGTGCTTTGTAGAAATCGGTTGCTATTTTACTTTTATTATTAATACCAATAATGGTAAATTATTATTCAGCTATGAT

**SEQ ID 1928**

VSNRFGIRNGFLVLCTLKPCFVEIGCYFTLFNTNNGKLLFSYD

**SEQ ID 1929**

ATGCTAAATTTATTATTCAGCTATGATTTAAAAAGATTTTAACTACTTGTGTTTGGTTTGTGTTTTTGGTTTTTGTGTATTTGGAGTGGGTCTGGTTGCCATTCGTATTTTGGTAACGTAATCCGA  
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**SEQ ID 1930**

MNWYYSAMIKKILTCFGLFFGFCVFGVGLVALAILVYTPKLPSLDSLQHYQPKMPLTIYSADGEVIMGYGEQRREFTKIGDFPEVLNRNAVIAAEDKRPTRHNGVDVWGVARAAGVNVVSG  
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 LRAQNGYVLVAGONQALDPNAYITMYKIMQDPPVVRVGFGTAAALGRTDILAGTKTNTNDKAWFVGPNPDPVAVISYFGDKPKSMRAGRYGATTEIAPVWVDFYMRFALKGKGQKGMKMEEG  
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SEQ ID 1931

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TGCTCAAACTCTTATTCGACAGCAAAAAACATCAGCGTACAGCTGTTTCCAGCTGAAAAAACAAAGTATTGACGAGGCCAACCGAACTTCGGAACTGGTTTGACGACGAGATGGCCG  
CGTCTCTCTCCAGTAGGAAAC

**SEQ ID 1932**

MLHLPQNAKPFITTVNHLKDLDPDTPLEIAFVGRSNAKGSSAINTL/TNHVRLAYVSKTPGRTQTHINFFELQNGNFMVDLPGYQVQVPEAVRAHWNNLGDYLRHRKQLIGLVLINDARHPLKE  
LDRMLDFFHHTGRPVHILLKADKLSKNEOKITLSOVKLLKPYSDRONISVOLPSSLLKKGIDEANRTVGSWFDADAADAAAASPEEN

SEQ ID 1933

TTGAAAAGGTTTCATGGGCATATCCCTGTCTTCCGCCGCCGTTTGTCCGACAGCAAAAATATGCGGTTGGTTTTATGTGAAACACAGTGG

SEQ ID 1934

LKKVHGHI LVFRRRLSDSKNRLVLCETO

SEQ ID 1935

ATGCCCGGAACACCCGTCGCACAACGATACCGTACCGCATCCGCGCAATGTTAAATGACCCCAAATCATCCGCCCCAGGATACTATGCTCACCAGATTTAGAAAAAACCGCATCCGCGAACC  
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CGTCTTTAAGTATGGGGCTGTCTGAAAACGACAGACGAACCAACAGCGAACCAGACTTGGCTGTGGGAAGACGGCAAAATCCCCGAAGGCTCGAAACACCGTTTCCAATACGGCCATG  
CTGACCGCAGCCTGCTCAAACAGCTTGTGGGCTGAACGATGCGCTTTCCGCCGACCGCCGGAAGAACAGGACGCTGCGCTCATCGACCGCTGACCGGCGAGTTGCGCCCTTTTAT  
CGCCCGTATCGAAACAAATCAGTTCGGTTTGGGATTTGCTCTCCACTGTPTCCATTGAGGGCGAGGAGCGCTTGGCGAAATGGATAGCCCCCGGTGCGGACGACAAAACGACTATATTTT  
AATGCCAGCCCCATCAGACGCGCTCCCACTTGCACACAGCTGTGGCGCGCGCGCGGACGGCGGGTGTGACTTCCGCCACCTGCAATCGCTCGGCAGCTTCAACTTGTATTTGCGCC  
AAACCGGCTGTCTGTGGCTGCCGGAACCAACACCTCGCCCTCAAAGCCCTTGTACTTTGAAAAACAGGGCGGAACCTACATCCCTCCATATACCGGAGCCCCAAAGACCCCGGAAGC  
CCACACCGCGCGCTCATCGAATGGCTGCCAAGCTGATTTCGCCCAACGAGCCATCGGCACACTCGTCTGTTTCTCGCGCAAAACAAATGCAGGATGTCGCCCTGCACCTGCCCGGA  
GACTACCTGCCGCTTGTCTGTACAGGCGAATTACCAAGCGCTCTCTCGCAAAACACCAACGATAGAGAAGGCAAGCCAGCATCATCTTCGGAGTCGACAGCTTCCCG  
AAGGGCTCGACCTGCCCGGACCGCTCGGTGCAAGTCATCATCGCAAACTCCCTTCGCCATGCCGACACCCCATCGAAAAAACCCAAACCGTGTGATAGAACACCGCGCGGCA  
CCCTTCATCGAAATACCGTCCCCGAAGCGGCACTCAAACTCATCCAGCGCTCGCGCGCTCATCGCACCGCAACAGACTACGGCGCGTAACCATCTCGACAAACCGCATCAAAAG  
CAGCGGTACGGCAACAAATTTATGGCCGCTGCCACCGTTTAAAGGATAGG

## SEQ ID 1936

MPPEPSNDIVPFRNVKMTFNPFPPT/MLTDLEKNAIRIDHYQNIQKLPGRFPRASQREMIATAVANAFSRT/ITREEGGEPKREGESIAVIEBPTGVGKSLAYLLAGGIDMAQTRGRLIV  
SSATVALQEQLVDRDLPLVEKSGLELTFALAKRGGRYLCPYKLYQLTQSNQNLGFEAPAVLWDSKPKPEELKLELIDIADEFSAARRFNGDRDAMPKEIDDAIWLKVTNRHGLKLAAC  
PNRPECPFYIARDMLFVDDVVANHDLILLADISMGGVILPAPENSPYCIDAEHHLPKKALSRFAEHSWNIAVWTLLEKLPQITGKIAALTDKAEALANLADAAASLDSLHEWQFHLAE  
PSLSMGLSENDRTTSEPTLWEDGKIPEGLEPTVSNATAARSLKHVVLNDALSARREKEQDGLIDRLTGFGLFIARIEQISAVVDLLSTFVSIEGEEPLAKWIARRADDKNDYIF  
NASPISSASHLANSLWRAAGAVLTATLQSLGSPNLLRQTGLLWLPETTLALKSPFDFEKQELYSIYASFKDPEAHTAAVIEWLKPLISPTAIGTLVLFSSRKQMDVALHLP  
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QRYGQQLLAGLPPFKRIE

## SEQ ID 1937

ATCGCGATATGCCCGCAGTGGGAGGAGTGGGCGAATGTCCGATTTTGGCCGAGGTTTGGCCGATGTAGCGGGGAATGCCGTTCCTGCCCGCTATCGCGCGCGCGCTTTGAGTAAGG  
CGCGCGGTTTGGTATCGGACCGGCTTGGGACATGCTCCGCCATCCCGGCGAGTCCGCTAGTPTATGCTTCGACGACGCGGAAATGGCGCGTAGTTTCGATTGTGGTGGAACTGTT  
GAAATCGCATACCGTGTCCGCGACTTCGTTCCGTTTTCGCGTGCACAAATCGACGCGCGGCAATGGTCGATATTGAGCGGGATATGAGCGAGCAGACGGCATTTGCCGTGTGTGCGGAC  
GGTGTGAAACGGCATTTGGCGAAGCGCGCTCCCTGTGGAAGAGGATGCGGCTCGGTTTGGTTTGGCGCGGACGATCCGCTGCCGGAAGGATATGCCGTATCGGCAACCGCGCGC  
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GGATGCGGTGCGTTTTCGCTGAACGGCAGTCGCGAATGCCCGGGTATATCGCAATCGTGAATGTTGTGCGACCGCGCAAGCTGCAGGCTGAAGATTTCCGCAATGTCGCGACCGGTCA  
ACGACGTGGTACAGCGGTAT

## SEQ ID 1938

MRDMAQWRQWAECPDFADGLPDVRELPFLPAMRRRLSKAARLVCDAAWDIASAHGPSVVYASHDGEARSFDLWLELLKSHTVSPTSLSVHNATAGQWSILRRDMSBQALAVCAD  
GVETALAEASLLIEGCGSVLVLAAADDPLPEGYAVSATRAPFAYALANVLTKGTRYSLTASDMPSEAGMLPEAYWSGLEWVRFLINGSRECRVYRNREWLWQPASCRKISAMSAPS  
TIWYREY

## SEQ ID 1939

GTGTTTCACATAAAACCAACCGCATATTTTGTCTGTCGGAACAAACGGCGGCGGAAACAGGATATGCCCATGAACCTTTTCAAACGCCAAATCTTTCACGACGGTAAACCATCTCAA  
GACCTGCCGACACACCGCTCGAAATTCCTTCGTCGCGAGGACAAATGCCGGAATAATCCAGTGCCATCAATACCTTGACCAACCATGTCCTTTCGCTACGTTTCAAACACACCGGGAC  
GGACACAGATATCAACTTCTTCGAGCTCGAAGACGGCAATTTATGGTGCATTTCGCCCGGTACGGTTATGCCAAGTCCCGAAGCGGTACGGCGACATTTGGGTCAATCTGCTCGGCA  
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ATCTGCTGTCTCAAAGCGCGCAAAATATCCAAACAGCAAGATAAACACCTGTCCCAAGTCAAACACTGCTCAAACCTTATTTCGACAGGCAAAACATCAGGCTACAGCTGTTTCCA  
GCCTGAAAAACAGGTAT

## SEQ ID 1940

VFHILPAYFCRTTGGGQGYAHEPFSKRQILHDGKPSQRPAGHTARNCLRRQEQCRKIQCHQYDQPCPSCLRFKNTGTDTAYQLLRAAERQFYGRFARLRLCPSPRSQTRTLGQSARR  
LPPPSETAYRAGFYDGPSPFKRTRHPYAGLPFHDRQTSHPAVKSRQIIQKRTDKNPVPSQKTAQTLFRQAKHQRTAVFQPERTRY

## SEQ ID 1941

ATGCTCTTTTATATTCAAATATGGGATTTTGAACCGATTAAACCGATGATTCGTAAACGTTTATTCTATACTAAATTTACATTAATTAACACTGTGTTTCACATAAAACCAAC  
GCATATTTTGTCTGTCGGAACAAACGGCGCGGAAACAGGATATGCCCA

## SEQ ID 1942

MLFFIFKGFIDPIKTDSDVNVLFYTKFTLNYHCVSHKTNRIPLSDKRRRRTICP

## SEQ ID 1943

ATGAGACGATGACTTTATTTGGCTTTGTTTGGCTGCCGCTGCGGTTTCCGCATCTCCCAAGCAGACGTTGGAAGGCAACAGGTTGCCGCAACGTTTGTGCGGCTTGCCTGCGAG  
CAGACGGTATACGCGCATTCGATGTATCCGCTTTGGCGGACAGCATACTGCTTACATCTATCATCAAACTATCGCATCCGCGACGGCAACGCAACCGCGGTTCGGAGCAGTGTGAT  
GAAACCGGTGTTAATGAATTTGAGCGATCAGGATATTTGAATGTATCCGCATCTATGCCAAGCAGCAGCCAAATCCGCGAAGCCAACTCTAAGGAAATCCCGAATTTGGCGCGGAA  
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AGCACCAGGCATATATTGTGAACAGATGAATGCCATCAAGTCCGCTCAGCGTAAATATCATGGAAGATATTGCAACCGTATGTCGGAAGAAGATTAAAGACGATGCTACTT  
TATCCAGGTTTGGT

## SEQ ID 1944

MRRLTLAFVLAAGAVSASPKADVEKGKQVAATVCAACHAADNSGLAMYPLAAQHTAYIYHQITIGIRDGRTHGSAAVMKPVVMNLSQDILNVSIFYAKQPKSGEANPENPELGAK  
LYRGLSDKVPACHSCHGPSGAGMPGGSEIQAYPRLGGHQAYIVBQMNAYSQGRKNTIMEDIANRMSSEDLKAVANFIQGLR

## SEQ ID 1945

ATGGAGCTGAAAAAGCAACACGAGCGGAAAGAAAGTGTGGAGATATACGGGATTTACTCATTTGTGTGTTTATTCGCCCATCAGGAATATGGGAAGCAGAATTGGGCGACAGAAAA  
CAACGTCGCCATCTACTGCTTGTATGCTTTTATTTTCAAGACAATGAAGACAGCTGCATGATTCACCGGTTGCGAT

## SEQ ID 1946

MELKANHGRERSVGDIRDLLIVCLFRHQEYKAEELGRQKTSRPFYCLDAFYFKMTACIDSNCCD

## SEQ ID 1947

ATGCGCTTTGGCGTCTGCTCAGTCTGCTGGGTATTCATCGGTTATCGGCACGGTGTACAGCAAAACAGCGCGAGACGGATTTATTTGGTCAAAATTCGGACCGTTTGGACTCGGA  
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AATGAAGCTTTCGCGGAAAGGTTAAAGAAAATCTCTGCGCGGATGCGGCAATCTTCTGCTGTGGATGTAAATTTGCCCGGAAAGTTGCCAAACGTTATCTGGAGGTGCGGGGTTT  
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GATTTTACAATACGGGTATGCCGCGGATTTTGGCAGCATATTGAAGTAACGGACAAGGCAACCGGTGAGAACTCGAGCGCACCATCCGCTGAACCATCTTTGACCTTGACCGGCA



TCACGATTATCAGCGGAGTTTTGCCGACGCGGTCGGATTTCAGCATTCAGGCGTGGAAATTTGAGGATGCTTCGCGGAACTGTCGTGTTGAAGGCAACTCCATACACCGATTCC  
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CGCGCCGTACTCAGGAAGGTAAAAATACCCAATATCGGCCCTTCATCGGTACCGCATCCGTGATGCGGCAGGGCAGCGCGGTGCAATATAAAACATATGCTGCCGATTTTTCGAGG  
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GCGGTGAGGCTTGCCCGAATGGCAGCAGGATGAAGCGCGGAACCGTTTCTGCTGCACAGTATGGATGCCATGACGGGGCTGACGGAATATCCCGCGCTATGCTGCTCCAGCTTGACGG  
GTTCCTCCGAGTTCGTTCTCAGGTTTCGAGATGACCCGTTCCGCGGCTCCGCTTTGGTCTATCTCGGCTCGGTATTTGTTGGTTTTCGGTACGGTATPPTATGTTTATGTGCGCGAAAAA  
CGGGCTGGGTATPTTTTCAGACGGCAAAATCCGTTTTCGTATGTTCGCGCCGACGCGAAGCGGATTTGCGAAGGAATTTGCAAAACAGCTCGAGAGGCTGCAACGGCTCGCGAAGG  
ACTTGAATCATGAC

**SEQ ID 1948**

MRPAVALLSLIGLASVIGTVLQQNQPDYLVKFPFPWTRIPDFLGLGYDVYASAWFVVMFLVSVTSLCLRNVPPFHKEMKSFREKVKEKSLAAMRHSSLLDVKIAPEVAKRYLEVGRG  
QGTVSRBEDGSVLIAAKGCTMNKMGYIPAHVALIIVICLGLGIDSMLLLKGLMAGRIVPPNQAVAYAKDFKPESILGASNLSPRGNNVISEGQSADVVFLNADNGHMLQDLEPFVFKLKKFHI  
DFYNTGMPRDFASDIEVTDKATGEKLEKLTIRVNHPLTHGITTYYQASFADGGSDLTFFKAWMLRDAASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSHNVEDMSEGAEREKSLKSTLADV  
RAVYQEGKKYTNIGPSQVYRIRDAAGQAVEYKWNHMLLOQDKDYFLHTGTRSGLOQQYRWLRIPLDKQLKADTFPMALREFLDKDEGRKRLVADATKDAPEATREQFHLAERNLTNTPAQKG  
YGLGEFTSDNIPKGGSDMRQGYFPEMLYKWNMAALDETIRRYGLPEWQDEARNRPLLHSHDAYTGITETAPMILLQDLGFSVRRSSGLQWTRSPGALLVYLGSVLLVLGTVFMFYVREK  
RAWVLPFGSKTRPAMSSARSERDYLOKEFPKHVESLQRLGKDNLN

**SEQ ID 1949**

ATGACTGAACACTATAAAACCCCTCCGGAAACACGAGCTGCTGATTTCAGAAATCTTTGATCCGCAATCTGAATCTTTGGGATGGGTATTTCGGCGTCTGCTTTTTCGGGCTACGGTTTTCG  
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TCTTCGCCGCTTTCGCCCTATATTTCGGCGCGGTTTTCGGCAAGTGCAAAATATGTCGCCACCAACCTGTGGGTATGGGAACCGGTGTCGCTTGCCTGATCGCTGCTTTCGCCGTAGCAGCTTTA  
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CTCGGACCTGTGGGAGCGCTATTGAGCTGGGATCCGAAGAGACTGGGCGTTATCGTTGTGTTGAAATACCGCGTGTGGCTGCTTTTCGCGCTGCTGGCGGCTGGCGCGGCAAAATG  
GTCGCGTGGTGGGCGATTATCGGTTTTCGTTAACCAGCACTTCGCGTTTATCGCGCTGAATATGTTTTCGAGCGCGTGCATCTTACGGAACCGCTT

**SEQ ID 1950**

NTHEYKTLPEHELLIQSLIRLNLDWVFAVLVFAATVVFQTRSGMHMDIYETVMLWASAGIAPVLFGWFFKPMRWVPLSVLLLAYAAVGLYGGNIKSAKIFLLRYFLSSQSAIMWQCAFV  
PFALFAYISGAVLASVKNVPTWTLGLGHTVFANVSAGAGPTGLLVRHESYLLRPDAGHIPVSNLYEVFILFLVITALMYLYYEGKFAVQKLGGFVPGFMAVVGVPLWYSVSREAHPTQP  
LIPALQSWMKIHPANFIGYGAFICISAMLGIAELVLSRAEEKGKLWLPPSALIDEVMYKALAVGLFPFTIATILGALWAADANGRYWSWDPKETMAFTVWLNYAVWLHLRLVAGRWCKV  
LAWMAIGLFVTAFAFIGVMFLSGLESYGLT

**SEQ ID 1951**

ATGTTGGTATTAGGAATCGAATCTTCTTGCAGCAAAACCGGCGTTGCGCTGTACGACACCGGAACGAGGATTGCGGTCGCATGCGCTGCACACTCAAATGCAATGCACGCGGAATACGGCG  
GGGTCGTGCGCGGAATTTGGCAGCGCGGACCATATCCGCCGCTTGTTCCTGTGACTGAAGCGTGTTTGGCCAGGCAAGCGCATCGTATGGCGATPATTGACGCGGTGCCCTTTACCGAGGG  
GCCCGGTTTGGCGGCTGCGCTGCTGGCGGCTTGCAGCTACGCCAACCGTGCTTTAGCGTTGGATAAAGCCCGTACATCCCGCTCCATCATTTGGAAGGACATCTGCTGTGCGCGCTGTGTG  
GCGGAGAAAACACCCGATTTCCCTTTGTGCGCGCTGTGTGTTTTCGGCGGGCATACGACGATATATGGCGCTCAGGGGACATAGGCGCATACGAGCTTTTGGGCGAGCGCTGATGATGCGG  
CGGGCAGGCATTTCGACAAAACCGCGAACTGCTGGGTTTGGCGTATCCGGCGGCTGCGAAACTGTGCGAACTTGGCGAATCGGGCAGGCCCGAAGCGTTTGTTTTCCGCGCCGATGAT  
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TGCCTGCGCTTTCAGATGCGGTAGTAGAAGTTGTGAGGCAAAAGTGAAAAAGCCCTGTTGCAGACAGGGTTCAGAACCGTAGTGGTCGCGCGGGGTCGGTGCAGAAACCGCAAACTCC  
GTGAAACTTTGCGGACATGACCGGTACAAATCCGACCCCAAGGACAGCCGAAACTCCGTCCGAAAGAGTCAGCTGTGTTTCCCGCGATGGCATATGCAACCGTGCATGCAACCGTGCAT  
GATTGCCCTTTGCGCGGTGCGATGCGCTGGGCAAGGCGAGGAGGCTGCGTGCTTCAACGTCCGTCGCGGCTGGTCTGTGTCGAAATGCTGCGTAA

**SEQ ID 1952**

MNLGISSCDETGVALYDTERGLRSHCLHQMAMHAYEGGVPELASRDHIRRLVPLTEGCLAQAGASYGDIIDAVFTQPGPLGGALLAGSSYANALALALDKPVIIVHHLBGHLLSPFL  
 AEEKPDPPFVALLVSGGHTQIMAVRGIDYELLGESVDAAAGEAPDKTAKLLGLPYPGGAKLSLSEASGRPEAFVPPRPMHSDDLQMSFSLKTAIVLTAVEKVRANGSETIPEQTRNTI  
 CRAPODAWVEVLEAKVKKALLTGFRFTVVVAGVGANKRLRETFGNMTVOIPTPKGKPKHSEKVSVPFPPPMAYCTDNGAMTAPAGAMHLGKGREVGAFNVRPRHSLSEIVK

SEQ ID 1953

ATGAACCTTCACCCGGTGTGCTCAACCAAGTCTTAAGCAGCGTTCAAAAAAAGGCAACACATTCCTCCGGCAGCCCGCTCAATTTCATTTCGGCGGAGGCGCGCTGTTGCCGGTGTGCCCTCCA  
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ACAAAGCGATTTCCAACTGCCGGAAAACTGAAGAAACATACAGCCGCACCGGTATTGCTGACCATGATAGCCCGCCCGCTTCAGACGGCATGATAGACGAAGCCGAACCGCCGGACTATC  
GAACAGGAAAGCGGCACAGACCCGAACTGCCGATGGCTGCCGCCGAATACCGCCTGCCCGAAGCATCGGGGACATCGCCGCCCGCTCGGCAACGATGAGGCGTTGGCGCGGAGA  
CCTATTGCGCGCAAGGTTGGTCTGTGCCGATTGTGTCGCGAAGAAACCGTCTTCCTCGCCCGCTTGTGCGAGGCTTTGAAACTGGATGACAATCTGGTGAGAGTTTGAAAGCGCAACT  
AGGGATT

SEQ ID 1954

MNFTRLNLQVLSTVQKKGNITVSGSPNLNPFGGALVAGVASMLNGKNRKTTTKIGSTAAALGYLAIRGYQNMQONKGRATVTSQDFQAPAGKTEETYSRVTILRTHIAAASDGMIDEAERTT  
 BOESGSDPETAAWLAAYRYLPASIGIDAAVGNDEALAAETYLAARLVCADLSRKETVPLARLSOALKLDNDELVSLERLQIGT

SEQ ID 1955

**TTGCCGCCGAAACCGTCAGTCGGCGATGTCGAAGTGGAAACGGCAAATAATCGGCGGCATAGTTTCTTTCAAAAATTTACACTGTGCCGCATTC**

SEQ ID 1956

LPPETROSAMSKWNROIIGGIVSPKNLHCAAF

SEQ ID 1957

TTGGATATCCCTCTGTTCAGGCATGAACATATCAATATTGTCCATCCCATCCGACAGATAAAAAATAACCGCTTGGAGCGGCATTGTCAATTTTCAGCTTGGTGCCCGGAGCCGGAATCG  
AACCGGCATGGGAGTGT

SEQ ID 1958

LDPELLFRHEHINIVHPHPTDKKITANS~~G~~IVIFSLVPGAGIEPANDV

**SEQ ID 1959**

TTGCGCGCAATACCTCTCCCTTTTTCAGACGGCATGTTTCGTTTACAATTACAGGCTGTTTCCCCCTTTTGGCAACCGGCATGCAACATCCTGTGACCGGCTGCTCAAAATGCCCTCTCCCTGCTGT  
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GACGGTCAAAGCCGTTTTCGCGAAACCGCAAAATGCGGTTTGGAACTTGCCCCCGCGCTTTTCAAAAAACCGGAAGACATCGAAACAATGTTTCAAAGCGGTACACGGCTGGGAAACAGCTG  
CAGCAGGCTTTTGGACAAGGGCGAAGGGCTGCTGTTCATACACGCCGCACATCGGCGAGCTACGATTTTGGCGGACGCTACATCAGCCAGCAGCTTCCGTTCCACCTGACCGCATGTACAAGC  
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GGCTGAAACCCCTGTTTCTCTGCGCAACGCTGCCCGACGGCAAGGCTTCTGTTTGCACATCTCGCCCGCTCCAAAGGGGAATTGAACGCGCAACAAAGCCCAAGATGCGCGCGGTTC  
ACCGCAATACCGGAATATTGGATACGCGCTTTTCCGACGCAGTATCTGTTTATGTACAACCGCTATATAAAACGCCG

**SEQ ID 1960**

LPQYFFSDGMRFLRQFRLFPPLRTAMHILLTALLKCLSLLSLSCLSHLTGNRLGHLAFYLLKEDRARIVANMRQAGLNPOTQYVKAVFAETAKCGLELAPAFFKKPEDIETMFKAVRGWEHV  
QQALDKEGGLLFIPTPHIGSYDLGGRYISQQLPFHLTAMYKPKIKAIKDIMPQAGRVRGKGKTAPTGIQGVQIKALRAGEATIIPLDHWSPQEGGGVWADFGPKPAYTHTLAARLAEVK  
GVKTLFFCCERLDPDQGFVLHTRPVGELNGNKAHDAAVFNRMTEYWIRRPPTQYLFMYNRYKTP

**SEQ ID 1961**

TTGCGGCAATATAGCCTTTTCTGCTACGATCGCGCTGCATTAAAGAGTTGGGAATTCATGCCAACCTGCTTTTCAACGGAAAGGTAGGTGGACGGTTGAAAAACCATGTGGCTCGCGG  
GAGCAATCCAAACCGCTTGATGCGGGAAATTTTTTGCTGTACGAAACGTACGGACAGAGATTCCAAAGCGCCGTT

**SEQ ID 1962**

LROYAFSATMRAALRVGNSMPTCF SNGKVRWTV EKPMLAGAIQTRLMREFFC LLYETYGQRFQSAV

**SEQ ID 1963**

ATGTCGACACGCGGGGAATATAGCAAATTCCTCTATTCTGCCATTTCAGTTGAGAAATATTCCTATTAAACGGCGCTTTGGAATCTCTGTCCTACGTTTCGTACAGGCAAAAAAATTC  
CGCATCAAGCGGGTTGGATTGCTCCGCGAGCCATCTGGTTTTCACCGTCCACCTTACCTTTCGGTT

**SEQ ID 1964**

MSTAGNIAKFPYSCHSVEKSYLNGALESLSVRFVQAKKFPHQAGLDCSGEPHRFFNRPPLYLSV

**SEQ ID 1965**

ATGTTGTTTGTTTTCACGGAATAATTCATAGAGCGAATATCTGTTTACTTCCGAATCGGTTTCCGAAGCCATCCGACAAAGTAGCCGACCAAGTATCCGATGCGATTTTGGATGCCATCT  
TGGCGCAAGACCCCAAGCGCGTGTGCGCGCGGAAACTTTGGTCAACACAGGCTTGTGCGTATTGCGCGGGGAAATCACCACACACGCCCAAGTAGGCATACATCAAAGTCGCAACGCGGAAC  
CATCAAACGCATCGCGCTACACATCTCCGAGCTGGGGCTTTGACGCGCAACGGCTGCGCGGTGCGGCGTGTACGACGACAACAATCCCCGACATCGCCCAAGCGGTGAACGACAGGCGAAGC  
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ATTTCGACGAAATCTTCGCGCGCTACGGGATCTTCGGCGCGGACGAAAGCCAGTTTACTTGGTAAAGCGACCGACCAAGCGCGCTCATTTGAAAGCGGCGAGCGGGGCTG

**SEQ ID 1966**

SECRET 1989

MVCFSRKISSEKYLFTSESSEVSEGHDPKVDQVSDAILDAILAQDPKARVAETLVNFTGLCVLAGEITTTAQVDYIKVARETIKRIYNSELGFDANGCAVGVYDQSPDIAQGVNEGEG  
IDLNGQAGDQGLMFGYACDEPTTLPMPFIATYSHRLMQRQSELKDRGLPWLRPDAKAQLTVVYDSETKVKRITDTVVLSTQHPDAISQEELSKAVIBQIIPVLPPELLTDETKYLNPTG  
RFVIGGPQDCGLTGRKIIVDTYGGAAPHEGGAFSPKDPKSVDRSAAYACRYVAKNIVAAGLATQCIQVSYAIGVAREPSTISIDTPTGTGKISEEKLIALNVEHPDLRPGKIVQMLDLRR  
IYGKSAAYGHFGREERPEFTWERTKAASIKAAAGL

**SEQ ID 1967**

ZGTCGGTTTCAATCATTTTCATAATGGTAAACGATTATTATATATGTGATTTCCCTGCAAACAAGCGGTCCGCCGCCCGCGGTGCCACTTATCCGGCTTTGCCTTATATATGCTTTTIT  
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 TGTCCAAGAGCTTGACAGCGGAAAAGTCATCATTTGACCAACCGCTCCCGGGCATACCCCTGCAAAATCCCGCGTCCACAGATGAAGCTCGTTACCGCTTTCAAACACTTTCCGACAGCAAT  
 TACCGCTGGGCGCCGAGTTTAAAAACACACGGTACGGTAAACGACGGCAGCTGTGACGAAACTCTGTATGTGGCGGCGACGGCGGCGCGCTTTTCAATCAGGAAAAACCTGTCTGCGCTCC  
 AAGCCGATCTGCGCGCAAAAGGCAATCCGCAATATACGCGGGCGCTGATGCTCGACACAGCTGTGGGGCGAACTCGGCAGTCCCGACCAATTTTGAAGCCGACAGCGGTTCGCGCTTTAT  
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 AACTTGAAAAATACCGCTTCCCAAGCTGCTGCCCTTCGGTCAA AAAAATGATCGCGCATCTTTTGGGCAATACAGCTGAAATTCGCGCGCAATATTCGCCAAAGCTGTTTGGGCAAGC  
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 CGGGCTGTGTGCGTTTAAAAACCGCAGCTCAACAATTCCGCGCTTGCAGGTTATTGCTGGGCGAAACCGATCGAGTGGCTGTGCTATCAACACGCGCGCGCGCTTTCCTGT  
 CTGCGCGCATTTGACCAACTTCGTTGCGCAAAAACATCATCTCCGCGCGCGGCTGCGCTGATGTGCGCAACTGATGTGCAAGAAGCGCGCGCT

**SEQ ID 1968**

VRPHFIMVTTIYIVISPANKFVRRRPGVPVFPALPYNCFYVTDSPMNFPTKTAASLLLLASLAAHALDTGRIQONEIAVYVQELDSKGVIDHRAGIPVNPASTMKLVATAFAAFKTPGCSN  
YRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRQLRDKGRINRTGRLLMDHSLWGEVGSPIHPFADSGSPMTPNPNPMLSAGMVNVEAERNAAGSTDLITDPPPLPHIPAQN  
NLKITASQAACPSVKILMRASFGNTLKLKRGNIPESCLGKPVGVRMFALDELIRQSPFTRNWLGGGRISDGGIGIADTPEGAQTLVAHSPKMEKIITDMNKRSDNLIARSVFLKLGDDGKL  
PAVSEQAASAVRRELAVSGIDVADLVLEWSSGLSRKERVITARMMAQMLEATYFSPFAQDFITDLPLAGTDGTLRNRKFGQSGGLRLRLKTFLLNNVRALAGYWLGDKPMVAVVIINSRAVSL  
LPDLNTPVAKNIISGGDGNLQCKMCKGSL

SEQ ID 1969

GTGGAACCGGCAATAATCGGCGGCATAGTTTCTTTTCAAAAATTACACTGTGCGCGCATCTCTAAOCCAAAGCCCATCCOCCCTGACAAATGCCGAAATTCAAACGCATCCACGCCATTTTTCCTC  
GACAACGCGCGCCCTCGGCGAAACCGCCCGAAT

SEQ ID 1970

VEPANNRHSFFOKFTLCRIITKAHPPDNAEIOTHPRHFFRORRPSANRPN

SEQ ID 1971

SEQ ID 1971

ATGTGGAAAGAAATTTTACTGAATTACGCTATTTTCCCTGCTCGAACTGCTTACCCTGTTTCGGCGCAATTGCGCTGATTGTGTGGCTATCGTACAGAGTAAGAAACAGTCGCGAAAGCGGCA  
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GATCCAGCGCAITGGTTTCGAGCGGAAGCTTCGCTGAAAAAGTTGTTGCCAACTTGTCAACCGCGGAGCGGATGTGATG

## SEQ ID 1972

MWKEILLNYGIFLLELLFVFGAIALIVLAIIVQSKQSESGSVVLTFDFSENYKQORQSFETFFLSEEBTKHQEKKEKKEKAPAKAEKKRLKEGERSAETQKSRFLVLPDGLYAHAVES  
LEHETFAVLLIAKPEDEVLLRLESPGVVHGYGLAASQLRRLRERNIPLTAVDKVASGSGYMAACVADKIVSAPFAVIGSVGVVAEVPNIHRLKKHIDVDVHTAGEFKRTVTFHGEFT  
EKGKQKFRQLEETHQLFKQFVSENRPLDIEKIATGRHWFGRQALALNLIDEISTDDLLKAFENKQVIEVKYQEKRSIIQRIQLQAEASVEKLFKLVNRRADVH

## SEQ ID 1973

GTGGCAITGAATCGCGCGAGATGTTCCCGAAGGCTGGCAGCGGGAATCTCGAATCGGACATCTGCGCCTTTACAATTTTCGATTATGACGACCGCTGAGGTGGAAGATGTGCGCTGC  
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ACCGAATCGCGACGTGGCTTGGAAAAACAACCGCGCGCATCATCAGCCATTCGCTCGGCAAGATGGCGGTTACAGTTCCCAAAAAACCTCGCGCTTCCCTGTCTGATTTTGTATATG  
CCCGTAACCGGACAGCGGGAAGTATTTTGGCAATTCGCGACGCTGTTGATGAAACGCTAAGTTGATGACTCGGCAAGGATTTTGTTCAGTCATATATCAATCAGTTTGTGCGTT  
TGATTGAAAGAAATGCCAA

## SEQ ID 1974

VALNAEMFPEGQAEIVEIGHLPLYNFDYDDPEVEDVPLPESTAFRETIKASDGLFVTSENNRTIPACLKNAVDIGSKPNADVAVKKNKPAIIISHSVGKMGYSYQKNLRLALSYPDI  
PVTGQPEVFLGNSPTFLDENKILDSARDFVQSYINQFVGLIERNAK

## SEQ ID 1975

ATGTCGCGAGCGTGAATGGAATGCAAGGCTTATCCCGCATATGTTGGCGGTTTTCGCTGCACGGCGGTTTATGTTCAAAATAAAATAAGAGAAATAATGCTGACGTTTATCGGATTG  
CTGATTATCGGGTTCATCGTATGGCTGTGCTGACGGAAGAGTGTGCGCCATCATCGCATTAATCTTGGTGCGCTGATTGGGCGGTGCTGCGCGGGTT

## SEQ ID 1976

MSAGVNGMQLSRICWRPCLHGRFVYQNKIKNNADVIRIADYRGHRNAVADGKSVAHHRINLGAADWGVAGGV

## SEQ ID 1977

TTGCTGGCGGGGTTTGATGATATCCCAATTAAGAAATTTTATTCGGCGGCGACGAATCGGTGACGAGATTGTGATTATGTTTATGTTTCCATTTTGTGTTTGGAAATCATGAACGATG  
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GACGTTTATTCGCTCGTCCCGCCCTTTTCCCGCTTTTACAAGCGTCTGCAATGATTCCTTACCTGCTGTTTTCGCTGCTGACTTCCAGCGCGGGCTAATCAACCTTTTCCCGCGGGG  
GGCGCGATCGGGCGGTTGCAAGCGTGTGGCGCGAGATGTGGCGGAATGTATAAACCTTTGTGACGCTGCAATATTCGCTGTGCTGTTTATCCTTGTGCTGTCCCTGTTTGGGTG  
TGCGTGAAGAAAGCGGATTTGTCGGGAGTTGGCGCGCTTCCCGCGCTGCGGATTTGATAAAGCGCGCGCTTTGTCGGAAGAAGAAACAAAATTTGGCGCGTCCGAACTGTTTGGGTG  
GAATGCTCCTGCTGTTTTCGGCGGATGAGCTCTGTTTTCGGGCTCTTCCCGCGGTTATGATTTATGCTGGCTGCAACGGCGCGGTGCTTTGAATTACCGCAGCGCGCAGGAA  
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## SEQ ID 1978

LLAGFDVSQLKEFVSGTKSVTQIVIMFMSILFFGLMNDVGLFRPMIGLILKLRGNIVAVSVGTVLVSVVAQLDGAGATTFLSVVPALLPLYKRLHNPYLLFLLTSSAGLINLLPRG  
GPGRVASVLGADVGLYKPLLVQIIGVVFILVLSLFLGVREKRRIVRELGAAPADLIPAPLSEEBKLARPLFWNVLLFLAAMSLLFSGIFPPGYVFLAATAALLNYSRQPE  
QMERIYAHAGAVMMASIIAAGTFLGILKAGMLDAISKDLVHILPDALLPYLHATGVLGLPLELVLSTDAYYPLFPIVEQITSQAGVAPEAAGTAHLIGSIVGTVPVPLSPALMGL  
GLAKLSMGKHRYSPFWANGLSLAILVSSIAAGIVPLP

## SEQ ID 1979

TTGGGCGCGATGCAACACACGAGCAGCGAGGCAAGCCTGCGACAGATCACAGGAACGATTCCGGCTTCAGCGCGCTTCGCGCTTACGGCAGAGGACGATTCTGCCCTATCGAAC  
TGACCAATATCGCAGCGACAAACCCACGCCAGAAAAACGAA

## SEQ ID 1980

LGRDCNTRTGRQSLRQITGTTIRASGFPVYGRGTIPAAIELTNIASDKPHAQKNE

## SEQ ID 1981

GTGTCGCAAGTTTGAAGACGGCGGCTATGCGGTGATTTGGTCAAAAACGGCGCGCAGGTTCGCGCGGCTGCGCGCTGCCAGCCTTATGACTTGATGCTGCTGGAATTTGGGTTTGCTG  
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GCAACGTATCAGGTAGAATATTGCGGAGGGAGGGTGGCATTGAGCAACAGGAGTTTTCGATTTGCAAGCTTTGCTGGCGAGCGCGGTGTGATTTTGTGCGCTCGGATTCGGAG  
GACAAGGTTTACGTTTGGCGCGGGAAGTCGAAAGCAATGCGGTGGATTTTCTGATTACAGGCTGTGCAAGAAATTTGGG

## SEQ ID 1982

VSASLDGGYAVDVKNGAQVAAAAAQPYDMLLDLGLPGRDGLDVLSEIRAAGCTVPVLIVTARDLISRLNGLDGGADDYTVKPFDMAEFKARMRAVLRRSGQAQCLSNGLSLNP  
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## SEQ ID 1983

ATGCCGAAATCAAAAGCATCCACGCCATTTTTCGACAACCGCGCCCTCGGCAACCGCCGAATTAGCCTGAATTTACATTTATCATTTGATATGCCGATTACCGACACCGCTCC  
CTGCTGCCGACAGCGGGCTATGTTCTGATAGACCGCATTAACCGATACGCGCA

## SEQ ID 1984

MPKFKRIHAIFSDNAAPRQTARISLNLHLSLIMPYRHRPLPAAQRAYGSDRPHYPIRR

## SEQ ID 1985

CTGCAATGCGCGGCTCGGGAATGCTTGAGCAGGCGTCTGTTTGTGAAATTCGCGCCCATATAAATAAGAACCGAAATAGGTACAGTGGTCTTGGTGGCGGTAAAGATAGCGTCCGTG  
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GCCGAGGTATTTGTTATAGCAATCTTTCAATTTTCTCCCTCAAGGAGAACGCGCTGATTGATGATTTGTTGCAAAAAACATATACAGTTTACGCGCGGCTATCTCTTGACGCT  
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CCAGAAACCCCGCAGGTGTCCGCGTGCAGTCCGCGAGGTTCAAGCGGTTTCGGAATAATTTTTCGCGCAACCGGCGTCCCGGCGAGCGCGGAGGTTTCTGTTTCAATAT  
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 GAGACAGCGGCCCGCAATCCGTCAATTTACGGCTGTATCGGCAGCTTGATCA

**SEQ ID 1986**

LQCAASGMLBQAPVFKVPPHIIIRTEIGQVVLVAVKIASVYFDRVFGQVFLCVHPMHIGNIFNPQIKDRILIALADVAHSFNRPEVLVYSKSOFFFLPQGRDAD\*CIIVCKNIYRFDGGYFLDG  
 FPEGSGFEPGYQEGRLFRKSRHGLAAHPQIIELGNENSGFYNFIPVFSAQRVVCQLLTHPNQTLRIEGQDQSFPPFPFPAADILIKQPFQVSGVVAEGQDGFRKILIFRNSGRAGQRAEVFLFYV  
 PS\*IQVVTDKHGGRGEIKAEKCLFEGHLFPFSKRLNQIIAQQCKSGRGRNRYGRQSKLFPVCNVMGEGKNPMVQV\*GIRDPADKYDGACRQDAGRKCPLVLTQDPKRRQQAEGKQGYV  
 RDKRIVFVDHEQADKQCAETE\*\*KQLPFSIFCLPSAVLRLPVNRQORTHQGLKPKQCKRVISIGLVEDVGIKPGRQKR\*CGQNKQDDADITQHP\*\*GFFVTTEYTPKRIQEVILFLYTRQ  
 PDMQYGVLVGCTQIELPQSEFQINIGQKNRRKLGYCFHLVBEI FVKEDLRSNHSRGHGGRNFRNINPLAPAGIKI PERKRTVLYIRFKNVDGNEESRDDKENVHPQESSGQPAVIQVENNDG\*H  
 GDGQPSVNFPRVSDSLHQ

**SEQ ID 1987**

TTGCCGAGGGAGGGGTGGCATTTGAGCAACCGAGAGTTTTTCGGTATTGCAGCGCTTTCGTCGGAGGGCGGGGTGTGATTTTGTCCGCGCTCGGATTCGGAGGACAAGGTTTACGGTTTGGGGCG  
GGGAGATTCGCAAGACAAAGTCGGTGGATTTTTCGTATTCAACGGCGTGTGCAAGAAATTTGGGTAAGGAAAGCATACAAATATGCCGCGGTGTCCGGCTGGCTGATGCCCGGTCAAGATGCCGTC

**SEQ ID 1988**

SEQ ID 1988  
LPRGGVALSNQFQSVLOALLARPGVILSRSDSEDKVYWGGEVESNAVDFLIHGLCKKLGKESIQNVRGVGWLMPQDAV

SEQ ID 1989

SEQ ID 1989

ATGCCGGACCGGATTTTTTAAAAATTTTAAACAATTCGCTTCAGGTGAGAATCAGCCTTGCCCTGATTGTGGATGTTGTGTCGCTGGCAATGCTTGCAGGATGATGTTTCTCTACTACGAAACCT  
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TCCACGACGAGGAAGACCTGTGTGCAGCTGCCCGCGCATCTGGCGGACGGTCTGCACACGCTTCAGGCGGACGGGGACGAGATTTATTACCGCGTCTATATCCGCACGACCGAACAGGG  
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CGCACAAAGCCATGCGCCCGCTCCGCAATTTGTCGCAAAAGTCTCGAACACGCGGAATCAACGGCCTGTCTGCTTCAGTGTTGTAACAATATCCCAAGTAAATTCAGAGGGTTCGTAACCGC  
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AICAAATATGCCCGCTCCCAACCGATGCGGGGCGGCAGTCCGCCGTTTTGTCAGCAGAGCATCAGGCGCAACAAACACCTGCTCGAACAGCTTTTGGCATTGCGCGCTTCGCACTCGGACGAA  
CCCCTTTGCAGAAAACGACATTCGGGCTGCAAAAGCGGTTTTCCGCAAAGTGTGTGCAGGAAGTATGCGCGCTGGCTTTGGAAAACTCTCAGGACATCGGTGTGGCGGTTCGAGGCGGATTCGA  
AGTGTCTGCCGACGAAACGGAATCTATACGCTGTTTAAACCTTTGGCCGACACCGCGCTGATGCTTCCGCGCAACGGGGGACGAGTAGATTTTGGGTTTCACGGACGAAGGGAATATATC  
CGCGTGTGGGTGGAGGATACCGGAACCGCATTCGCGAATCCGAATCCGCCCGCGCTCTCGATCTGATTTATACCGTATTTTGGGAACGGAGCAGCAGGGGCGGGGCTGGGCTGTGCGATTG  
GCTGACGCTGTGCCCAAAAAATACGGCGGATATTTGGAACTGACCGACAGCCGACGTTTCGGACACGGGCTGTGTGATACGCGCGCTGTGTGGAACGAAGAAACCTTGAA

SEQ ID 1990

SEQ ID 1990

MPDRFFKILKHSIQVRI SLALINMVPVLAMLAGMFSYETTFHETEARLQDDLLRQAALYVGPISKPETLPEGDGDTRILVMPQQEDPVVSLPAHLADGLHTLQADGDDYYRVYIKTTEQ  
RIAMVQENEVREDLAEADARQSVLPILALPILITLFWITHKAMPVRVKLSQSLQRRINGLSALSVYNIPSKIRGFVTAINLLKRVDEDIRRQRFPVADAHELRTPTALSIQAERI  
NMPLPDPAGQSAVLQQSIRRNKHLLEQLALARSQSDETPLTKTTFGLQSRPQVLQELMPLALEKRDIGVAVGGDEVSADETEITVLKTPADNAVRYTPNGGRIDLFTDEBKYL  
AVWVEINGNGIPESECPVLDPFYRILGTEQQAGLGLSIADTLAKKYGGYLELTDSSRRFGHGLLIRALLDKETLK

**SEQ ID 1991**

[illegible]

**SEQ ID 1992**

SEQ ID 19992

LHPICACAGRNCKNIFITFSGKTM SGLPIPKDIARPPEITLVNITPQETRVAVLEENNICELHIERNSGHSLVGNTYLVGVRRVLPQMGSQAFIDIGLERAALFHVIVDVLQRRNPEETQR  
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DLPLSLRVLVRMDVGCITQKILVDSTVNHGRMTFRFAEQYVHGALGRIELFKGERPLPETHNI BQEISRALQPRVNLNPGSYLIIESTEA MTTIDVNTGGFVGARNFDETIFRTNLEACHTIA  
RELRLNLNGGIIIDFIDMAQESHREAVLQELAKALAFDRTRVTLHDFTSLGLVELTRKRSRENVLQCEPCSPCQGRGLTKPTQTCYIEQREIVREARRYDASFRILAAFNVIDLFL  
DEESOSLAMLIDFIGKPIQSLAVETAYTQEQYDIVLM

**SEQ ID 1993**

SEQ ID 1993

ATGCAAAATATTTTATTACATTTTCAGGAAAAACCATGTTGTGCAGGACTCCCATCCCCAAAGACATCGCGCGCCGCGCGGAAACGATATTGGTCAACATCACGCGCGAGGAAACGCGC  
GTGCGCGTGTGGAGGAAAAACAATATCTCGCAGCTGCACATCGAGCGCAACAGCGGGCACAGCTGGTTCGGCAATATCTATCTTGGCGTGGTTCGCGCGCTACTGCCCGGATGCAGAGCG  
CGTTTATCGACATCGGCTTGGAAACGCGCGCGGTTTTACACATCGTCGATGCTTCGAACAACGCGCGCAACCCCGAAGAAACCCAGCGCATCGAACATATGCTGTT

**SEQ ID 1994**

SEQ ID 1994  
MOKYFYIIFRKNHVVETPHPORHRAPARNDIGOHHAAGNARGGVGGKQYLRAAHRAQORAQPGROYLSGRGAPRTARDAERVYRHLRGTRGVFTTHRCPRTPQPRRNPAAHRTYAV

SEQ ID 1995

SEQ ID 1995  
ATGATAATCAATATAGGGGCAATCGCTCCGTTTGGCAAGTGC GGAAACAGATGCACGTT CAGACGGCATGTGCGGAGTGTGTCAAAGTTCTTTTTTAAAGTA

SEQ ID 1996

SEQ ID 1996  
MTINIGATAPFGKCGTDARSDGECGVCOSFFPKV



**SEQ ID 1997**

TTGCAAAACTTTTCGGAAACCCAATATGCAGACCGGTATTACATGTACACAGGTCCGTTTTCGCCCTACTCGCGATGGCGAAAGCGCTGCTGCACGGCGAGGTGTCGGACATATCGACGAAATCCGCTGTCGATGCAAGCCCGGAAGCCCTTTGCCGAAATGCAGCGGCTTTCGGGACAGCGCAGCGTCCCGAGATTTCATCGGCCGAAACGCACGTCGGAGGATTACCGACCTCTACCGCCTTCAGCAGGAAGCGGGCTGGACGGACTGCTGAACCTT

**SEQ ID 1998**

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**SEQ ID 1999**

ATGAGCGAAGACTGCAACCCGCTATTACAGCATCAGAGGACTGTATGTGCAAGAGACTTGTCTTTGGAAAGTCCGCGCAGCGCCGCAAAATCTTTTGGAAACAGGGGGATCCCGAAGTGGATATGC  
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 TATTTTCCGCTCTGAAAAACATCCCGAAGAAGATGTGCAGCTGCTGTTGGGCGTGGCGGTGTCCGAACATCTCTTCCCTTACGCGCGCGAAGCGGTTTCCGTTACGGTAACGCGCGCGCGC  
 TTCCCGCGCGCTTGCCTTGGCCGATTAAATTTGAAGCGATTACCAACAAACAGCAGGAAGCCGAAGCCGCGCGGGCT

**SEQ ID 2000**

SEQ ID 2000  
MSEELQPVFSIERLYVKDLSLEVPHPAQIFLEQGDPEVDMRVSTGSQKLEDGYIDVDTVTVTAKLDNERTWFLNEVTSQSGIFRLNIPEDDVQLLIGVACPNIILFPYAREAVSGFVTRAG  
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**SEQ ID 2001**

SEQ ID 2001  
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CGGCAAGCGCGGACAGGTTTCGCGCTCGAGCTTGTTCAGACCGGCAAGTGGCGGGGAAACCCAAACCGGCATAGCCCCACGCCCAACGCCCAATATGCGCAATACGGTGTCTGCTCGGTCAAAAT  
GCGCTGCCAGCGTCGAGACGGGCAGTTTTTCCGCCAAAAGCCCAATACGGCGTTTGCCATCGCGAGGTTGCCCTCGGAGTTTCAAAGTGTGATGGGTGTGACTTTGTGCGGCAGGTGGAA  
GAGCCGACTTCGCGCCGCTTGACTTTTTGTTTGAATAAACCATAAGAAATAAACCACCAAGCTCGCGGCTGAAGTTCGATGAGAAATCGTGTGTCGCGCTGAGGGTTTGGAAAAACTTCG  
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GCATCAGGGCGTGGGACAGGTTGTGATGTCTTCGCTGGTGCAGCGAAGTGGATGAACCTCGCTACGGCGGCGCATTTCCGGCACTTCGGCAAAACGTTTTTTCAGCCAAATATTCGATGGC  
TTTGACATCATGATTGTGCTGTGGCTTCGATGGCTTTGACGGCGGCGCGCTCTTCTAATGAAAAGTTTTTCGATGACTTTTTCGTAATTTGCGAATTTTCGGCACTTTGAGGGCGGCGCATTCG  
GCAATCTCGCGCTTCGGCGGCGAGGCTTTGAGCCAGTTTAAATTCGATTTTTCGCGCGGCTTCATCAGTTCGTACTCTGAAAABAATCGGCGCAATGCTTCAACGGATTGGGCATAACGGC  
CCTATCGGCGGAAAGCAGGCGGATGGGTTGATCATATCGGCATCTCTGTTTCGGAAAAGACATCAAAAATATGACAA

**SEQ ID 2002**

SEQ ID 2002  
NPFRQPSLAHQGGQLKQFGFGPGGNFRSDKAPQHFQCDAAFTARQVQFQFVRJGDTVAHYGLNRLGBQLPSDQIGGKRGRVRLLEQVTAQVGGETQHGHLAAHAAHIAQYGAVGQI  
ALRPA\*DGQFPRQKAQYGVCHAEVALGVFKVDGVDVFRHGGRADFARFQFLPEITQ\*NITPNVAEAVDENRVDAAEGLEKLRIHVVRLLDQGVGVEGQTEADFEVAACWPFTHIGIGGHVG  
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FDIMIGRFGDGDGGRVF\*\*KVDFDVFDFGKRFGEGRHFNRLGGQGFEPU\*FDFDARLHQSVL\*KNRAQCQFNGLGITAV\*GGKRGDGVDIHILFGKIDKN\*Q

**SEQ ID 2003**

ATGAGGGATAACCGCTTATAATCATAATTTTACAGTCGCGACAGAGAAAACCGATGCCTTGGAAACATCCCCATCTTCCCTCACATGGTTGAGGGCTTGTGCTATTCGCCGTA CTGATTGTCTCTTT  
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**SEQ ID 2004**

NR1T VII I I L Q S A Q R K P M P W N I P I F L T W L R V L L I P V L I V L F P L Y P F S W F S E E A V N V A A A V I F A V A A L T M F D G F L A R L W K Q T S D F G A F L D F V A D K L A V A V S L L L V K L D R T Y V I F A H I T I G R  
E T T I S A L R E W M A O M G K R S S V A V A T V G K F K T A A O L A I P F L L L N F P D F Y G F N L V V I G N I L M F I A S L L T V W S M L Y Y L K M A K E I A

**SEQ ID 2005**

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**SEQ ID 2006**

LAETSVILSCFWVSGDIGRFLWTRLFPYKTKMPSSETSDGIGRQESSPGGFGFLLLVNRFKINRRKQDGREAGARYRTGNRPARVREEDVTRTHAQOQLHIFPGDVPQTENTALGYFVQ  
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**SEQ ID 2007**

SEQ ID 2007

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**SEQ ID 2008**

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**SEQ ID 2009**

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**SEQ ID 2010**

LTHFDPKSRYSOVGGNPAMRIRRGISGKRQAPRRHSRAGGNLEMKNHGVI GND

**SEQ ID 2011**

TTGGGTTTCGGACGGCTTTTGGCTCATCATTCAGCGAAAACAAAATCTAAAAACCGTCATCCCGCAAAGCGGGAATCTAGTTTATCCGGCTTCAGCAATTTCCGACACATTTCCACAC  
GCTTCGATTCCGTCACTTCTCCGGTTTCAATCGTTCCGATAACACCGTGGTTTTTCATTTTC

**SEQ ID 2012**

IGSDGFWLI IORKOKSKIPSFPOKRESSLSGFSNFRHISTRFDVISPVSIVSDNTTVVFHF

**SEQ ID 2013**

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SEQ ID 2014

MSKLIKAGIVGATGYTGVELLRLLLAAHPDVEVAAVTSRSEAGTAVADYVPSLRGVYGLAFQTPDEAGLEQCDIVFFATPFGNLIAMDAPRILLEQGVRVVIDLSADFRIIDPTWEHWYNGTHA  
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IRGMHATVYHLISDGSDEPTVLRDYRDSPPFDILPAGSTPSTRVSGANLCRISIROAAQSDVMVVLVSVIDNLVKGAAQAVQNMNMFGLBETHGLDAIPLLP

**SEQ ID 2015**

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CGGACAGCGTTTCGGACGGCATACCCGCCAACACACAAAGGAAAAACCA

**SEQ ID 2016**

MKTLVLLLLSFSTTTAFAAAYGLGLGOAPKYPVGFRAFGYVYSGRQGWVLKTEADAIKLDTLTKRFVYRPSAANQNPVGOAVGQRSDGIPANHTKEKP

**SEQ ID 2017**

ATGGGCGTGTCGCACTGCCAACTGCCCTGGACGGATGCGCCGGAAACTTCGTCCGGAACTCCTTTACAGACGGCATTTCGACACGCCCTCACTCAACGTGTACAGCCCCGAACACCATG  
ACGGAACAACCTGACGCCGCTC

**SEQ ID 2018**

MGVSDCELRWTDAPETSSGTL LSDGILARASLNVSPEHHDGTTDAV

**SEQ ID 2019**

TGCGGTCTGAAGCCCGTGTTCGACAGATACGCAATGATTTCGTCTTCGTCTGTCGATATGGAGAACAAAGAGCGGCCCTTCGGAATCATACCGCGGCCAAAAGCTGCGCGTTTATC  
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**SEQ ID 2020**

CRLLKVFVFRQIRNDFVFFVVRVYGEQSGPFGNHTARQKLVVYPLRQARPKRLSNQNDTRRRHFARLHQGGDFKQFVORPFAARHHDICLGLAEKHCLAPFGTKGKPGQDVLIRIRFLLVRQGVV  
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SEQ ID 2021

ATGAAGCCCGATTATAGCAAAAGTCGTCGAAACCGTTTTCAGACGACCTTTTATTTAATTACAATAAAAAATGTTAACACAAAAACAAACCGCTTTTTCGGTTGGAGACAAATTT  
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**SEQ ID 2022**

HKPDYSKRSSENRFOTTFYLITIKMLTTKNKPLFSVWRQIFN

SEQ ID 2023

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## SEQ ID 2039

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## SEQ ID 2040

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## SEQ ID 2041

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## SEQ ID 2042

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## SEQ ID 2043

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CGGACGATCGGCTGCGGTAATTCGACACTTTTGGATATTTTAAAGCGCAATCTACTCCGCAATCAGGCAAGTCATGATAAATGGGCACGACATTTACAGCTTACGCCACGTTTATC  
CGCAATTTGAGTGCATGCTCAGGACGACGATGTTTTA

## SEQ ID 2044

MDYLNLSLGLTKLPVLITQTEVABEGLACLAAGVGYFYTDLRALRSKYCLSLKGENLADIVRFADDMGLTGRALRLDLDELGLSLRPLCILHWDNLHFFVLESVSDGAAMDPASGR  
KVKTEISRKPTGLALELWPNTRFEAGEEKQIRILFMLRGISGLGRTLPQLLALAAAMEVFAFLQNVSPKIGRGESLALIGRSGCGKSTLLDLILSGNLPESGKVMINGHDYISLPRFI  
RNLAMVRQDDVL

## SEQ ID 2045

ATGATTTCGCGAAGAAATCTCCGCCATGCCCTATGGGCTATGAAACCTTGATCGGCGATATGGGCGGCACTGTACGGCGGCAAAAAACAGTATCGATTGGCGCGGCTTATATTGG  
AACCGAAATCTTATTTTAGATGAAGCGGCGAGTCAATTTGGATATTGCCAATGAAAAAGCAGTCAATGCAAACTTGAATGGCTTGTCTATTATAAAATTTATGGCGGCACACAGAAAGGA  
AACCGTGAATCAGCAGATAGGAAATGCTTTAGGA

## SEQ ID 2046

MIREESAMPMEYETFLIGDMGSALSGGQKQRIVLARALYCEPKILFLDEAASHLDIANEKAVNANLGLSIIKIMAAHRKETVESADRKMSLG

## SEQ ID 2047

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## SEQ ID 2048

MTFLQRWQGLADNKICAFANFVIRFSEERVPAQAASMTPTLLALVPLTVMVAVASIPVDFRWSDFSVFVNQTVIPQGDWVFDYIDAPRDQANRLTAIGSVMLVVTSLMLRTIIDN  
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GAFVAVPFFLLWLLNLTLLVLGAVLTSSLSYNQGEAFRRGFDSSRGRFDVLKILLLLDAAQKEGRTLSVQEFRRHINMGYDELGELLEKLARYGYTYSRGQGVWIKTGADSIELSELFKL  
FVYRPLPVERDHVQAVDAVMTPLQTLNMTLAEFDAQKQQQS

## SEQ ID 2049

ATGAACCCCAATCCCTCAAAATCTGCTCTACTATTTCCCAAAACGGCAGCACCCGCAATCCCGCACGCCGAATCACTCGCGGCATCGACAGCGTTGAAGGTTGCGAAGCCGCTATTGC  
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CCGCTTACCAAAAC

## SEQ ID 2050

MNPPLKILVLYSQNGSTRNPARRITRGIDSVEGCEAVLRTVPKVSAVCEAVKKDIPDSGSRPDRRRQYRLRTRQTLGGTRQVQIRRVFRRHGVQMPSEVCLYNPRLYCPTSRFANL  
PRYQN

## SEQ ID 2051

TTGACATATCGAATCTAGTTTGGTAACGCGGAGGTTTGCAGACCGGAAGTTGGACAGTAAGACGCGGATTTATACAGGCAACCGGTTTCAGACGGCATCTGAACGCCATGCCGCTG  
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CTTCGACAGCGCGGACACTTTGGGACGGTGCAGCAATACGCGTTCGCAACCTTCAACGCTGTGATGCGCGGAGTGATTGCGCGTTCGCGGATTCGCGGCTGCTCCGTTTTGGGAATAGTA  
GAGGACGAGGATTTTGGGGATTGGGTTTCATGGCGGATTCGTTAA

## SEQ ID 2052

LTYYRLLVLTREYCEPRSWTVKTRIIQANAFRRHLNAMPSEHAAYADLTASSAKRLPKAKILFSSAVRTGAAGVNIFFDGFADGGHFGDGAQYGFATFNAVDAASDSACGIAAGVLTIV  
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**SEQ ID 2054**

**SEQ ID 2055**

**SEQ ID 2056**

**SEQ ID 2057**

**SEQ ID 2058**

**SEQ ID 2059**

SEQ ID 2060

SEQ ID 2061

**SEQ ID 2062**

**SEQ ID 2063**

SEQ ID 2064

**SEQ ID 2065**

**SEQ ID 2066**

SEQ ID 2067

SEQ ID 2068

SEQ ID 2069

AFGCCCAACGGCGTCATCTCCCGGCGCAGGGCGGAATCCAGACCTTGATTATTCAGGAATATTTAAAAATTGCAGCAATTCCAAATCTCTGGATTCCCGGCTGCGGGGAATGACAGTGTGGA  
CGGTCCTTATT

## SEQ ID 2070

NPNRVIPAGAGIQTLIYQYKILKIAIPNLWIPACAGMTVNSVLI

## SEQ ID 2071

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## SEQ ID 2072

MKFPSTLLVLLVAEEHYIAWLEMTQIPGEKAAEMFKLPYEFMEQKRVQTLFGNQGLYNGFLAVGLLWQFAAPDNAVYGVATVLFGLFVLLAAAWGAPSSNGKILVKQSPAFPGSGGV  
GGMKKISVAPENPQYRIVBIFESLQEGWNTGMPAVFVRLGKCNLAGCWNCDTDLFTFGMSLSDLILRLKTYAARNIIITGGEPTIQLHDLTDLALKAEGYFLCLSTNGLKAPPQIDTV  
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## SEQ ID 2073

GTGTGCGCGCTTCCGCGTGAACATGCCGACATTTCCGCGCCCAATCAGGACGAAGCCTTAATGAATAAGATGCCGCGTGGGTACACGCCAGGCTTCC

## SEQ ID 2074

VCRFRVKLPTFPFPPNQDEALMKNKPRIGTRQAS

## SEQ ID 2075

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## SEQ ID 2076

LSFHRKIRKMNIFYEBSQFKVAVVVQKNDATYQVDTQHGKRTKVKANNVFAEFDGMAAPLENAQAQAADIDTDLLEWVCGEERPTAEALAEYYGHAPTKTELAATLIALYAAPVYFK  
KAGGVFAAPBETLKLQALAIERKQQAQIDAWAELKRGEMPEIAADLRTILHAPDKQSLTYKAFTKAADALKTSAYELAKRTGGTISIPQYLDQGFELKYFPKGTGFDLSLPEMPD  
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## SEQ ID 2077

GTGTACCAACCGCGGCATCTTATTCATTAAGGCTTCGTCTGATTGGGCGCGGAAATGTGCGGAGTTTACGCGGAAGCGGCACATTTCCCGGTATGTCAAACATCGGCAAAACGGTA  
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## SEQ ID 2078

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## SEQ ID 2079

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## SEQ ID 2080

LNLADTLCCQCAQAGLGRKLCRLKQHSVSDGIFLLPPKGNRPNGNRCGLNMVGMRFEPPTPSRRTKCATGLRYIPN

## SEQ ID 2081

TTGTGATGCGCGCAATGGCAGGATTGGGAAAAAGAAATGCCGTCTGAACACGATTTCTGTTTTCAGAGCGCATTTTGTGTTGCCGCAAAAGGGAAAAACCGCCCCGCAATCGATGT  
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## SEQ ID 2082

LSVRANGRI GENEMPSFATCFREHFFVA AKREKPPRQSMRSSEYGRNERIRTSDDPVFVNEVKYRAALHSELIKA

## SEQ ID 2083

GTGATTATAGCGCAAAAAATACGCGCTGCCTATACCGTTTGGCTTTTTCGCCGTGTCGGCGGATTTAAAAAGGCTCTCCGACTTTTACGCGCGCGCGCGCTGCTGCGCGGAGCAAG  
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## SEQ ID 2084

VILAQKIRRAATVLPFCRVSGFKRPLRLRLRPPCPAARQGRQRLAFLGNFLSA

## SEQ ID 2085

TTGGAGCAACCGCAATGACCGTCCCCATATTCGCGCGCGCGCGTCAATGGCAGACATTTGCCGCTTCCGCTGACCGAAGAAAGAAAAACACGCTGCTGATCCGCAATCGCGCGCA  
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GAGGCTTCCGCTGCGGCATCGATTGTGCTTCACGCCGCTCTTAGATTGGACTGGGAACTGCGCGTCATCGGCAACGCGAGCTTCCACGCAATCCGGAAGCGGTGCGCCGCTCG  
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GAGGCTTTT

**SEQ ID 2086**

LEYTAMTVPHI PRGPMVADIAAFRLTEEEKRLDPAIGGITLFRNPNQIBQLKTLTAIKALRTPLELIAVDHGGGRVQRTIEGFTRLPAMNVLQINDKDGAASAAETAGQVGRVLAT  
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EIHLLQILRRDIGFKGVIPSDLLTMEGACGAGGIKERARISFEAGCDIVLVCNRPDLVDELDRDGFITPDNQLAGRWQYNENSLGHEAVQAVMTGFGQAQAQAFVAGLASPDQTAGGVKVG  
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**SEQ ID 2087**

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SEQ ID 2088

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SEQ ID 2089

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SEQ ID 2090

MMLAGGGEFCPSEVYVFDSLYAASRRNGEPEETPRPYDANRDGLVIGEKARGFSYWKWNTPNGAVRKFTFNSSATAPTATASI SAKAOPYSS

**SEQ ID 2091**

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CGCAGGTGCATTGGCAACCGCCATTGCCCTGAATCGGGGTGCTGCTTACACTTACGCCCTGCGTGTCATTGGAACCGGTTGAAACGCAAAA

**SEQ ID 2092**

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**SEQ ID 2093**

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TAAAAATGCCCGGTAAATCGGTTATGACGGGCAATTTATCATTT

**SEQ ID 2094**

VLSVRNGGYLSASGLGFVGKMGGNIPCRKKYLFKINOLIFVKCPLIGIDGHFII

**SEQ ID 2095**

[illegible]

SEQ ID 2096

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**SEQ ID 2097**

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**SEQ ID 2098**

VRISQILTAALQNETLENSDGRCRISTYAV

**SEQ ID 2099**

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**SEQ ID 2100**

VPEDREALSLPGVGRKTANVVLNIAFHPVMAVDTHIFRVSNRTKIAPGKDVREVEDKLMRPIPKFELMDAHHMLIHLGRYTKALKPQCQCTCIINDLCRYPAKS

**SEQ ID 2101**

ATGCGTATCGACCCCAATAACGGGGTTCGGAACGCTGTGTTCAATACCACTGTTGCGCTTTTGGCGCCACGCGCAGCAACGATTCACAAAGCCTCGCGGTCTCCGGCACTTAGCCGTTG  
TATTTTCCAGCAGCATGCGCGAGGTTGCATAATGTGTTGGAATTTGTTATACAGCCCGATGGTTTCGTGTATTCATACAGCCGTCACAGCCCAATCCAGCATCGCTCGCGG  
TATCGCAACCGGAACACGCTTCGCGCTGCGCTGTGTACGCGCATCGGTCGCTCGCGCAAGCAGAACGGCGAT

**SEQ ID 2102**

MRIDRNGVSERCQYHVCRFAPHARQRFQSLAVFRHLAVVFFQHDAAGLHNHVFGLGFIQPDGFRVPHHVAQAIQHRLRRIGNRKQLRRRLVYADIGRLRRKQNGD

**SEQ ID 2103**

ATGCCGACCGCACAAACCGCATGCACAAAAAATGAACAGACAAATCCGCCAAGAAATCTTCGAGCGTTTCCGCGCCGCCAACCCCATCCGACCAACCGAGCTGAATTTCACTCCCTT  
TCGAGCTTTTAAATCGCGTTCGCTTTTCGCGCAGCGCAGCGATGTCGCGGTAAACAGGCGACGCGCAAGCTGTTCCGCTTCGCGATACCGCGCAGGCGATGCTGGAATTTGGCGTTGGA  
CGCGGTGATGGAATACAGAAACCATCGGCTGTATAAAACCAAGTCCAAACACATATGCAAACTCCCGCATGCTGCGAAAAATACAAACGCG

**SEQ ID 2104**

MPTAQTDCTKMMNRQIQEIERFRAANPHPTTELNFNSPFELLIAVLLSAQATDVGVNKATAKLFVADTFQAMLDLGLDGVMEYTKTIGLYTKSKHDMQTCRIVLEKYNG

**SEQ ID 2105**

GTGCAGTCGGTTTGTGCGGTTCGCCATTATAACGCACGCTTCAGCGCGGTAATATTGCAATTCCTCCACAGAAATGAAGCGTAACGCGCGCTTTTGGCGATAAACGACATCAGCCCGCTTGT  
CACGGATTCAACCGCAGCCAGCGCGGTAAAGCGCAGTGCCTCGCCGACGACGGCAGCCACGCAACGCAAGCAGCCAAATACCGAAACCGCGTATCAGATTCACTGTTTTCAGACG  
GCATTTTTCGGGAAGGCGAGCAACCTCCATCCAAATAGGAAACCATATGCTCCCAATCCGTTGGCAAGGCGCGCAGCAGCAACGCGCGCTATGCTGTTTGGGGAAGTTCGGGACGAACAG  
GGCGAAGGCGGCTTCGACGCTGCGCGGCGAGGGTGGCGGAAGTGAAGCGGAAAAAGCGAGGCGCGCTAGGTTAGGAGGGTATCATTCGCAACAGTCCCAACAGGTAAAAATCGCG  
GACGGATTATACGTATTTTACGCCCCCGCGAAGGCGGAGGACGCTGCAAAATACGCGCACAGCGCTATGCCCTTTTTCGCGGGCATACGACATCTTTCGCGCTCCGCTT

**SEQ ID 2106**

VQSVCAVGIIITHSGGVILHSPQNEGVTRFADNQHPACPRIQPQAGGKQCVADDQPRKRKQPNTEPYQIQCFRRHFSGRQQTSHPIGNHTAQSVGKAGAQQRAVCFVGEVADEQ  
GEGGFGRAGQEGGSEGGKSEGGVGVGGYHCKQSQTGKNRRRIIRYPHAPBGRRTVQKYGTAVCPFFVGHITFFPLRF

**SEQ ID 2107**

ATGCCCGACAAAAAGGGGCATACGCTGTGCCGTATTTTGCACCGTCTCCGCCCTTCGCGGGGCGGTGAAAAATACCGTATAATCCGTCGCGGATTTTACCTGTTTGGGACTGTTG  
CAATGATACCTCTTACACCTACGCGCGCTCGCTTTTTCGCGCTTCACTTCGCCCACTCTCTCGCCGCGCAGTTCGGAAGCGCGCTTCGCGCTGTTCGTCGCAACTTCCCAACACAGC  
ATACGCGCGCTTCTGTGCGCGCGGCTTCGCAACGGAATGGGCGATGTTGTTCTATTTGGATGGGACGTTTGTCTGCTTCCCGAAAAATCGCTGTGAAAAACACTGAATCTGTATACGG  
CGTTTCGCTATTTGGCTGCTTGCCTTGCCTGGCTGCCGCTGCTGCGGACGCACTGCCGCTTACCGCGCGCTGCTGCGTTGAATCCGTGGAACAGCGGCTGATGCTGTTATCGCA  
AAACGCGCGCTTACGCTTCACTCTGTGGGAATGCAATATACGCGCG

**SEQ ID 2108**

MPDKKAYGCAVFLHRPPPGGGVKIPYNPSIPTCLGLFAMI PSYTYAALAFSAFTSATLLPGTSEAFALFVRNPKHAYGALLCAGLANGLGSMSVYWMGRLLPSRRMPSEKTLNLIR  
RFGIWLAFANLFPVGDALPLTAGLRLNPNWTSGLMLVIGKTARYAFILWGMQYIAA

**SEQ ID 2109**

ATGCAGTCCGCGCAACAGGTTGACGGTTGCCGTTCGCCCTTTTGTGGAAGATGATTGCCCGCAGGAAATGCGGATACGTTCTCCGCGGTGCCGCACTTCGTTCAATTTG  
ATGATGTGCCAGCGCAATTCGGTTCGACAGCGCGCGGACCTGTCCGGTTTGAGCGCGTGAGCGGCTTCTTCAAAGCGGGAACATTACGCGCTTCGCGCAACAGCGCAAGTCCGCC  
CATTCGCGCGCTTTCGCTTTCGGAATATTCGCGTCCCAACCTGCGAAATCCGTGCCGTTGCGCGCTGCTGCTAGATTTCGCGGATGGTACTTTCGCGCGGACGCGCGGCTTTTGTG  
GTCGCTTTAATCAGGATGTTTGGGCGCGTATTCGCGCAACGTTGCCCTTCGCGCAGGTTGATGCTTGTTCGCGCTGCTGCGGAGGCAATCAATTCAGCTTCGCTCAGCGG  
CTGTTTTCATCACTGCTGCTGGCGGACTTTTCGCGCAATGATGTTGTCGCGAAGCTTCGCGCGTTCGCGCGTTCGCGGCTGAGGTTTTCGAGGCGGATTTTGTGCGACGCGCATCGATT  
CCGCTTCACTTGCTGAATGTTGCGCGCTTTCGCGCTGTTACAAATCAGGATTTGTTGCAAGCTGCATCAGCACTGTCGCGACAGCTCGGATTCATCTATCTGCGCTCTTCGCGCAG  
GGTGGCTTCGCTTCGCGCAACGCTTCGCGCAAGCGCGGTTGGTGTGACTTCGTTGTCGCGCAACGCGCAATGCCGTC

**SEQ ID 2110**

NQVAQQVDGCLSGFLLDVLPHGIADFFLRRAGIAHFVQFDDVPAELGADRADLSGFERVDGFFKGGNHVAVGKPAQVAALARACVLGISACQTCIRAVARLVVDFADGTFRADGGVFA  
VGFNQDVLGAVLAQRCAFQGDALFLRLLEBGINFSFAHAAVLHCLLADFGNDVVGKLAALGGAEVFEGGILCDDGIDFRFTCLNVAAPARLYNQGLVDKHLQHLGSLGFTYLRVFGQ  
GGFGNGFGKPAVGDDFVVGNDSNAV

**SEQ ID 2111**

TTGAATACCAAGGCTCGCATACCGGCATAGCGCGCATTAACGCTTCGCGCGGATTTGGCAAGCATACAGCGCAGCTTCAAAGCGCAAAAAACGCGTCAAAATATATGGAATGGC  
GCGAACGTTTCCCGAATTTGAAGCGCAACTGGATGCGCGGATTGAGGATTACGCGCGCGCGAAACATTGGACGCGCAAGCGGCTCAGAAATATGGGCGCGTTCGTACCTGTGCGTCGA  
TGCAGCGGAGCAGGCTTTGATGGATGACAGTTTGTCTCGGGACGAAAGCATATACGACGCGAGGATGGGCGTTCCTTCGCGCTCTTCGCGCGCGCGCAACAGACATCGGAGATGTGGGA  
GAATTTGCTGTACCGCGCAGCTTCGCGCAACTTCGCGCGCAATACCTATGTCGCTATGATGCCGACACCGCGGACGCAATATCGGCATCTTTTCGGATTAAACAGGACGATCATCCCG  
ACATCGAGCGCGTTCCTTCGCGCGCAAGGCAATAGTTATGCTTACGAGGCGCAATAATACGCTTACGCGGATGATGCGCGACACCGCGGACGCAATATCGGCATCTTTTCGTA  
ATGTTTTCGACTCGCTTATGCGCGCAGCGCGCGCAACGCGGAAAGGATTTACGCGCAACTCGTTCGCTTACGCGCGCAACGCGGATCAATATCGCGGAGGCGGAGGATTTTCGTA  
TTGGAAGAAATTTGGAACACGCCAACGCGCGGTGCGAAATTTACGCGCAACTCGTTCGCTTACGCGCGCAACGCGGATCAATATCGCGGAGGCGGAGGATTTTCGTA  
GCGATGCGGATTTTTCGCGCGGTATGCGACTTCTGGTTTACGCGCGCAAGCAGCGATGCTTACCTATTTTCCACGCGCGCGCGCGCAAGGCGCAATCTCGCTTCAGACGCGCAT  
CAGCACGCGCGCTTCGCGCGCAAGACATCGCGCGGATTAATCTGCACGCGCAGCGGACGCAACCAACGACAGATATGGAAGCGCGCGCTTCGACGCGTTTTCGCGCAACATACGCGCT  
GCAGTCCGCGCAAGCGCAACCGGACACAGCTGGCGCGCGCGCGCAATCGAAGCGCGCTTCGCGTGGGCAATTCGCGACCGCGCAAGCAATCCGAGGCGAACTTCGCGCGCGCT  
TTGGGACGGCAGAACGACCCGCACTGCCCGCAATTAAC



**SEQ ID 2113**

SEQ ID 2114

**SEQ ID 2115**

SEQ ID 2116

SEQ ID 2117.

SEQ ID 2118

SEQ ID 2119

SEQ ID 2120

SEQ ID 2121

SEQ ID 2122

SEQ ID 2123

SEQ ID 2124

SEQ ID 2125

ATGCCGCGCGGTGAGGCACATTGCCGTCGTGTCGCTGTAATTGCCGCAATGGGCTATACCATCAATTTCATTGGAGTGGCTGCCGCATATGTCCATTATTGCCGCCATCGTGTGCTGTAATTTGTACGGCTTGGCGCGCGGTTTGAATACACAGATATGCAGGCAGGAGTAGATAGCGCGCTTGAATCAGGGTATGGCGCGGTTTACCCTGTTTTCCTTCATCGGGCTGATGGTCAGCGCGCTGATGATAGCGCGCGGATTCGCAGCGCTGATGTATTACGGTTTCGGGCTGATTTCCCGACTATATTTTATTTTTCGCGCTTCGCGCTGTGTTCGGTATCGGCTGTCCATCCGACAGCAGCCTGACCGCTCGGCCACTGTCCGCGTGCCTTTGCTTTATGGGAGTGGCGCGCGCTTTCAGGCGGATGACCGGCGGCGCGGCGATGTGTTCCGGTGTGTTTTCGGCGATAAATATGTCGCCCTTTCGCACACACGGGCAATTTCCGCGCTCCTAGCTGTTTTCAGACATCAAAAACATGATGTACACCACCATCCCTCGCTGGCTTATCAGCGCGGCACTGATGCTTTGCTTCTTCCACGCTCGCGCGCAGGATTTGAACAGCGTCGAATCCTTCCGACGCCAGCTTGAAGCCACGGGATTTGGTGACCGCTATTTCGCTGATTCGTTTGCACGTGTTGGTCTGTTTGGCAATTGATGCGCGTCAATGCCGTGGTCGCCATGCTCTTTTACCGTCATTGCCGCCGTTGGCGGTAACTGATCTGCACAGCAGCGCCGATCTGGCTCAGCTCGCGCGGCTGTTTATGGCGGCTACAACTCGAAGCGAAGCGTTTAAAGACATTGCCAACTGATTTCCGCGCGCGGCTTGGAGAGTAGTGTCTTTACGACAGCACTGTTATCTCCGTTAGTGTGGCGCGGCTGCTGCTTATTCGCTCGGTGTGATTCTTCTTGTCTGAGGAGCGGCTACCTTTCAGCAATGCGCGGACGCGGCACTTCAGGCTGACCTAGCTCTCGCTGGGTCAATTTCTGATTGAGAGCAATTTTTCGATCACTTCCTGTTTCGGGAGGCTTCAACCTGTTTACGACATTTACGACACTCGGCTGCAATCTGCTGCAACTCTGTCGCGCACTTGAAGATGCGGGACGGTGTATTAAACCCGCTCGTGC

CGTGGAGCGTGTGCGCGTATTTATCAGCCACGCCCTTGGCGTACCGGTTTGGGAATATCTGCCTATGCTTTTTCTGCTATTTGAGTTTGGCTTTAACCTGTTATTCGGCTGGACGG  
GCTGACTTTGAGCAAAAAA

## SEQ ID 2126

NPRGEALAVVVALIAAMGYTIIISLEWLPHMSIIAAIVVLLIYGLARGLKYNDMQAGNIGALNQMGAVYLPFFIGLMVSAIMMSGAIPTLMYYGFLISPTTFYFSAFALCSVIGVSGSS  
LTACATVGVAFMGMAAFQADMAITAGIVSGVFGDKMSPLSDTTGISASIVGIDLFEHIKNMYYTIPAWLISAALMLWLLPSVAAQDLNSVESFRSLEATGLVHGYSILIPFALLVVL  
ALMRVNAVAMLFVTIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFKDIARLISRGLESMTPTQTVILGMSLGLLFPALGVIPSLLEAVRTPLTNAGRATPSVAMTSVGVNFLIGE  
YLSILLSGEYTFKPVYDKLGLHSCNLSRTLEDAGTVINPLVPMSVCCGVFISHALGVFVWEYLPYAFPCYLSLALTLPGWTGLTSLKX

## SEQ ID 2127

TTGCAGCAGCCCGGCTTTCGCGCCGAAGACATCGGCCGGATTAATCTGCACGGCACCGGGACGCCACAACGACAGTATGGAAGCCGCGCGCTTGCAGCGGTTTTCGGCAACAATACGC  
CCTGCACGTCGCCAAGCCGCAACCGGACACACGCTGGCGCGGGCGGCGCAATCGAAGCCGCGTTCGCGTGGGGCATTCGCCAGCCGCGCAAGCAATCCGGAAGGAAACTTCGCGCCCG  
GCTTTGGGACGGCGCAAGACGCCCGCACTTCGCCGCCATTAACCTGACCGGGCAGCGCTGGGAACCGCAAAACCAATTCGCGCCAGCTCGTCTGTTCCTTCGGGGGAAGCAACTCGCTC  
TTAATCATCGA

## SEQ ID 2128

LQHAGLAPEDIGRINLHGTGTHHDSMESRAVAAVFNNTPCTSAKPTQGTHTLGAAGAIEAFAWGIADRSNPEKLPRLWDGQNDPDLPAINLTGDSWETEKRIASSSFAGGSNCV  
LTIQ

## SEQ ID 2129

ATGTGCACTGCCCTTTTGGCGGCAATGATGAACCTTGCACGGCAAGGGCTGTACACATGTGTACGGCGGGCAGCGGTTATCTCTGCATCGACGGCGAACTTCCCGCGCTCGGTG  
GCACGGCGGATATGTATTTTCCCGCGCGCTTGGGTTCATGTGTGAGCCACGACGGAGAAATACGGAGAAAGTTTACAACCGGACATACGCAAAAACGGCACATTTATGGTCAACAGTG  
CGGCAACGGGCTGGATATGAGCGTGTTCGCGCCGTTTCGCTACGACACCCACGCGATTTGATGAACGGGCTGCCGGAACCGTTTTCTGAACATTGCCCATCCAAGTTTCAGTAT  
GTGGTTTCAATGCTGCACTGAAAGCGAAAACTTTGACGGGACGGTTTCGCTGTCTAACGCAATTACCGTCCGCTCTGCTGGTCTTATCTCGCGCGCTATCTCGAACAGGATAAGG  
ATGTGCAACTCTCGGCGCTATTGAAGGTTGGCAGGACAAACGTTTGGGACATTTGATCCAAAAGTGATAGACAAACCGGAAGACGAATGAATATTGACAAAATGGTTGCCGCCGCCAA  
TATGTCCGCGCGCAACTGATGCGCGCTTCAAAGCCAAAGTCGACTACGCCCGCAGCGCTTTGTGAACCATATCCGCTGCAAAAAGCGCATTCGCTGCTGAAGAAAACCCCGGATTTCG  
GTTTGGAGGTGCGCGCTGCTGGTGGCTTTCAGTCGAAACGCAATTTCCGCAAGCGGCTTCAAACGGCAATATCACGTTTCGCCGGGCAATACCGGAAGAGCGGGCAAAAA

## SEQ ID 2130

MCSAFWADNDETQREGLVHITAGSGYLCIDGETSPRPVGTGDIIVFPRLGHVLSHDGKYGESLQPDIRQNGTFMVKQCNGLDMSLFCARFYDTHADLMNGLPETVPLNIAHPSLQY  
VVSMLQLESEKPLTGTVSVNALPSVLVILILRAYLEQDKDELGVLRGWQDKRLGHLIQKVIDKPEDWNIDKMVAANMSRAQLMRRFKSQVGLSPHAFVNHIRLQKGLLLKKTTPS  
VLEVALSVGFQSETHFGAKFRQYHVSEFGYRKEGGQK

## SEQ ID 2131

TTGTATCGACTTAATCTGAAACACAAAAGCAGGATTAAGACACAAACAGCAGTAAGCTTTATCAAAGTAGGATTTCAAGTTTGCTTACT

## SEQ ID 2132

LYRLNPETQKAGLRHNKAVSFIVKGISSLLT

## SEQ ID 2133

GCCAAAGGCAGGCGAAGTACCGCGGGCTTCGGTACCTTGTGCCAAGGCAGGCGAAGTACCGCACTTTGCGGGCGAAGCCGCAAAACGCCGAGAAAGCGGGGGGATTGGCGATAAGCGCG  
AGGGGGTGTCGCCACAGCGCTGCCGCGCGCGAATTCGGAGCAA

## SEQ ID 2134

AKGRSTAGRLYLVRQAKYRTLRAKPQTAKRGGIGDKREGVSPQRCAANAQ

## SEQ ID 2135

TTGGCACTTTATAAATATCAGCGCTCAAGCGAGTATTTTGGGCAATCGATGGCGGTATAGCGCAATCGAATTTGTGAAATTTGCGAAGATTAATAAGTCTGAAAATGTTATGATGTT  
TCTCTTTTCTGGAATAGAAGAAATCAACATGACATTTGGTTAATATCATTTCTCGTAAATTCGGAATGGTAATTAAGAATCCTTGAACGATGTCACAAAACATACAAATTTGAAT  
TTGCGAAATTTGTCGATAATTTGCAATTTTGTATGATGATTTGCTT

## SEQ ID 2136

LALYKQPSSEYFGQSMAVIAQSEVFVFAKINKSENVICDFSPFWNRRIKHDIWLSFPDENSENVIKESLNDGHKTYKFEPCIEVDNCFNDVFF

## SEQ ID 2137

TTGCCCGTTTGTAGGATTTCGCAATGGGAGATAAGCAAGGGATGACAAAGCGGTTCGCGCGTGATGACGGACGCGCGGGCGGACGGCAGGAAGCGGCAACCCCTTCGAATCTTCCCG  
CCCTTATCTAACAGGGGGGTACAGAAACCGAAACGGCGGGCAGGGTTTCAGAAAGTCTTCGAATGTTACGAAACGTACA

## SEQ ID 2138

LPVFEDSQMGDKQMTKAVAGVMTDAPADGRKPATASNLPPPYLTGGVQKPRRAGFRKSSNVTKRT

## SEQ ID 2139

ATGGACGGCGCACAAACCGAAACAAATTTTGAACGCTGATTGCCGACTCGCCCGGAACCCGATTCGCCGAAGACGTATTAACCTGCTTCGGCAGGGCGCAAGACAGGAAGTTT  
TTGATGCGGACACACTGACCGGCTGGAAAAGTATTTGACTTTGCCGAGCTGGAAGTGCGGATGCGATGATTACGGCAGCGCATGAACGTATTTGAAAGAAAACGACAGCATGAAG  
CATCACCGCTACGTATCGATACCGCCCATTCGCGCTTCCCGTCACTCGCGGAAGACAAAGACGAAGTTTGGGCAATTTGCACGCCAAGACCTGCTCAAATATATGTTCAACCCCGAG  
CAGTTCACCTGAAATCCGCTTTCGCGCTTCCGTTTTCGTCGCCGAAGGCAATCTTTGACCGCCCTTTTAAAGAGTTCCGCGAAGCAGCGCAACCATATGGCAATGCTCATCGACGAAT  
ACGGCGGACGCTCGGTTTGGTACCTTTGAAGACATCATCGAGCAAAATCGTGGTGACATCGAAGACGAGTTTGAAGAACGAAAGCGCGGACACATCCACTCCGTTTTCGCGGAACG  
CTGGCGCATCCACGCGGTACCGAAATCGAAGACATCAACGCTTTTTCGTTACGGAATACGGCAGCGAAGAACGACCATCGCGCGCTTGTCTATTGAGAAATGGGACACCTGCGC  
GTGCGCGCGCAAAAAGTCTTATCGCGGTTTGCAGTTCACGCTCGCCCGCGCGCACAAACCGCCCTGCACACGCTGATGGCGACCCGCGTGAAG

## SEQ ID 2140

MDGAQFKTNFPERLIARLAREPDSAEVDNLRLQAHEQEVFDADTLTRLEKVLDPFAELVRDAMITRSRNVLKENDSIRITAYVIDPAHSRFPVIGEDKDEVILHAKDLLKYNFNE  
QFHLKSVLRPAVFPBGSLTALLKEFREQRNMAIVIDEYGTSGLVTFEDIEIQVIGDIEDEDEDESADNIHSVSAERWRHAETIEDINAFGTETGSEEDTIGGLVQLGHLPL  
VRGEKVLIGGLQFVARADNRLRLHFLMATRVK

## SEQ ID 2141

ATGTTCAATGCTTCAAGAANTGAAACGGCGTGGAGTCTATCATATTTGAACGTTTCTTCAGACGGCACCGTCAGGTCTATGTTATATTACGCCACAAAACAGGAAACCGGCCAA  
TGAAACGGCGCCAAAATACCTTCTTAACGTTGCAGCGGCAACGTTTCAATTTGAACCTTTGAAACGCCCTTTCGCCCGCGGCGCATCCCGCGGAACGCGATTTTACCCTGGCGGTG  
GTCGCTTGAAAAACGAATACCTCCGCGCGACATCGGTTTGTATCTTTTGGACGAAGAAGACCGCGCTACACCGCGACTACCGGGCAAGATPATGCCCAATGATTTAGAT  
TTGCGGCTCAACGAAGCGAAATCCTGCCCTGCCAAGTTTTCGGAAGACGTACGCGGATTTGATATCTGCCCGCAAGTCTTTTAAAGAACCGCGCAACAGGCGAAAACCGCTGAAC  
GGCATTTGCCCACTTAACCATACAGCGACGCTGACCTGATGGGATACGACCATCAAGACGATGAGGCGGAATATGGAAGCGGAAGAAATCCGCTGATGCGGGCGGAGGCTA  
TCCCAACCCCTACCGAGAGGACGACAT

## SEQ ID 2142

MFNAFKWKRRGVHILNVSSDGTVRSMYLRPQNTKPMTRAKKYPFLTLQRQPHLNFENASSAAGIPAERDFYRHWSALKNEYLRADIGLILDEEBARAYNRDVRGKOYATNVLS  
PALNEGELLPQVSERLYGLDILICPQVVLKEAABQGRTPERHFAHLTHGTTHLHGXYDHIXDDAEIHEAREIRLHRAAGYFNPYREDGH

## SEQ ID 2143

TTGAACGCATTGAACATGAACCCGAAAAAACTTGTATCGCCACGCCGGAAGCCCTGCTGCCATGTGGCAGGCGAAACATATCCAAGGCCGTCTGAAGCGCTGTATCCGATTGCGAAG  
TCGAAATTTTGGGCATGAACACGCGCGCGACCGGATTTTGGACAGAACTTTGTCAAAGTCGGCGGAAAGGCTTGTGTGTCAAAGAGTTGGAACATCCCTTCAAGACGGCGCGCGCA  
TTTGGCGGTGCATTCGATTAAGGACGTCGCGATGGAFTTCCCGAAGGCTTCGCCCTTGGCCGCATCAGCGAAGCGCCAAATCCGTTTGACGCGTTTGTGTCCAACCGATACGCGCGTTG  
GAAGAAATGCCGAAGCGCGGTTGTGCGCACATCCAGCTTGGCGCGGAAGCCAGTTGCGCGCGCGCTATCCGCATTTGGTAATTAACCCCTGCGCGCAATGTACAAACCGGTTGT  
CCAACTCGCAACCGCGGAATACGATGCAATTATCTTGGCTGCGCGCGGTTGCGAGCTCTGGAATGGAATGAACGATCCGCAATGATTTGTGCGAATCCGACAGCGCTGCTGCGCGCG  
ACAAGCGCATTTGGTATTGAAATTCGACGCGCATCGGAAGATTTGTACGAAGCTTGAAGCCGTTAAACACGATACACACAGCGCTTACCGCGAAGCGCGCTTTGGCGCGCGCT  
TTGGCGGAAGCTGCCAAGTCCGCTGCGCGCTATTCAGTGAAGAAACGGGCTGCTGATCTTGGCGGATTTGGTGGGCATCCGACGCGATCGATTGTGTGTCAGGCGGACGCGCAAG  
CCCTGCGCGATATGCGGATGCGCTTGGAGTGGGTTGCCAAAAAACTGCGCGACGAGCTGCGCGAGGAATTGATTGGAGCAGTATTGAATACGGAAT

## SEQ ID 2144

LNALNPNFKLVIASRESILANWQAKHIQGRILKALYPDCEVEILGMTTRGDRILDRTLKVGKGLFVKELEQSLQDGRADLAHVSIKVPMDLPEGFALAAI SERANPFDAFVSNRYARL  
REMPEGAVVGTSSLRREAQLRARYPHLVIKPLRGNVOTRLSKLDNGEYDAIILAAAGLQRLLEDRIIRMLSESDSLPAAGQALGIEIATHREDLYELKPLNHDTTHACVTAERALAR  
LGSGCQVPLAAYCTEENGILLRLGLVGHDPGSTVLQADAQAPAGTADALGRAVAKKLADDGAEELIGAVLWFTEN

## SEQ ID 2145

TTGTTTTTAATTAATTTATTAATAAGTTTACTACCTTATTTGTCATTCCCGCGCAGCGGGAATCCAGTTTGTCTGGTTTCAGTTGTTTTTAATCAATTCCTGCAGCATTTGGTTTC  
CAGATTCGCCCTCGCGCGGAATGACGCGGAAAGTTTGTGCTTCGGATAATCTGTCGCGTTCAAATTT

## SEQ ID 2146

LFLNLNFKPSPYFVIPAQAGIQARFQLFLINSCSIGPDSRLRGNDGKVFVASDPTVAFKF

## SEQ ID 2147

TTGGTTTTCAGATTCCCGCTGCGCGGAATGACGCGGAAAGTTTGTGCTTCGGATAATCTGTCGCGTTCAAATTTGAATTTGAGAATGATGATATTCGATTTTTTTATTTG  
GCTGTACTAGATTATCCCTAAATTCACACCAATCCCGCAGGATTTT

## SEQ ID 2148

LGFIIPACAGMTAERFLMLRIILWRSNFEFENDDIRIFYCGCTRLSLNSTPIQDF

## SEQ ID 2149

TTGCTCCCTGCGCTCAAAAGAAAAATCATGCCGACGGTATTGTTTATGCCGATAGCCCGGCGAGCGCGCAAGTTGGACGCGCGCGGTTTACCGTTGCCGCAATCAACCGTTCCAAGG  
AATTTGCAGACCGTCGGAACCAATTAACGGCATTTGGAACCTTTGGAATCAGGCAAAACGCGCTTGGCAAAATACAAACGGAATCGATCGTAAACCTTTCCCGCGTTGTTGAGGGAATG  
CGAATTTGCACTTAACCTCGGCACACCGTCCCGCAGCTAAAAATCTGCGGGATTTGTTGGAAT

## SEQ ID 2150

LLPAAVKKIMPDIYVADSPGSRGKLDAGGFTRCRINRSKEPADRRNHINGIGNFNQAKRALRKYNGIDRPFPLLRCEFRILNSGTPSRQLKILADWCGI

## SEQ ID 2151

GCGGATGTCGACATACGCGCGGAATGACGGTCGCGCAACAGTTGACGTTTCCCTGTCGCGCTTTTGTGGAAGATGATTGCGCGCAGGAATGCGGATACGTTCTCCGCGCTGCGG  
GCATCGCGCACTTCGTTCAATTTGATGATGTCGCGCGGAATTTGGTTCGCGCAGCGCGCGCGACCTGTCGCGGTTTGACCGCTGCGCGGCTTCTTCAAAGCGGGAACCATACCGCT  
CGGCAAAACCGCAAGTCCCGCCATTTGCCGCGCTTGGCTTTGGGAATATCGCGCTGCCAACTTCCGAATCCGTCGCGCTTCCGCGCTGCTGCTAGATTTCGCGGATGTTACTTTC  
CGCGCGCAGCGCGCGTTTTCGCTGTCGCGCTTAAATCAGGATGTTTGGCGCGGTAFTTGGCGCAACGCTGCGCTTCCGCGCAGGTTGATGCTTGTTTTTCGCGCTGCTCGAGGAAGGCA  
TCAATTTACGCTTCGCTCAGCGCGCTGTTTTCGATCAGTCCCTGCTGCGCGCACTTTTTCGGAATGATGTTGTCGCAAGCTTCCGCGCTTGGTGGGCTGAGGTTTTCGAGGCGCGGAT  
TTTGTGCGACGACGCGCATGATTTCCGCTTCACTTGCCTGAATGTTGCGCGCTTTCGCCCTGTACAATCAGGATTTGTTGACAAGCTGCAATCAGACCTGTCGCGACAGCTCGGATTC  
ACTTATCTCGCGCTTTCGCGCAGGTTGCTTTGGCTTCGCGCAACGCGCTTCGCGAAGCGCGGTTGTTGATGACTTCGTTGTGCGCAACGACGCGCAATGCCCTCTGAAAAGCGGATACCG  
CCCTGCTGTTGTCGCGGTCGCGCTTCTTTTTCGCGCTTGGCGCGAGCTTTGACCGCTTGGCGCGCGGTTTTCGCTTTTTCGCGCTGCGCGTGGACATCGCTGCTGCCAGCAATGCGG  
CGCAATCATCAGGCTTTGATTTTCATCAT

## SEQ ID 2152

ADVDIRAGMQVQVQDGLSGFLEEDVLPBGADTFLLRAGIAHFVQDDVPAELGADRRADLSGFERVDGPFKGNHYAVGKPAQVAAIARACVLGISACQTCETRAVARLVDFADGTF  
RADGGVFAVGPNQDVLGAVLAQRCAFGQDALFLRLLEEGINFSPAHAALVHLHCLLADFPGNDVVGKLAALGAEVFEGLILCDDGIDFRFTCLNVAAPARLYNQGLVDKLHQLHSQLGF  
TYLRFVQGGGFGFNGFGKPAVGDDFVVGNDGNAY\* KADTALLLCGCFPLLRGGSFDRFGFGFCLLRGVDIGCCQCGGNGHGFDFH

## SEQ ID 2153

TTGATTATAATGGCGGATGAAAAAATACCTTATCCCTCTTCCATTGCGCGAGTCTTTCCCGGTGCGAGTCTATTATGTGCCACATTGACGGAATCCCGGTGAATCCCATCAATA  
CCGTCAAACCGGAAGCACTGCAAAAGGTTTTCGCTCGCCCTTCGCATTGCGCGGATGTTGCCAAATCAGCGATGAAGCGACGCGCTTGGGCTATCAGTGGGTATCGGTAAATGAC  
CAAGTTTCAGCGCGCAATATCTGAACAACTTCAGAAAACGCTTGGTTCGCGCAGCAATCCGCTCGATGACAGTATGAAATCTACCTGCGCTTCCGCGGTAGACAGCCAGCGCGCGGAA  
ATCAATACGGAACAGTCCAGCTGTATATCGAGAATGCTTTCGCGGCTGCGCAGCAGCTTGGAAAAATATGGATGCCAAACCCGATAATCCCGCATTTACCACTTTTGTATGGAAGTGA  
TGAAGATGACGCTTTGAAA

## SEQ ID 2154

LIDAGMKKYLIPISIAVLSCQSIYVPTL/TEIPVNPINTVATEAPAKGFRLLAPSHWADVAKISDEATRLGYQVIGKMTKVQAAQYLLNFRRLVGRNAVDDSHYIYLRSAVDSQRGE  
INTBQSKLYIENLRGWQQRWKNMDAKPDNPAFTNFMVEMKQPLK

## SEQ ID 2155

TTGTTTTTAAACAAAAACAGATGCCGTCTGAACCTGGTTAAGTTTCAGCGCGCATTTTCATATGGCTGCGCTTTTACAGTATATTCAAT

## SEQ ID 2156

LFFNKKQMPSELVKVQAAPSYGCAFYISIFN

## SEQ ID 2157

TTGTTTGAATTTGTTATAGTTTATTTGTTTTTAAACAAAAACAGATGCCGTCTGAACCTGGTTAAGTTTCAGCGCGCATTTTCATATGGCTGCGCTTTTACAGTATATTCAATTAACAA  
AATAGTACAACTCGAGCTTGAAGTT

## SEQ ID 2158

LFEIVIVYCFILKNRCLNWLFRRHFMMAALFTVYSIRKNIVQHSYLRV

## SEQ ID 2159

ATGGCATACTCTCGGACTTAAGAAACAAAGCTTTAAACCATAGCGGATTAACAAAAATCAGGACAAGCGCGCGGACCGCAGGCAATGATACGGAACCGGTTGCGCGCGCGCTCC  
ATCACTTAGGGAATCGTTCCCTTTGGCGCGCGCGCGGCAACCGCTACCGGTTTTGTTAATCCGCTATATACGCAATGCAAAACACCGGCAACCGCGCAGCAAGCTTAACTTG  
TCAAGAAACACGCTTACTCTCGGATTCGCTTAAAAAACAAACAGGCGAGC

## SEQ ID 2160

MAYSADLRNKALNHSGLTKIRTRRTAGSTNGTEPVRPALHHLRESFPLGRGSGATPYRFLIRYITDNAKTPAKPQORLTQETRTCFALKNKQAA

## SEQ ID 2161

ATGCCGCCAAATCGGATAGGCAAAAACCGCTCGATATGTGCGGGCGCATCCGGATGCTGTCTGCATGAAATCGCCAAACATTTGATTGTACGGCAGCCGCGGTTGCCATGCGCCCAA  
ACAGATGCGGATGCGCGCAAAAAGACCGCCGCTTACAAAGGACAAGACCGGCGCAAGTAACGCATTATTTGACACGGCGCGCGGATTTCCGACTGCCAACGCGTTTGTCCGGATGA  
AACAGGATTCGACCGCGCGCTGTTCGCCCTTATGCCCGCAGCTGAAAGGGCAATGGCGAAAGCGCGGATAGGGTGAAAAGATACCGCGCTTATCTTTGGTGTCCGCACAAGTCGGC  
AACCGCGGATGCTCCGATGTTTGTCAAATACGGTGGCGGGGCTCTTTTGAAGCGCGGTTTCAGCAATGCTTACTGCCCGCATTTGGCTCAAAAATCGGTGATTATTTTCAGATAATG  
CGCGATTTCCGCGTATGGTGTCTTACGGGGAACCGCGGAAAAATGGGACATAAGGTATTTGCTCCCGCACCTTATTCGCTGAGCCCAACCGGATGAGAAAGTGTGGCGGAATATTAA  
CGGTATCTGCGAACCGTTTGTCTGATTACGCCCGATTGACGATGCACTACTGTCTATTTTGATTTTAAT

## SEQ ID 2162

MPPNRIGKNRLMSGGIRMPVCMKSPNLIIVRQPPFAMRPNRCGRWAKKTAAYKQDPKAVTHYLTPAGFSDCQVCPDETGFDRRLFRPYARSLKGMMAKARIRVKRYRLSLVSAQVG  
NRPIAPMVQNTVAGVFFEARQQLLPAQAQSVLISDNARFRMGALRGTAELGHKVLPPAPYSPENPIEKVWANKRYLRVLSYARFDALLSYDFN

## SEQ ID 2163

TTGCTGCTGTACAAATATCATTTTCTTTTCCACTCAACCATCAGGATTTCCCAATGCCACCAATTCGATGTCGCGTAATCGGCGCAGGTCGGCAGGTCGGCGCATCCGCCCTGC  
TCCGCAAAAAGGTTATCAAGCTCGCTGTGTGAAAAACAGCACTTTCCGCGCTTCGTATCGCGAAAGCCGTGCTGCGCACTGTATGGAATGCTGGAAGAGCGGTTTTCGCGATGCC  
GTTCCGACCGCGCGCGCTTTCAGT

## SEQ ID 2164

LLPVQYHFLFHSNHQDFPMPTQFDVAVIGAGPAGSASALLRKKGYQVCVLENSTFRASSAKACCTVWKCWKFPVLPMPFAPGPAFS

## SEQ ID 2165

TTGAAAAACGGTCCGCGCTTTTCTGCGGCGCAGCGCTATACCGAGTTTGATTTCACCGATAAATTTTCAGACGCGCCCGCAGCGGTTTACCAAGTCCGCGCGCGCTGTTCGACAAAATCC  
TGATTGAAGAACCGCCAAACAGCGCTTGAAGTACGTTTCGGGACGCGCGTAACCGCGTTTCGACACAGCGCGGATTTTCCCGCTTGAACATCGAAACGACACCGCGGAGAGCTATGA  
ACTGACCGCGAAATTCGCTTGGACGCAAGCGCTACGAGCGCGTGTCCGCGCGCTGTAACCTTGGAAAGCGCCCTCGCACTCGCCGCGCCCAACGCAATTCACGACATCGAAGC  
AACATATACCAACCGGAAATTCGACCGCAACAAATCTGATTACCAACCATCCGCAACACCGCGAGCTGTGGATTGGCTGATTTCCCTTCGGCGACAACCGTTGTTCCGTCGGCGTGTG  
GCACACCGCAACAACTTCGCGCGGGAATCGGAAACGGTGTGAAAAATTTGTTTACGAATGCCGATGTTGAGCGAAATTTTGGACAAAGCGGTTTGGGAAAAAGATTTCCGCTTCGGCTC  
CATCAAGGCTATTCGCGCAACGTCAAATCACTGCACGCGAGGCAATTCGCGCTGTGGGCAATGCCGCGAGTTTCCTCGACCCCGCTTCTCGTGGCGGTAAACATCGCGCTGCACATC  
GCCGAATCTGCTGCGGATGCTGACAAAACAACTCAAGGCGAAGCGCGGATTTGGCAACCGAATTTGCCGAAACCGCTGATGATCGCGGTAGACGCGTTCGCGACCTATGTGGAAGCGCT  
GGTATGATTTCGCTTCGCAACGCTGCTACGCGCGCGACCGCGGAAATCAGCGGTATGCTTTCTTCGATTTCGCGAGCTACCGCTGGGTACGGAACCGCGTTCTGTGGCGAA  
ATCCGAACACCGCTGACTGCTTGTGCAAGATGGCTGGTCACTTGAAGCGAA

## SEQ ID 2166

LKNGAAF SWGSRYTEFDTKFS DPGTVYQVRAVDFKILIEAARQGV EVRFGHVTA FN S GDFARLNIETDYGESYELTAKFVL D ASGYGRVLPRLLNLETPSHLPPRQTHFTIID  
NITHPKPRDNKILITHTPQHRDVIWLIIPP GDNRC SVGVVGT PDKLAGESETVLKKFVYEC PMLSEILDKAVWENDFPFRSIQGY SANVKS L HGRHFALLGNAEFLDPVFS S GVTIALHS  
AELAADLLTKQLKGEAADQTEFAEPLMIGVDARFTTVDGWYDFRQNVVYAPDRSPRISRLMSLILAGYANDTENPFVAKSEQRILTALSEWVQLESE

## SEQ ID 2167

TTGTTCCGCAAGAAAAATAAAATTTCCGGCATCAGAAGCAGGCAAAAACAATTCACAAGCCTTGCCCGAAGGTTTACAATCCGACCGTCTTATCGCAACGACCGTTTATGGATACCGCA  
AAAAAGACATTTTACGATCGGGCTGGATGCTGTGGCGCGCGCTGCTTACCGTTATGAACGTATTGAT

## SEQ ID 2168

LPKKNKISASEAGKNTPFKRKYVNPVLIATTVYGYRKRHFRIGLDAGGGELLHRYERID

## SEQ ID 2169

GGGCGGTTTGTGCGTCCGCGGAAAGAGAGTGGCGGGGATGAGCGGGAACCGCGACATCCTCTGCTGCGGGTTCCTGCGCAGCTGCTGAGGCTCTTCAACTGAAGTGA AAAA  
AAGACGGCGTTTGTGATGTTTTCGCGGTAACGTAGCGTTGGCGGTACACGCCCGCGCCCGCAGCAGCGCACTGCTTTGTATTCGACCGGCAAGCAATTTCTATCGGTTTGTG  
CTTCAAAACCGTAGTTGTAGCGGACGAGCGCAGACAGGTTGCGCGTACGCGCGCATTGTGCGGACAGGTCGAGCTGGCTGAGTTTGTGTA AAAATAGGAACCGTCCGCTCCAGGTAGAT  
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GACCGATACCGCGCGGAAACGCTCTCCCGCTGCGCGCTCAAATACGGCTCTGCACCGCGTGGAAGGCTGTGCGCGGTTGATGCGGTGTTGCCGTATAGAGGTTTTCGCG  
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CCGAACAGCGCGTATTTGCTGCGAAGTTGCGCGGTCGATTTGACACGGGCAAAACGCGCGGACGCTGCGGATGCTTTGCCCGGAAACTGTGACGCTGTAATAAGTGGCT  
GCAGCCGAGTTTGGGCGGAGTAGCCCGAGCTGTTGCTGAAATCCCATTTGATACCGGATACACGACAGTCCGCTGCGCTGCTTGGCGCGCGTGTGGCTGAAGCGGTAAATTTGTC  
GGACACGCGGATTTGCGCGCTGCTGCTTTTATGCCAATCGGCAGAAAGCGGGGATGATGCGGTAAAGTTCTGCTTTGAGCGCTTTGGTTTGCAGCGCTGCTGATTTCTGAAC  
GAAAGCGCGGATTCAGGCTGCTCCCGCGCTCCCGCCATATCCAGCCATACGCGCGGTTGAGGTTGACGTTGCGCGGATTTCTTCCCGCGGTAAAGTCCGCTAGTAGCCG  
TGTGCGGAGCTTGGTTGAATCGACACCGCGCTGAAGCGTGTGGAATGCTGCTGCCGCTGCGCATTTTCCCTGATAGCGGTTGTTCTGCGCGCTTTCTTATGCTGCGGCAACCGAGT  
CAAGTCCGCTGCTGCTGTAATCGGGACGAGGTAACGGAATTTGCTGCTCAACCTGCGCGGCTGCGCGATATGCCGGGGCGAAAGTGGCATGAAAGTGGGGCAAGGTTGAAA  
TAATAGGGGACGGAAGGGAACGCGCTCCGAACCGGAGATACGAGCGGACGAGTCCGCTTTTTCGCTGCGCTCAAGCGGGAAGTCCGCCAAGCGGTATAGAAAAGGGGAACG  
CGCGGAACAGGAAGCGCGGTGTTGGCAACGCGCTATGCTTTTCCCGATGCGCTTCGACAGAGGCGGCTTCACATACCGCGGCACTCCGCGGAAACAGGTTGTAATTTGGTTTC  
GCTAGTTTGTAAAGCGCTTCGCCCAACATTTCCGCGGTGCGGCTGACGCTTTCAGCGCGCGCTGCGCTTGTTCGCTTTCATACGAGGTTGTCGCGCTGCTGATGCGA  
TTGTAGGTCAGGTTTTCGCCCGAATCAGCGTACCGTCTGTTGGAGGGCGAAACCGGTCGCTACGGTAACCGGTGTCGCGGACTGGTGTAAATCCGCCAATCGGATTTGAGGACTCGC  
GTCGCGCTGCGTCTGCTGCGGGCTGCGCTTTCGTTACTGCAAAACAGCGAGGTGCAACCGGAGGTCAAATCGGAAGCTTGTGCGGATTCGGAACGCGCGCTGCGCACGCGCTTTCGCGACA  
CGCGCGTCCGCTCTTTCGCGCGCAACGATTCGCGCGCGAATGCGTGCAGAACAGAGCCCAATGCCAGCAGTGGTTTGTAGTGA AAAATAACAGGACCAA

## SEQ ID 2170

GPVVASGGKRVGGDVAGNEDIHPACGV SADA AEVFLK\*KKDGVFVGVFAGNVALGVHARA PAATAFVFCGKHFYRFPFKTVVAD DGRQVQRPLCGQVELAEFVVKIGTIVRLQVD  
FFVAFVTVAGVQHFSGGAVACADGVMPAFVVLVVVDAVEGETPAYAAGGECHPVGTAAIRI FADA AVKHRIILBIEFLDTGAETLLPRRAVQNTALHGGKAVGGVDVAVIVFA  
EKL PVAAEAFRRTEIGQVWLRGRNITVEQARLDGLHDSAAEQARIAFEGCAVDIDNQAPDAAGCPAETVEAVISGVQPEFGADVAPAVAEIIPDTGIHDQSAVLAAVVAEAGKLC  
GHADLRPA CFVMPIGRKAGHDGVRFFVVAALVQRLVFLNRKAGIQAA SRRPAI IQPTAAVEVDVAGDFFAAVKVAVVAAGDLVEIDTRLKRVGNVVPVLPFLIAVVPAAFLIVRQPG  
QVGLSAVIGTQVTDLSVKRRRAAFADNAGGESGIEVGGKVEIIGDGKGNVTRGTRYGRDQSAFAVAVKREVRPRRIEKGNAEHGGVFNAYAFSPIGFDRGGLDIPAGISGGTGVGLGF  
RQFVTPFAHQHFGGAADALQPPSALFGFHTDVVRFAGLLIEIVGQGFAPNQRVTLLGEPEVAVTGNVAVRLVVRIGIEDCAVPFDNANFRAHLNRLSHPHVGNNARIVFGDCCFAAALD  
GGFSLGAAAFVIAQAGRTGGIGSLGFGFALRTAFCDTFVRFLFRNIGGAMRAEFAEQHQWFE\*K\*TSQ



## SEQ ID 2171

ATGAGTAATCCATTTCTCTTTAGGTTTGGGTACGGAACTGGTTTCCGCACTGACCCGCAAGGTTACGAAACCCGACGCCATCCAAAGCCGGCCATTCCCAAAGCACTGGCCGGAC  
ACGACCTGCTTGGCCGCGGCAAAACCGGACAGGCAAAACCGCTGCTTTATGCTGCCAGCTTGGAAACGCTTACGCCACCGCAGCACTCGCTGCAATGCACCCCGTGCG  
TATGCTCGTGTGACCCCGACGCGCAACTTGGCACCATAACGACCAAAACGTCAGGGCTACATTAACAACTGCCGCTGCCGATACCGTCTCTTCCGGGTGTCAACATGGACAAA  
CAAACCGCGACCTGCGTCCGGCTGCGAAATAGTGTGCGCACCGTCGAGCGGTGCTGACCATGTGAAACAGAAAAACATCAGTTTAAACAAAGCCGAAATCGTGTCTTGGACGAAG  
CAGACCGCATGTTGGATATGGGGTTTATCGACGACATCCGCAAAATCATCGAGATGCTGCCCGCAACGCCAAACCCCTGCTCTTTTCCGCCACCTTCTCGCGACCGATACGCAAACTGGC  
GCAAGACTTCATGAACGCCGCCGAAACCGTCCAGGTTGCCGCCCAAAACACCAACGCAACGTCGAACAACATCATCGCCGTCGATACCTTCCAAAAGCGCAACTGCTCGAAGCG  
CTGATTTGTCGATTCGATATGAACCAAGTTATCTGCTTTTTCAAAACCAAAACAAAGCGTGCAGCGGTACCGCGCAACTGCTGCGCGCAACCTGTCGCGACAGGCGATACCGCGGAC  
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TTACGAAATGCCCGCCGACCGCGAAGACTACATCCACCGCATCGGACGACGCGCGCGCGTGGCGGATTTCCCTGATGGACGAATCCGAACAGAAATGTTTGGAGGC  
ATCAAGAACTGACCGCAACAGCTGCTCATCGAACGATCGAAGGCTTCGAGCCCGATGTTGGGAACAGGAAGGCTCAAACCGGAAAAACCGAAACAGCGAACCGAGACAAACCA  
ACCGCTACGAATCCGCGCAGGCTCAGCGCGAAAAAATACCGCGCGGAAACACCGGCAACAGATCGCGCGCGGCTCGCGGAAAAATTCGCGCGCGCAGCGCGGAGCGCGCGGAC  
CCGAGCTGCGCGCTGCTCAACCGCGTTACGCGTAA

## SEQ ID 2172

MSNFFSLGLGTELVSALTAQYENPTPIQAAAIKALAGHDLAAQTGTGKTAAPNLPSLERLKRATASTSPAMHPVRLVLTPTRELADQIDQVQGYIKNLPRIHTVLPFGVNHDK  
QTADLRAGCEIVVATVGRILIDVVKNI SLNKAIEIVLDEADRLDMGFI DDIRKIMQMLPRQRQTLFSATPSAPIRKLAQDFMNAPEVVAQAQNTNANVEQHI IAVDTFQKRNLLER  
LIVDLHMNQVIVFCKTKQSDRVTRVLRRNLSAQAIHGRSQQSLRLELNAFKDGLSLRVLVATDIAARGLDIAELFFVINYEMPAQPEDYIHRIGRTGRAGDVAISLMDRESBQKHFEA  
IKELTGNKLLIERIEGFEPRWBEQSGKPEKTETSEPRQRNRYESARAQREKNTREPTTANDAGAACKIAGRSRRSRRGHRTCALLQPRYGVK

## SEQ ID 2173

TTGGGGCGGGCACCGTTTATGGCATAATCCGCACACAAATTCGGTCCCGCGCGTTTCAAGGCGGCGAGTTTATTTCCCGCTCTATCGGTTTCCCGCTTCAGACGGCATAAGGTC

## SEQ ID 2174

LGRAPFYGI IRTQIPVPAVHRAVYTFVLSVSRFRHRHV

## SEQ ID 2175

GTGCCCCCCCCAATCGCGGGCGCGTCCGACAGTTGGAATCCTGCTTAAAAATGTACAATGGCGCACTTTTTTGAAACGCGGGCCCAATATGACATCGCGGTTATTTTATCGACAACC  
CCATCGCACTTTCGCGGATGGCGGGCATTTCCGACAAACCTTCCCGCGCTCTGTCGGCGGTTTGGCGAGGTTGGCGGTTGTCGAAATGCTGGCCAGCGATCCGACGCTCAGGAATAC  
CGGAAAAACCTTGCACCGCAGTGAATTTTCCGATGAAGCGCGCATGTTGCCGTGCGATGTCGGCGAGCGACCCGAAACAGATGGCGGATGCGCGCTTACACGCTCGGACTCGGGCG  
CAGTGTATCGACATCAATATGGGCTGCGCGCGCAAGAAAGTGTGCAACGTCGAAGCGGTAGCGCGCTGATGCGAGACGAGCGCTGCTGTTGCCGCACTTTTGGAGCGGTGCTCAAGCGG  
CGGGCGTACCCTTACCTTCAAAACCTGTTGGGTGCGACGACGACATCAAAACCTGCCCGCATCGCCAAATCGCGAAGATTGGCGCATTCGCGCTTTCGCGTACGCGCGCGC  
GCGCACGCAATGTACAAGCGGAGCGCGTTACGAATCATCGCGAGACCAAAAGCGCTGTAACATCCCGCTGGGTCAACGCGGACATCACTTCCCGCAAAAGCGCGCGCTC  
CTCAACAAACCGCGCGGACGCGCATGATAGGGCGCGCGCGCAAGCGAGCGCGTGGTTTTCGCGGATTGGAAGCATATGCGGACACGCGGTTTACCGCTGCTGCTGAGTTGG  
CAGAATCGACAGCGCCCATTTTGAACACATCCGCGCATGACGCGTTTATGTTGAGACCGTGGTGTGCGCATCGCACGCAACACATAGGCTGGTACATCGCGGAAATGCCCGACG  
CGAACAGCGCGCGGTGAATCAACGCTTGACAAATGCGCGCGCAATACGACACACTTGCCTGTTATCTTGAAGGCTTCCGGAACCAACCGCTTGGCGTGGCGCTATCGGAA  
GGG

## SEQ ID 2176

VPAPIAGASADWKSCLKNVQWRTFLKRGPIIMHIGYFIDNPIALAPWAGIADKPFRLCRAPGAGWAVEMLASDPTLRNTGKTLHRSDFADEGGIVAVQIAGSDPEQMADAARYNVGLGA  
QVIDINMGCPARKVCNVQAGSALMQDEPLVAAILLEAVKAAGVPTFLKTRLGHWDHQNLPALIAKIAEDCGIAALAVHGRARTQMYKGEARYELIAETKSRLNI PAWVNGDITSPOKAAAV  
LQQTAAADGIMIGRAQGRPWFRLDKHYAEHGVLPALSLAECRAAILNHRAMHAFYGETGVRIARKHIGYIEMPDGEQARRRINRLDAAAYQDITLAGYLERLAGKTRDRACGYRE  
G

## SEQ ID 2177

ATGCCGCGGTTCCGGTTCCGACGGCATCTGCTGTCATGGTTCCGAGGTCGGCGGAATCCCGCGCGGGAATGTCGAAACAAATAATGCCGCTGAAACAGGATGGAACGGGTTTCGCCA  
AAAGCGTTTCAGACGGCATTCCTCT

## SEQ ID 2178

MPPFGFGRHLSAIFGGRABSRPANVENNKRLKTSGTGFAKRLSDGIPS

## SEQ ID 2179

ATGAACCTGCGACTGCGGACATTGCGCAATGTATCGAGCAGAATTTGAACCAATATTTCAAAGACTGAACGGCACCGAACCTTGGCGGTGATACGATATGGTACTGCATCAGGTGGAAA  
AGCGCTGCTGGTGTGCGTGATGGAGCAATGCGCGCGCAACAGTCCAAAGCTTCCGTGATGCTGGGACTGAACCGCAATACCTTCCGTAAAGAACTGATTCACACGGTTTGTCTG

## SEQ ID 2180

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## SEQ ID 2181

GTGAATATGTCGCGCAACCGTCCGTATCTTGGGCAFCGACCCGGGCGAGCGGTAAACGGTTTTCGGCATCATGATGTCAGGGGGCGGATCATTTTACGTCGCTCCCGCTGCATCAAAA  
CGCTGCGGATGAGCTCTGGCAGACAGGATTCGCTGATTTGCGGCAATATCGCGGAAGTCTGTCGCTTTACAAGCGCAACAGGCGCGGTGAACAGGTGTTGCTCAACGCTCAATCC  
GGCATCGACGCTGATGCTCGGTGAGCGCGCGGAGCGGATTTGGCGCTTTGGTCAGCCATAAGTCTCCGTTTCGGAATACACGCGCTTGCAGGTCAAACAGGCGGTGCTCGGCAAGGC  
AAGCGCGGAAAGAACAGGTGACGATATGTTGTCGCAATGCTGGGACTTTCGGGAACCGCGAGCGGATGCGCGGACGCTCTTCCGCTCGCGCTGACCCACCGCTTACGCAACCAAG  
GGCTTCCGCGCAACTCAATCTTCCGGGATGCAAGTCAAGCGGAAGGTTTCAA

## SEQ ID 2182

VNMSATVRLIIDFGSRVTGFGI IDVRGRDHFYVAGCIKTPADEPLADRIAVIRHIGEVVAIVYKPPQAAVEQVFNVPASTLALGARGAALALVSHKLFVSEYALQVQAVVKGK  
KAAKEQVQHMVQMLGLSGTPQADAADGLAVALTHALRNHGLAALNPSGMQVGRGRFPQ

## SEQ ID 2183

TTGAGTGAAAATTAACGAGCAAAATTCGCCCTCAAGTCCGTTTACCGTTAGAAATAGTGTTTATGTAACCCGAAATGCCCGGATCTGTTATGCAACGGCAAAACCGAAC

## SEQ ID 2184

LSENKRAKIPQVGLFVRIVFIVIRNARILLNGKPN

## SEQ ID 2185

ATGCGCTCTGAAAAAGCTTTCAGACGGCATTTGCGTACCGCGTCATTTCAGGGCTGCATCTTCATCACTTCCATCAAAAAAGTTGGTAAATGCGGGATTATCGGGTTTGGCATCCATATTT  
TTCCACGCTGCTGCCAGCGCGCAAGGCAATTCGATATACAGCTTGGACTGTTCCGTATTGATTTCGCGCGCTGCTTACCGCGCAACGAGGTAGATTTCATACATCTGTCAT  
CGACGGCATTTGCTCCGACGAGCGTTTCTGAAGTTGTTGAGATATTCGCGCGCTGAACCTTGGTCATTTTACCGATACCCACTGATAGCCCAAGCGCGTCTTCATCGTGTATTTT  
GGCAACATCCGCCCAATGCGAAGGGCGAGCGGAAAACTTTTCAGGTTGCTCCGTTTTCAGCGTATTGATGGGATTCAGCGGGATTTCGCTAATGTTGGGCACATAAATAGACTGGCAC  
CCGGAAGGACTCGCGCAATGGAAGAGGGATAAGTATTTTTATACCCGCCATATAATCAAGTTTGCCTTGAGAAAAAAATTTGTCGCAAGAAAAATAAAAATTCGCGCATCAGAA  
CGAGCGCAAAACACATTCCCAAGCGCTTCCGCAAGCTTACAAATCCGACCGTCTTATCGCAACGACCGTTTATGGATACCGCAAAAAAGACATTTCAGATCGGGCTGATGCTGGT

CGGCGGCTGCTTACCGTTATGAACGTATTGATTAAAGAGGCATCGGCAAAATTTGCCCTCGGACGGCGGAATTGGTCTTTTGGCGCATGCTGTTTCAACCGTTACGCTCGGTGCTG  
CCGCGGTATTTCGCGCGGACACCTTCCGACGCCCATTTGAAAAACCACTTAAACCGCATATGGTTCGGGACGGGCGCATGCTGCTGTTTACGCGGTAACGATCTGCTTTGAC  
AACCGCGGTACCTCGAGTTACACCTCGTGCATTTTTCGCGGTATTTTCCTTCCGTGATTTTGAAGAAGCGGATTTCCGTTTACACGACGGCGGTGCTGCTCTTGGTTTTCGCGCGTG  
GTATTGCTGCTTAATCCCTCGTTCCGACGGGTAGAAACCGCGGCACTCGCGGGTGGCGGGCGGCGATGCTCCGCTGGGCGTATTGAAAGTCGCGCACTGCTCTTGGCGGCG  
AACCGGCTGGCGCGTGTGTTTACCTTTCGCAACCGCGGTGGCGATGCTGCTGTTTGGGCGACGCTGACCGGCTGGCACACCTGCTCTTCCATCGCGGTTTATCTGTCGGGCAT  
CGCGGTGCTCCGCGTGTATGCCCACTGTGATGACGCGCGCTTACAAAGTCGGCGCAAAATTCAGGTTGCTGCTGCTTTCCTATATGACCGTCTGCTTTCGCGCTGCTGCGCATTT  
TTCTGGCGAAGAGCTTTCTGCGAGGAATACTCGGTATGTGATCATATTCTCAGCGGCAATTTGAGCAGCATCCGCCCCATTGCCTTCAACAGCGGCTGCAAGCCCTCTTCGCGC  
AAAGA

**SEQ ID 2186**

MPSEKAPRRHLRTASFGHLHHPHQKVGKCGIIGFGIHTPTLLPAAQGIIDIQGLFRIDPAALAVYRRTQVDFIHTVIDGIASDQAFSEVVQILRRNLGHFTDTHLIAQARRFIADF  
GNIRPMRREAKTPCRCPFRDIDGIDHDFRQCCHINRLAPGKDCRNKGRDVPFTHRYHNQVLEKTNCSARKIKFRHQKQAKTHSTSLAARFTIRPSLSQRPFMDTAKKDIILSGWMLV  
AAACFTVMNVLIKEASAKPALGSGELVPWRMLFSTVTLGAAVLRRTDTPTPHWNHNLNRSMVGTGAMLLPYAVTHLPLTGTVLSTSSIFLAVFSLILKERISVITQAVLLGFAGV  
VLLNLPSPRSQEPALAGLAGGAMSGWAYLKVRELSLAGEPGWRVVFYLSATGVAMSSVWATLGTWHTLSFSPAVYLSIGVSALIAQLSMTRAYKVGDKFTVASLSYMTVVSALSAAF  
PLGEELFWQELGMCIIILSGILSSIRPIAFQRIQALPRQR

**SEQ ID 2187**

TTGGTTTCACAGGCGCGCAAAAAGCCCAACATACGTCCGGCTTGGGAATTGGTGGGTCCGGTGGGTTGCAACCCACGACCAAGGGATTA

**SEQ ID 2188**

LVSQGGKKAQTVVRWELVGPVGPFTTKGL

**SEQ ID 2189**

TTGCCGCTGAAAGAAATGTGTACCGAGATGAAATTTATATTTTTTGTACTGTATGTTTTCAGTTTCTGCCGTTTCCGCTGCTGCACAAAGATTGCCGCGCTGATCGGTTCGCTTCCCT  
ACCTTCTGCTCAAAACCGCGCGCGGTATCGCGCAATCAATTTTGGCAAAATGTTTCCGCAATGGGACGAGAAAGCGTAAACCGGTGTGAAACAGCATTTCAACACATCGCGCAAACT  
GATGCTCGAATACCGCTTATATTTGTTACGCGTCTGCCAAATGCGCTGAAATCGCTGTGCGCTACCGCAATTAAGCATTTATTTGGACGACGCGCTGGCGCGCGGGGAAAAAGTCATCATCTG  
TACCGCACTTTTACCGGCTTCAGATGGCGGTACGCGCTTAATCAGATGTCCGCTGATCAGTATGTAATCCCAAAAAAACAAGATATTGGACGAACAGATTTTGAAGCGCGCA  
ACCGCTATCAACCTCTTCTTATCGGGCGCACGAAGGCTCGCGCCCTCGTCAACAGTTCGCAAAAGCAGTGGCGCGTCTCTGATCTGCCGATCAGGATTTTCGACGCAACAA  
TTCGTTTTCGTTGATTTTTCGCGATTCAGACGCAACGATACCGGCTTGAAGCGCATTCGCGCGCTTGCAAATGCAAAAGTATACCCGCTATCCCGTCCGCGAGGCGGCAATACG  
GTTACATTGCAATTTATCCCGCTTGGAAATCTTTCCGAGTGAAGACGCGCAAGCGGACGCGCAACGATGAAACCGCTTTATCGAAGAACGCGTGGCGGAACACCGGCAACATATTTCT  
GGCTGCAACAGCGTTTCAAAACCGCTCCGGAAGGCGAGCCCGATTTTAC

**SEQ ID 2190**

LPPEKRMCTEMKFIFFVLVYLPFLPALLHKIAGLIGSLAYLLVKPRRRIGEINLAKCFPEWDEKRTVLKQHFHKMAKMLEYGLYWYASAKCLSLVRYNKHLYLDDALAGEKVIIL  
YHPTAFEMAVYALNQDVPILISMYSHQNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKSSAPFLYLPDQDFGRNNSVFPVDFPGIQTATITGLSRIALANAKVIPALFVREADWT  
VTLQFYPAWKSPFSEDAQADQRMRNRFIEERVREHPQYFWLHKRFPKTRPESGPDFY

**SEQ ID 2191**

TTGAAACCGGGTTGTACAAACAGGATTTGCCGACGGTTTAAACGGTTCACTGTTGTTGTAACCAATGCTTTTAAATTTGACAAAAACGAAATCGGTTTAAAGGCTTATTCGAG  
AACAAAGGGGAGTGGATGCCAAAAACCGGTTAATATATTA

**SEQ ID 2192**

LKPGLYKQDLPDFNGSVVCKNNAFLKLTKEIGFKGLFREQRGVDAENPVNLL

**SEQ ID 2193**

TTGTTAATCCACTAATATATTAACCGGGTTTTCGGCATCCACTCCCTTTGTTCTCGGAATTAAGCTTTAAACCGGATTTTCGTTTTCGTAATTTTAAAAAGCATGTTTTCACAA  
CAACTGAACCGTTTAAACCGTCCGCAATCTGTTTGTACAACCGGGTTTCAAAATTCCTCAAAACCAATCGGGGTTTGTATCTGAACGCGCTGATTTGTTTGTAAATTTTATGTAGTCA  
G

**SEQ ID 2194**

LLIHYNILGFSASTFLCSRNLKPIISFFVNFKAFLPQTTEFLKPSKSLYNPFGPKFPKTIQVFDLKRILICFVILCSQ

**SEQ ID 2195**

GTGAAAAAGGCGTACATTCGCTACACAGAATTACAGATACAGCGGACCAATCCCGCTGAAAGGATTTTCCGCTCAGTCTTGGGTTGGTCCGGGTTTCATCGGATACGGTGAAACGAA  
AGTTTCCGCGCAGGGTTGAGCTACGCGGTAAGCCGACGGCGAAAGCGCTGATGTTTG

**SEQ ID 2196**

VKKGVHSATQNYRYSAMPSEIRIFRSVLRLVGVSSDTPVKRPAGAGLSYAGKAAGESLYCL

**SEQ ID 2197**

ATGCAAGGTACTGCCATGAATACGATTTTGGCTTTTCGATATTGAAACCGTACCGGATGTGCAAGGATTCGCTACGTTGTATGACTTGGCGTCTTCCCTGCCGATGACGAAGTGGTCTGT  
TCGCGCAGCAGAAACCGCGCACAGACCGCGCGGATTTTATGACGACCACTCCATCAGTTTGTGGCGGTTTCTGCTGTATGCGCTGGGGGACGGAAGGTTTCATGTCCGCAACAT  
CGGCGAGATGGACGATGGCGAAGAGTCTGATTTGCCAAGTTTTCGAATTTGGTTGAAACCAATACCGCGCACTGGTCACTGGAACGGCGCGGTTTCGACCTGCCGTACTGCAATAC  
CGCTCCCTGATATACGGCATCAACGCGCGCGCTATTGGGATACGGCGACGGCGATTTTCGCGGACGCGGATTTCAAGTGGAAACACTACATCAGCCGTTATCAACCAAGCCACTGCG  
ATTTGATGGATTTGCTCGCGCTTTACAGCCGAGGCGAATGTCCGCTGGACGATATGGCGAAACTGTGCGGCTTTCCGGGCAAGCTGGGTATGACGCGCAGCAAGGTGTGGAGGCGGT  
CCACGCGCGCAGGCTGAAGGAAATCGCAATTTTTCGCAACCGATGCCGTGAATACGATTTGATGATCTGCGCTTCTGCTGCTGCTGCGCGCAGATTCGACGCGGACGAATACGAAATG  
GAAATCAAGCGGATCAGAACTATCTCTCCGCCCAACAGAGCAACACCGCATTTGGCGCAGAAATTTGTCACAGCGTGGAAA

**SEQ ID 2198**

HQGTAMNFIADFIVPDVQGIPTLYDLPLSSLPDEVVFLAQQKRAQTGGDFMQHLLHQVAVSSCMRWGQDKVHVGTIGEMDDGEEVVIKPFELVEKHTPQLVSWNGGDFLVLHY  
RSLIYGINAARYWDTGDGDFGDRDPKNNYISRYHQHCDLMDLLALYQPRANVPLDDMAKLCGPGKLGMDGSKVWEAFHAGRLKEIRNYCETDAVNTYLMYLRFLVSGRFDADYEY  
EIKRIRNYLSAQTEDKPHWAEFVQAMK

**SEQ ID 2199**

TTGGACAAATTCGCCAATCGGTTTGTCTCTGTTTGGGCGGAGAGATAGTTTCTGATCCGCTTGATTTCCATTTGTAATTCGTCGCGGCTCGAATCTGCCGCTGACCGACAGAAACGC  
AGATACATCAAAATACGTATTACGCGCATCGTTTCGCAATTAATTCGCGGATTTCTTCAGCGTCCCGCGTGGAAACCGCTCCCAACACTTGTCTGCCGCTCCACCGCTTGCCTGCGGAAAGC  
CGCACAGTTTCGCAATATCGTCCAGCGCACATTCGCGCTCGGCTGTAAGCGCGGACCAATTCATCAAAATCGAGTGGCGTGGTGATTAACGGCTGATGTAGTGTTCCTACTGAAATC  
GCGGCTGTGCGCGAAATCGCGCTGCGCTATCCCAATAGCGCGCGGCTGATGCCGTATATCAGGAGCGGTAATGACGTAACGGCAGGTGCAAAACCGCGCGGTTCCAGCTGACAGT  
TGCAGGCTATGTTTTCACCAATTCGAAACCTTGGCAATCAGACTTCTTCGCCATCTGCTATCGCGGATGGTCCGACATGAACCTTGTCTGCGCCGACGCGATACAGAGAAA  
CCGCCCAACCTGATGAGGAGGTGCTGCATAAAATCGCGCGGCTGTGTGCGCGGCTTCTGCTGCGGACAGCACCCTTCTGCTATCCGCGAGGAGAGCGCAAGTCATACACCT  
ACGGATACCTGACATCGGGTACGGTTTCAATATCGAAAGCCAAATCGATTCATGCGAGTACCTTGCAATCAAAACAGACTTGCCTCTATTGTGTCTAT



## SEQ ID 2200

LKFCPMRFVFLCGEIVSDPLDFHFVVRVESADQETQIHIQIRIHGIFAIADFLQPARVERLPHLAHVHQLARKAAQFRHIVQRHIRPRLVKRBOIHQIAVALVITADVVVFLKI  
AAVAVIAVARIPIARGVDVAVYQGAVMYQGVETAAVPADQLRRMFNQFERLGNHDFPAIVHLADGADNMLVLPAAHTAGNRHNLMEVVLHKLAAAGLCAAFLLRBOHHPVIRQGRROVIR  
TDTLHIGYGNIESQNRHSGSTLHRSKTDLRLLCH

## SEQ ID 2201

TTGTCCAAGCGTGAATAAGAACTGCTGTCCGAAGCGGTACGCTTGTGCCCGCTTTCGGTTTCAGACGGGTATGGTGGATTAAATTCAAACCGGTACAGCCTTGCTCTCTCTGCC  
TTACTATCTGTACTGTCTGCGGCTTCGCTGCCCTTGCTC

## SEQ ID 2202

LSKGRNRLNLSGGTLVPPFRFQYATYGLNSNRYSLASPCITCTTCGCFVALS

## SEQ ID 2203

ATGCAACGGCAACCGAACTGAAAAATGGCTTCAGACCGTTTATCCCAACGGGACTTCGATCTGTCTTCGCGGGGGGATGCTGATTTCGCGCGCTATTTCGCTGCGGGGTTTCAG  
ACGGCGGACGCTGCTGTATGGATGCGCGCGCCGACAAGATGAGTGTCCGCGCTTATTGGAAGGTGAGAACTGTTTGACATGGTCAATGTCGCGAGGTATTCACGCGGACACGGA  
TTTGGGGTTTGTGGTATGAAACGACTTGGCAATACGACGTTTGTACCGCGATGCTTCAGGACGAGGGCGAAGCGGCACACAAAGCCCTGTTGCTGGAGGCCATCGCGGAGCTGTGCGGA  
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ACTACCGCGAGCGCAAGACAAATACCGTCCGGAATCCGCGCTTCTTAAACTATCTGCGCGCGGTATGCGCGCTTATGCGCAACTCGCGCGCTCTACGCGCTTGTGTCGAAGTGT  
CGCGGATGAAGAACTGGAACCGGCTTACGTT

## SEQ ID 2204

MQRQTELNWLTQVYPERDFDLSPAAADADPRRYFRAAFSDGSSVVCMDAPPDKMSVAPYLKVKQLFDMVNPQVLHADTDLGFVVLNDLNTTFLTAMLQEGEAAHKLILLEAIGELVG  
LQKASREGLVPEYDREMLREINLFPWFVAKELGRELTFKQRLWQQTADTLPLLAQPKVYVHRDP IVRNMLTRGRPGVLDQDALYGPISYDLVSLRLDAFIEWEEFVLDELVIRY  
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## SEQ ID 2205

ATGAAAAAGTCAAGCTATTGATTGTTCGCAAAAACGAAGCAAAACCAATTCGCGGAATGATTGAAAGTTGCGCTTTCGATAAAGAAATTATCGTTATCGACGACCATAGCGCGCAACA  
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TGCAGACGAACGCTGCACGCGGAACTATCTGATGAATCTCAAAATTTGTCGAACCGCGGATTATGCGCGCTATTTCGCGAAGCGCGCAACCTTTTCCCAACCATCTCCGCGCACAC  
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CCGTCGGAATTTGGGTTTTTTCAAAATTTATATCTTGAACAAAGGGTTTCTGATGGAATAATGGGTGGATTATGCGCTCAACACAGCTATTACAGCATGATTAAATATGTCAAACTA  
TATTATCTGATCAAAATCCGCGGAAAAATTT

## SEQ ID 2206

MKKVSVLIVAKNEANHIRECTIESCRFDKEVIVIDDHSDNPTARIEGLGAKVFRRLHNGDFGAQRTFAIQAAGGEWVFLIDADERCTPELSDEISKIVRTGDYAYFVERNLPFNHPATH  
GAMRPSVCLRPKKGSSVQKRVHETVQTPYPRRLKHFMYHTYDNWQVFNKFNKYSISAERYEQKPVSVFVVDIILRPIMGFKIYILNKGFLDGRWIMSVNHSYTMKIVYKL  
YYLYKSGKF

## SEQ ID 2207

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AACCGCAACCGCGAAGCGGTGGCAATTCGATTATCAGGCGCAACCGCAACCGAAGCGGTGTTGCTGATGACCGAAGCGCAACGCGCTTCCGCTGCAAGGTGTAAACCGAAGCGCTTC  
CCTGCTGCTGCGCGGTTTACGCGCGCGGATGATCTGAACATCTGATCAGCGACGACGACTGCTGCTGCTGCTGCGCGCACGACGAGCTTTCACGCTGCGGAAGCGCGCGCAAC  
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CAAAGTCAAGAAATCGACCGCTTCAACCGCGAGTCCGCGCGCGCTGGTGCAGCGCTTCAACCTCTGCAACAAGCTCGAGCGCGCAGCGCAAAACCTTGGTGAACAAAGATTCAGCTGC  
ATTCGCGCGCAGGAAGATTGTCGAAGACGCTGGCGAAATCGTGGCGAAGATTTCGGT

## SEQ ID 2208

MSKTVRYLKDYQPPAYRILETELHFDIAEPQVVKSRUTVEPQAGEPLVLGSAKLLSVKINGAAADYVLEGELTIAADVPSERFVEVETELPAENKSLMGLYASGGNLTQCEPBG  
RKITFPYIDRPDVMKFTTTIADVKRYVPVLLSNGNKIDGGEFSDGRHWKVEDPAPKPSYLPALVAGDLAVTEDRFTTHSERNVKLEPYTTEADKPKVFVESLENAKMWDETRFGLYD  
LDIFMVAVGDFNMGAMENKGLNIFNTKFLVADSRTATDTDFEGIESVVGHEYPHNWGTNRNTRCDWFLSLKEGLTVFRDQRFSGDRAGRAVRRIENIRLLRNQFPEDAGPTAHPVPRV  
SYEEMNFFYTWTYVYKGAEEVVRMYHTLLGEBGQKGMKLYPQRHDQAVTCDPFRAMADANGINLDQFALNYSQAGTVLEABEGLKNNVFELTIKQVTPPTPDMAKQPMNIPVKVGLL  
NRNGEAVAFDQYQKRAFEVLLMTEAQAPLEGVTEAVVPSLLRGFSAVPVLYNPYSDDLLLLLLHSDAFTCEWAAQTYLRRVAANLAALSDGIGLPHKEKLLAAVEKVISDDLLDN  
AFKALLLVGPSEAEWLDGTENIDPLRYHQAREALLDLAVRFLPKWHELDROAKQENQSYEYSPETADWRTLRNVCRAPVLRADPAHETFAEKYGENAGNMTHEWGLLSAVNGNESDTR  
NCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQVQVQALQHPKFSLENPNKARSLIGFSRNVPHFHAQDGSYRFLADKVIIEIDRFNPQVAAVLVQAPNLCKLEPHRKNLVKQELQC  
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## SEQ ID 2209

TTGTTTACCAAGTTTTCGGGTCCGCTCGAGCTTGTTCAGAGGTTGAACGCTGCACACAGCGGGCGGCGACTGCGGGTTGAAGCGGTGATTTTCGATGACTTTGTCGGCGATGAAG  
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CCTGTTCAGGGTGTCTGCTGCGGCGCT

## SEQ ID 2210

LFHQVFAVRLVLEVERLHQAGDLRVEAVDFDDFVGDEAVAAVLCVKMRDVAAEAADERTGFVGVFETEFRLQGGNLNLQGVAAAA

## SEQ ID 2211

ATGAAGATAACACTGCAAAATTAAGAAAGAAAGTACAAAAAGAACCGCTCCGTTCTTTGTACCGGAAGTTACCGCCCGTCTGCCGCCGATATTTGGGTATCCATCCCGATTGCGCGG  
CACTGTTTACCGTAAATTCGACCGGTACCAACCATCGTTTGGCTTGGCTGCGGATGAGGTTTCGAGGGCCCCCGCGGGCCGGCGCAAGCTGTTTCGGCGGACGGGTAAAGGCAG  
ACCGGTGCGGGCGGTAGGAAAGCGGTGTTCTTCGGCATTCGAAACGCAACGGCGGGCTTATACCGTTGCCGAGGACATGCCGAGCCTGAAACGTTGCTCCCTGCCGTCAAAAA  
AAATCATGCCGACCGTATGTTTATGCCGATAGCCCGGCGAGCGCGCAAGTTGGACGCGGGCGGTTTACCCGTTGCCGATCAACCGTTCCAGGAATTTGCAGACCGTGGAAACCA  
CATTAACGGCATTTGGAACTTTTGAATCAGGCAAAACGCGCTTCGAAAAATACAACGAATCGATCGTAAACCTTTCCCGCGCTTGT

## SEQ ID 2212

MKITHCKLKKVQKEPLRSFVPEVTARSAADILGHPDAAALFYRKIRTVNHLALAADEVFEGPAGPASCFGRRRKRGRGAVGKAVVFGIPKRNGRAYTVAEDNAEPETLLPAVKK  
KSCRTVLPMPIARAAAASWTRAVLFAASTVPRNLQTVGTTALGTFPIRQNPCEMTESIVNLSRR

## SEQ ID 2213

ATGCCGACCGTATTTGTTATGCCGATAGCCCGGCGAGCGCGCAAGTTGGACGCGGGCGGTTTACCCGTTGCCGATCAACCGTTCCAAGGAATTTGCAGACCGTCCGAACACATTA  
ACGCGATTGGGAACCTTTTGAATCAGGCAAAACGCGCTTCGAAAAATACAACGAATCGATCGTAAACCTTTCCCGCGCTTGTGAGGGAATGCGAATTTGACTTAACCTCCGCGACACC  
GTCCCGCGACGTAAAAATCTCGCGGATCGGTGGAAT

## SEQ ID 2214

MPDGIVADSPGSRGKLDAGGFTRCRINRSKEFADRRNHINGIGNFWQAKRALRKYNIDRKPPFLRLBCEFRINSCTPSRQLKILDRCGI

## SEQ ID 2215

TTGGGTGAATTTTGAATTTGAAGAAAACGGTACAAAGATTACTCGGAAATCGGAGTGCATGGCAATTTTGGCGCGCGCTTGTCCGATTCAATAATGGAAAGTATTATCGGGTA  
ATCGGATTGTTTGGTTTCCCAAAAAGCCGAAAC

## SEQ ID 2216

IGEYLEFEENGTKITARIGSAMHFLGAACRISINGKYIYAGNRIVWFKAERS

## SEQ ID 2217

ATGCATTTCTTTATCTTTATTAATCAAAATTATTTGATAAGCGTAGGGTGGGCACCTTGCTGCCACGCGTCTGTTTCAAGTTTATTATTGGG

## SEQ ID 2218

MHFLYSLFNQIINISVGMALAAHAFCKFIIG

## SEQ ID 2219

TTGAAAAAGATAATAAATCTAAGGTAAAGGAGACTAATTTAATCAGGCATGGCGTGTATACCGCCATGCAATAAATAATATATCTGATGAACAGGTATGATTTGCAAAATGTCTT  
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AACTTTTAAATCTGGAGAAACACTATATTCGAATTTAATCTATTAAAAATCAATGCAAAAATTAATTTTTTTTGGCGTTTTGATTTTGATGCCCTTACTTTAAAGCGGTGTGAGTC  
AGGTGGCAGATTATAATTTTGTCTCGTATGCAATTTCTTTATCTTTAT

## SEQ ID 2220

LEKLIINSKVRFTNFQAMVRIRAMQINNISDEQVMIVKMSCYLKKDEIFPNRIERYGYQSDIKKINPPFLNLPVVKPYYPYLYDTHLNQIYDLAWSNDPLMFELFILDRESIKYIDRO  
KLFSGETLYSNFSIKNQKNYFFCGDFDAPYFKSGVSQVADYNFVPAFSLFFI

## SEQ ID 2221

ATGCAATTGATATGCGCGATGAGACAGGTATAGGAAATTTTGAACCTTCGAAAAACATGGTCTGCACAATATCGGGATATGGAATTTTCACTACCGAATTTTGGAAATTTGAAAC  
GGACAGGGCGGAAGTCTATATCAACCGCAGCGGCTTATCATACGAAGCGCGGATGCGCTTCTTTCGCTTCGCTAATGGGGGAATACCTGGAATTTGAAGAAAGCGGTACGAA  
AATACCGTTGAAATCGGCAGCGCGTGGCATTTAATGAAATATAAGAAATATTAATACACATTTAAGAGGTACGAAACTTCCAGGTCTAAGTGGAGGTTCAAGATAAGGGCATTTT  
CATCTTTGAAAAAGA

## SEQ ID 2222

MQLICADWTGIGNFMKTFKRTWSAQYRIMKISVRNFWNLKRTGAEVYINGRRVYHNEAGMASASLSLNGEYLEFESGTRITVEIGSAMHFNFTIRNINHLRGTLPGSNHWVQDKGHF  
HLNKR

## SEQ ID 2223

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AAACACATTTCCACCTGATGATACACACCGGCAAAATGCGGCTTATCCGTTTTCGAAACCTGACCGGGGTGCGCTGATATTTGTCAACATAATGTCGTCGCAACAAACCC  
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TGATTTCAATATCTTTGGGTGCGCAAAAGGAAATATCGAACATCATCAATCGGGATTTGCTGAGACAGGCTTACGCTGAATCTTTGGCGGAGCAATCGAACGCTGCTTTAAACCC  
CGAAGCAAAAAACGCACTGCGCAACGCGAGGACATCAATCGCTGCGCGCGCTTTTACCATTCAACATACCGCGGACAAATTTATGGATGCAATA

## SEQ ID 2224

MEKEFRILNIVSAKINGGGEQYVYDVKALGLRGCTMPTAVNKNDLMRRRPSSEVSVFTTTLHTFNGFLSLYALTRPIRENHISHLMIHTGKIPALSVLLKKLTGVRILPVKNHVANKT  
DFYHRLIQKNYDFICVSRVLYDVQYADNPFKEKYRIVHNGIDTGRFPSPQEKPDSEFTTAVYAGRISPEKLENLIEACVILHRKYPIQLRLKLAGHGDPMYCRKLRGVSASCAEPFVSF  
EGFTEKLASFYRQSDVWVPLSLVPEAFGLSLCEAMYCRTAVISNLTGAQKEIIEHQSGILLDLRLTPESLADIERLVLPNPEARNALATAGHCQVAARFTINHTADKLLDAI

## SEQ ID 2225

ATGGGCGGATGCTGCTCAAAATGCCGCTGAGGATAATGATGCACATACCGAGTATTTCTGCCAGAAAAGCTTTCGCCCGAGAAAAATGCCGCGAGACAGGGCGGAAAAAGACGACGCTCA  
TA

## SEQ ID 2226

MGRMLLKMPLRIMHIPSISQKSSSPRKNADRAEKTTVI



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GATATTCGCCGACTGCAACTCATCGCCGCTCTCGGCTCAGCCTCATACCTTTGCCGCTCATCTACCGCCCTGGTGTAGAAAGCATAGACCCCTGTTCTCAAGTCCGCTCAAG  
GCAAAGGGCGGCTTTGGCAGCTATTTCTCATCTCTGCTGTATGAACCTCGTATCGGCTTCCAGCTCTCGGACATCTGATGTCGGTGGGACTTATGATGCTGCCGCCATTACCC  
CCGCTTATGGGCAAGAAATATGGGACGCTCATCTGTGTCTCGCTCATCGCCCTTTTTCGGTGTGATCGGCTGCTCATTTCTTACCACATCGAAATCCCTTCCGCCGCCGCCATC  
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## SEQ ID 2242

MYALASVFLSLSAAPVGVFLVMMRSLIGDALSHAVLPGAAGVGMFAGLSLPMGVGFAAGMLMALLAGLVSRTTFLKEDANFAAFLSSLAIGVILISNGSSVDLHLHFGSVLAV  
DIPALQLIAAVSGLTITLAVIYRPLVLESIDPLFLKSVNGKGLWHVIFLILVMMHLSVGPQALGILMSVGLMLPAITARLWARHNGTLILLSVLIALFCGLIGLILSYHIEIPSGPAI  
ILCCSVLILFVILGKEGGLPKWPKNHRHHT

## SEQ ID 2243

TTGCCAATCTCCCTTTCAAACTGCAAACTCATTATGACACCTTCCCTCTTACTGTGAGGATTGACCTTCCGACTCTCTCTCGCCCTGATTGCCGTATTCCTTTTATGGGGTGTTTACCTTT  
GGCGGTATCGGTA

## SEQ ID 2244

LPTSLSKLQIMTFSLLSGLTFRFLALIAVFLNGVILMAVS

## SEQ ID 2245

TTGGCGGTATCGGTATGAGCATCATCGTGAACCTGACGGTCAGTACCGCGCGCGCCCGCGGTACACACGTCGACATTACTTTTGAAGAACATAGTATGTGGCGGTGTTCGGTTC  
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CGACATCGACCGTTCCACGCTATGACCGTTTTCGACTTGGCGCAATGGGCTGTGGTATGAAATCGGTTTTTCAAAGGATTAATACCGCTCAAAAAACACGCTTCACGAGCCTTG  
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TGGTGGCGCTCA

## SEQ ID 2246

LGGIGMSIIVENLIVSVRRPVAHVHDITFEHSMWAVFGPNAGKSTFLKSLMGLQPIDTGSIRLDGLTRQNIAYLPQSDIDRSQPMPTVFLAAMGLWYIEGFFKGINFAQKQVHEAL  
ERVGMRFARRQIAHLSNGQFQRVLFARMLVQNAKFLLLDEPFNAVDAITTYELLDLQKCHCGHAI IAVLHDVEQVRAYFPNTLLAREKIAAGATETTLTBSYLAQASAKMQQBSFD  
WCAS

## SEQ ID 2247

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TACTGTTGAGAAATCGAAGTCAAACGCCGTGGCGAGCTACGCCGTGCCAACTGTACTACCTGCGCGGTCTGACCGCAAGCTGCACGCATCAAGAAAACTGCTGCAACGCAAGGT

## SEQ ID 2248

MNLIQLEQEEIARLNKEIPEFAPGDTVVVSVRVBGTSRSLQAYEGVVIARRNRGLNSNFIVRKISSGEGVERTFQLYSPTVEKIEVKRRGDVRRAKLYLIRGLTGKAARIKEKLPARKG

## SEQ ID 2249

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CAAGGACTTTTTCGCGCTCAAAGGCGGTTTGTTCGCCGACCATTTTTCGAGGACTTCGCGCTTTCGACGCTGATTTTTCGTTGACCATCGCATCGAAATATGCTGTTTCCGACATC  
TTTGCTTTTCGCGCGGACCATATCGACGCGCGCGGCGGAGCGTCCAGCGCGCAGCTTTCTTTCGCCAGACGAGTGTTCGGTACGCAAGGTACATATGCTCTTTAAAGACTTGGCGGT  
TTGCTCAAAACAGGTTTCGAGCGCGGCGAGTGCAGCAAAATAGCCGAAAACTCAAGCACTTCAACCTTTCCTGCTGCTGCTGTTGGGGAAATCGGCTTGGCAAGGACGCTGTAGTTTTCG  
CTTCGACAGCTCTGCCGGGCGCGGCTGCCGAAGCGGCGAGCGCGCTGTCGGCGGGGACGCTGTTTGGACTTTGCTGTGCGACGCGGCAAGGCGCAACAGGCGCGCAACCGCGAGGCG  
GAGGCGGAGGTGTCTGATTTTCATACGCTCTCCGTGATGTTGGAATAAATCGGATATTTGATTTTTCGCGGTGTGATACAGTTTTCGCGGCAAAAGGACGTTTTCGTT  
TCGGGAAACCGCTTCAGACGGCATCAAACCGATGCCATCGGAAGCGGTTTCTGCTGTACATAACGCGCGCGCCCGACGGATACGCTGTTGGGGAACAA

## SEQ ID 2250

MPSENVSDGIPQTGLLRGLFTTYFVRQKVDGVHTGLPVGKDFIPADNRRGTVDLGEGQLLHFAGARLTFGGFVGGKDFFAVKGGLFAQPFDFRLLQLDLVDHRIENMAVRHI  
PAGGSHIDGGGACQQRHFFLPDDVFGTVHIVFKRLGVFAQNRFEAGAVRTKIAEKLKHFNLACLLGNRVKGDGVVLPFDQSCRGGGCRSGRRVAGGDAGLDAVARKGEGQGNABG  
EGEVSGFHTALRDVGNKSDIGLILLYFRVLIQFAAEKGRFRPGKPLQTASNMPSENAVSVVQYAPPRDTAVGEQ

## SEQ ID 2251

ATGCAATATAAGCCGCTTTCAGACGGCTATGCCGTCTGAAAGCCTTTGATGCAACAAACCGCCAAATATATTCGTTTATTTGAAAAAACACCCCGAATTCATCTTCAAA

## SEQ ID 2252

MQYKPLSDGLCRKAPDATNRQIIFVHKRTPRIHPSK

## SEQ ID 2253

ATGCAAGGAATGATAATGGTCAAAACATCTGCCACTCGCCGCTCTGACTGCTTTGCTGCTTGCAGCGTGGCGCGTTCGGACAAACCGCTGCCGAAAAACGGCACCGCGGAAAAACCAA  
ACGTATTGAAATTTATACTGGTCGGAATACGTGATCCGGAACCGTTGCCGATTTTGAAGAAGAAACGGCATCAAGGTTACTTATGATGTGTACGACAGTGATGAAACGCTGGAAG  
CAAGGTGCTGACCGGAAATCCGGTTACGACATTGTGCGCGCTTCAATGCGTTTGTGGGAGGAGATTAAGGACGCTGCTATCAGAAATCGATAAGTCGATGATTCCCAATATAAA  
CATCTCAACCTGAAATGATGAGGCTGATGAGCGGGTGCATCCGACCAAGCAATACGCGCTGCGTTTATTTGGGGACAAATACCTTCCGATCAATACCGAACGCTGAAAAAGGCTT  
TGGGTACGGAACAGCTCCCGACAAACAGTGGGATTTGGTGTTCACCCCGAATACGCTTCAAACTCAAAATGCGGCATCAGCTATTGAGACAGCGCGGCAAAATTTATCCCATGGT  
GTTGAATATTGCGGCAAAACCGAACAGCAATACGGAAGACATCAGGAGGCAACCGCCCTGCTCAAGAAAAACCGCCCAATATCAACAGCTTTTACTTCTGCTCCGCTTTATGAT  
GATTTGGCGCGCGGATACCTGCTTAACATCGTTTCGCGGAGATTTGAACATCGCCAAACCGCTGCCGAAGAGCGGCGGCAAGGAAAAATCCGCTGATGATCGGGAAGAG  
CGGTGGGATTTGGGTGATTTCTTCTGATTTCCGAAGATGCGAAACGTCGCCCAACGCGCAAAATACATCAACGACTTCTCGATCCGGAAGGTGTCGGGCAAAACCGCAATTTCTG  
TACCTTACCGCTTTCGACGAGCGCGCGGATTTGATGAGGAGCAATTTAAACAGCAATACGATTTTCCGAGCGGGAAGATTGAAAAACAGCTTTATCATGCTGCTATCCG  
CCGCGGCAATTGAAGTTTATGCTGCCAGTGGCAGGATGTAAGCGGGGAAA

## SEQ ID 2254

MQGMLNVKHLPLAVLTALLAACGSDKPPAEKPAFAENQNLKIYNSEYVDPETVADFEKKNGIKVTVYDVSDEYLESKVLTKSGYDIVAPSNAPVGRQIKAGAYQKIDKSMIPNYK  
HLNPEMRLMDGVDPDHEYAVFPYWGNTFAINTERVKKALGTDLKLPDQWDLVFNPEYTKLKQCGISYLSAAEYIPVNLNLYLKNPNSSNTEDIREATALLKKNRPNKIFRTSSGID  
DLARGDCTVTIGFGDLNLAKRRAEBAGGKEKIRVMMKPEGVGIWDSFVPIPKADKNVANAKHYINDFLDPEVSAKNENFVTPAPSSKPARDLMEDEPKNDNTLFPSEGLDKNSFTMVFIR  
PAALKFVVRQWQDVKAGK

## SEQ ID 2255

ATGCTTATCCAGGAGTACCAATTTTCCCGAAATGTTTCGACAGCAATTACCGCTACCGGTAACGGGACGCGGCAACAGACAGGGAATCTGGCAGTTTGAAGCAGTCAATCCCGAAAGT  
TTGCCGACACAGATTGGGCTATATCGACAGCCGCCGTTCGGCGCGGTCCGGGAATGATATGATGGCTCCGCCGTTCATGCGCGGATAGAACGCCCAAGCAATCTTCCCAAC



CGCAAAAGTCATCTACCTCAGCCCCAAGGAAAAACCGTGACACACCAAAAAGCGGCAGAACTGGCAGAACTTACGCATCTGTAATTCGTCTGTGGCAGCGCTATGAGGGAATAGACGAAAGA  
CTGCTGCAAAAGCAGCGTCTGATGAAGAAATCAGCATCGGAGACTTCGTCTGTTCCCGCGGAGAGCTTCCCGCCATGATGCTGATGGATGCGGTATTGAGGCTCGTATCCCGCATATTGGGCG  
ACATTCACTGCTGCCGAACAGGATTCGTTCTCAAGCGGTATTTTGGACTGCCCCACTACACCAAAACCTTAGAATTTCAAGGCATGGCTGTTCCGGAAGTATTGCGCTCCGGAATCATGG  
CTTGATACGCGAATGCGCGTTGGAAACAATCGTGCGCCGCACTTGAGAGCGCAGCCGATTTTGGAAAAGCGCGTTTAAATCCCAAAGGAATCCCGCCTCTTGAATAAAAATCCTACAA  
GAGCAACGCGGAACTCAATCA

**SEQ ID 2256**

MLIQAVTIFPFMFDSITRYGTVGRANRQGIWQFEAVNPKRFADNRLGIYIDRRPFGGGPGMIMMAPPLHAAIKHAKAQQSSQAKVTYLSPOGKPLTHQKAKLAEIHLIILLCGRYEGIDR  
LQSSVDERISIGDFVVSGGELPAMMLDAVLRVPGILGDIQSAEQDSFSSGILDCPHYTKPLEPQGMVPEVLRSCNGLIAEWRLQSLRRTLERRPDLEKRVLIKPSRLINKLIQ  
EQREIQS

**SEQ ID 2257**

ATGACAGACACTCAAAACCGGGTAGCCATGGGCTACATCAAAAGGGGTATTCCGCATAAAAGGCTGGCTGAAAAATTGCCGCAACACCGAATATTCCGACAGCCTTTTGGACTACCCCGAGT  
GGCAATTGGCCAGGACGGCAAAACCGCTACGGTTACCCCTTGAAGCCGGAAAAAGTCGTCAACGGCGAACTCCAGTCAAAATTCGAAGGCATAGACGACCGGCATTACGACTTCTCATTTGG  
CGGTTACACCATCAAAATCCCGCTGAAGCATTCGCCCCGACAGAAAGACGAATACTACTGGGCAGACTTGGTCGGCATGACCGCTGCTCAACAAAGACGATACCGTTTATAGGCAGGTA  
ACCAACTGATGAAATCCGCCCAACACGATATTGATGATTGACGGAGAACACGGGCAGATTCTGATTCGGTTCCGTTTCCCAATATATATCGAAACCGTCGATACCGGCAGCAAGACCAATTA  
CTGCCACTGGGGGTTTGGACTAC

**SEQ ID 2258**

MTDTQNRVAMGYIKGVFGIKGWLKLAANTSYSDSLDPYHMLAKDGKTVSVTLEAGKVVGELQVKFEGIDDRDSAPSLRGYTIKIPREAFAPTEDEYTWADLVGHTVNVNKDDTVLKGVS  
SNLMEETGANDVIMIDGEHQIILIPFVSQIETVDTGSKTITADGGLDY

## SEQ ID 2259

ATGGTAGTTATCCGTTTGGCAGCGGGCGGTGGAAGAACCGGCCCTTCTACAACGTCTGTTACTGACTCAGCAGCGCGCGGAGCGGCCCTTTCATCGAAGCGGTAGGCTTCTACAAC  
CCGTAGCCCAAGAAAACAGAGCGCGTCCGCTCAATGCAGACCGCCTGAACCACTGGATTGCACAAGCGCGCAAGTCAGCGACTCCGTTGCAAAACTGATTAAAGAACAAAAAGCCGT

SEQ ID 2260

MVVIRLARGGSKHRPFYNVIVTDSRSTRDGRFIERVGFYNPVA NEKOERVRLNADRLNHWIAQGAQVSDSVAKLIKEQAV

SEQ ID 2261

ATGATGGAAGCTCATCATCCAAACCGCGCACAGCAAGGCTACCTGAGCATGAGTGCCGACATCTCTCAAACCAATACCCCCATGATCAAACTTGCTGAAAAATCAGGATTACCTCTCAAG  
AATCGGACACCGAAAAAACCTGTACCGCGCATATCTGAACCTTTCGCGCAGACAAAAACAAGGAAAAACAATAAAAACTTTCGCGCACCGGCCACAAAAAACC

SEQ ID 2262

MMELIIOTAAOOGYLSMSADILKTNTPMIKLAEKSGFTLKESDTEKNLYRAYLNLAADKTTGKTNKNLRTGHKIT

SEQ ID 2263

TTGGATGATGAGTTCACATCAATTTCTGTGCCAGCCCGCTGCCGCGCATATGTTCCGCCAGTGTGATGCCAAATTCGCATTCGTTGCGGTTTCAGGCGGCTGTGGCGGACGACGCGACGATG  
CTGTGTGGCATCCCTTCCCTCCATGCCGTTCCAGTGG

SEQ ID 2264

LDDEFHHFLCQPAAAHMFRCDAKFAFVAVQAAVADDGDDVAVGIPCRPCGSQH

**SEQ ID 2265**

TTG CAG CGC GCA AAT CCC GCG CCG TGC TCG CCG GAG CCG CTG CACT TCC CCG TAC CGG CAC ACC CCA ATA AG CCG TCCA ATT TCCA ATT CGG CAG CCA CCCC CTCTAT GGG GAC ATC CTT GAC CG  
CAC GGT GCA ACG GGA CAA ACC ACT GCG GTT ACT CCG CCG GTT TACC ACG CTG CAG ACG CCG CACC TTG CCG CCG TT TGC GAA CTG CAG CGG CACA CAA ACC CTG ATC AGT TCT GCA CACA CT  
GAC CGT CAT CCG GAA TAC CGG CAA CACA TT TTT GGC CAT CAC CTT CAAC CT TAA CCG GGA CAA TAC ACG ACG GAT TTA CAT TTA AAG CAC CCG GAA CAC ACG ACG GCC AAG CGA AG  
AAC CAC AGG CAA AG CCG CCA AACC CTG GAAC ATG CCG CCG CAAA ATG CAG AGT GCG CCG CCA TAC CTG GAA CACA AAAA ACC GAC ACG CCG CGA ATT TTT CCG CCA CACA AAG GGA AG CCG  
CGG CAG AAC TGT CCG CAG CAAA ACC GAA CCG GAG CCG CCG TAC CCA AAG CTG TCT TGG CCG CCA TAC CCG CAG CAC ACG CCA CCA AAG CACT GTG CCT TAAAAA CAA CAC GAC CCG TTAC CATTAT  
CCCC TT TACC CCG CAG CAG AAG CCA ACG CAG GTT TCG TCG CAG CTG CCG CCG CCG AAG CAG CAG TACA CAG CGT TCA TGA CCG CCA CAA CCG AAG CACT GCG CCG CAG GTT TGG CAC GC  
CTG GCA CCG GAT TACC ATG TGA CCG CACT GGA CCG GAG GAT GCC CAG CAG AACA TCG TCG CCG TCG TCG CCG CAC AG CCG C

SEQ ID 2268

LQRIIPCSPKFCTSPYRHTTHNAVQFGQSFHPLYGDILTARCNQQTAVLPPFTTLDSSRHARFAELDGTQTLDDQFIHTLTVLPIEYRQIHGIGITLNLNGGQYSSDFLLKTPGTHDTPKKE  
NTGKAAQTLEHAAAKMQSAAAYLEHKNPATAEFLRHTSEAAABELGSKTETGAAPVNLAPYPAAEHPTLSLKNNTVTIITPLPEDAEAKQGFVRSLGPEARYTRFMTHTNELPAATLAR  
LCPNDVHCPEHGRQCPMTATSSPSSATAA

SEQ ID 2267

[illegible]

SEQ ID 2268

SEQ ID 2206

LQRLPLFVPPQVLCYNALPSHFLINFMNSNETWSSSKIGFVLAAAGSAIGLGAIKWPPTYTAGTNGGAVFFLLFLIPTVLVAVLPVQLAEFYIGRTGGKNAVDSPKRVLRPGTQWLHVGRGVAA  
 ACGILLSPVSVGGVWNLVNVHSHFTGAIHAGADPEALPGTTISNPAGSLSYQALPHLIPVWVWKGGISDGIKANKYLMPLGLILFIALAVRSLTLPDAMEGVSFLKPNHSTYFKADTHTT  
 ALCPAPFALSIGVSMITTYASYLKGDKQDMPSGHTIMMNNLLVSLLAGLVIPFAVAFGFEENQGGPLIFTVLPAVPMKMPPGTGLFAVPMHLLVVFATLSAPFSHLETVIASITRQDERKR  
 KKHFWLIGTAIFIVGIPSAISFGANGEEKVGGKTIIDLWDYVLSAVIMPEIGALSVSITPTAWIDKQSVLKDAGAGSTVPRVILLMLLNTLEYLAPIAIIIVFVNSLGLIL

SEQ ID 2269

TGTGCTTCAAACAGCGGCTGCAAGCCCTCTTTCCGCCAAAGATAAAAAATGCGGTCGGAACATCTCTTCAGACGGCATATCCGGGCTTTTATTTCGCCGCTTCACATCTGCACCTGGGCGCAC  
 ATTAACCTTCAAATGCCCGCGCGGATAGGCACCATGATAAAAGTGTGTTTCAAATCTTCCCGCTCGGAAAAATCGTATTGTGCTTTTTAAATTCGTCTCTCCATCAAAATCGCGCGCGGCT  
 TGTCTGAAGGCGCGTAGGTAACGAAATTGGCGTTTTTCCGCGACACTTCGCGATCGAGGAAGTCGTGATGTAATTGTGCGCGCTGGCGACGTTTTTCGCACTCTTCGGAATCACGAAAGA

ATCCACCCCAAAATCCCCACGCGCTCTTTGCGAATCATCAGCGGATTTTTTCTGTGCGCGCCGCTTCTTGGCAGCGCGTTTGGCGATGTTCAAATCTCGCGCGAAACCGATTGTTACGCAG  
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TTTTGCCCAAAATAGTTTCAACACCATGGGATAAATTTCCGCGCGCGCTGTCCAAATAGCTGATCGCGCATGTTTGTGATTTTGAACGTGTATTCGGGGTTGAACACCAAAATCCCACTGGTTGTG  
CGGCAGCTTGTCGGTACCCAAAGCCTTTTTACAGCGTTTCGGTATTGATGGCGAAGGTATTGTGCCCCCAATAAAGCGCACGGCGTATTTCGTGGTTCGGGATCGACCCCGTCCATCAGCCTC  
ATCATTTACAGGGTTGAGATGTTTATAATTGGGAATCATCGACTTATCGATTTTCTGATACGCACCTGCCCTTAATCTGCCTGCCCAAAACGCATTGAGCGGCGCGACAATGTCGTAACCGG  
ATTTTCCGGTCAGCACTTGCTTTCCAGCGTTTTCATCACTGTGCTACACATCATAAGTAACTTCGTGACCGGTTTTTCTTTCAAATCGCGCAAGCGTTTCCGGATCGACGATTTCCGACAG  
GTTATAAAATTTTCAATACGTTTGGTTTTTCGCGCGGTGCCGGTTTTTCGCGCAGCGCGTTTGTGCGAACCGCGCACCGCTGCAAGCAGCAAAAGCAGTCAGGACGGCGAGTGGCAGATGTTTG  
ACCATTTATCATTTCTTGCATATCGGGTTGGAGAAAGCGGCCAATTATAGCCGATTTGTAACAGGGCTTCAGACGGCATTCAAATCCCGCAATGCCGCTCTGAAAGCGCGCGCTTCCATAG  
C

**SEQ ID 2270**

SEQ ID 2270

LPSNSGCKPSHAKKCRPNILQTYAIRLFPRLHILPLAHHKLCRRPDRHDKAVQIFPARENRIVVFKFVLHQIARLRARRRVGNELAVFRHRHRIEEVVDFVVRGVDFRIFRHNHER  
IHPNPALFPRHHADFPFLAARFPQAFQDVQISAEETCYAGIAARQIQIDKGRSKAFDIGAVFLEQGQCLPDVFIARAARVPAQIVQHGINFRRAVQIADAALFEFERVFGVEHQIPLVV  
IQLVNRQSLFPHAGFDGEGICPPKIRGFFVVGVIDPVHQPHFRVEMFIIGNHRLIDFLIRTCNLNPAHKRIGRRDNVVTGFSQGHAFQRFITTVVHISNLDAVFLFKIGNGFRIDVFRP  
VINPOVVLVFRRCRFFGRFRVFTAARCKQQSSQDGEQMFDDHYHSLHIGLEKAAIADIGNRASDGIONPAMPSESRRFHS

**SEQ ID 2271**

TTGCACAAACAGCTTACCCCAAACACACACAGCGGGTGCATCTCCAAAATACGCACATACCGTCCGCAAGGAATATATCATGCCGGCACAAACCGATCCGGGCTACTTCTTCAGC  
CAACCAACATTATCTCGATAGGCGCGAGCAACACCGTACAGCCTGGGTGAACCGGTACTCAGAACCTGCTGAGTACGCCCTTTCAAGGAAAAATCACCCCGTAAACCCGGCGCACCA  
CACCATAGCCGGGCTTCCCGCTACACGAGCTTCAACAAAATCCCGGAGTGCAGACTGATTATACCGGTACCCCGCCGACAGTTACGACACCTCTCTCAAAACCTGCGGTAAAAAG  
CAGCTCCGACACATATCTCTATACAGAGCTGGGACAGCTGTCTGCGCGAGAACTGCACACCCGCCGAAACTGCCATCCGCAAAACACACGGCAACGGAGTCAACATCACCGCTGCACCA  
CGCGAGGCACTCAACTGCCCTCACTCGGACTCAACATCAGTACCCAAAGACGGATATGCGCGAGGCCATACCGCCATACTGACCGGCAATGCCCGCGTCAAGCGCAAAATCGACAACTATCT  
GAACAAACTCCGTCAAGGCATAGCTCCCGCAGCTCAGCCTGCATCTCCGGCATCAGCCCATACATCTCCGCGGATTTGGCTCAACCGCTTCGGACACAGCCTGCACACAAAACCGCGCTCTA  
CACCAACACCTTGAGAGGATCAGCGAGCTGTTTCAGCGCAATTCGCCCAATTTTACCGCCATACGCGCTGATTCTCCACATCACTGCTTCAGACAGAAACCGACCGTCCGTACTGC  
ACTGCCCTCGCCGACACTGCAACTTCTCTATCAGTTTCAAGCGCGACGACCTCGAAGCGGCACTGAGCGGCCAACTGTCTCGGACCTTCCACCCCTGTCTCCGACTCGACATCTGTCTCGACAC  
GCCTCCGAATGGCTGCACGCGCACGCAACAAAACCTTCACTCTCCATTTTCCCAACTTCCCCACCAATCCGCAACGGACACCTGACCGGCACACCCACACCTTCAATCTGCCACGAC  
ATCGCCTTACGTCAGCTTGCCTGCGCGCGCGACACCAAGCGCTCTGACCATCTCTCGTCTCCGACACAGGATTACAAAAAACAGCAGCGCCCTTCCCGCTGTCCGACAGACAGCG  
CCAAACCTCTGCTCGTCAGCAGCCCCCTTTTCAGACGGCATAAACATTTTCAGACACCCCGACAGCCCTTTCGACGCTTTCCTTACCGTACGACCCGCGCGCTGAAACAGGCACAGCT  
CGACATTTCCACCGCGCAGCATGCGCTGTGAAACACCGCAACCCCAAAACAGCCGTGACGAGCCCAATTCGCGCTGCTCGCGAAGCCCTGCACCTCCCCCTACCGGCA  
CACCAACCA

**SEQ ID 2272**

SEQ ID NO 2272

LHKQLKQNDKHTAGASPKITHIPSAKEYIMPAQTDPGYFMPNHHIILIGASEQPYSLGERVLSNLLSTPFGQKIPVNP RHHTIAGLPAYTTSLNKIPGSADLIITVTPTPDSYDTLLKTCRKX  
QLRHIIILIQDWSLSAAELHTPAETAIRKHHNGNLNTACTTACIQLPSLGLNISTQDGYAAGHTAITLGNAAVSRQIDNLLNKLKRGQTSRHSISLHPGISPITSAADWLNRFPGHSLHTKTAVL  
HHNPFEDQRRLFSALRQPTRHTPLLIHITCTLTETDRAVLHCLARHCNPLISFNADOLEAALSQAQLSDLPLSLRLDILSDTPAEWLHARAPKNLTLHFPNLPHIRNGHLTGTPTPSICHD  
IASRQLARPDQAVLITILPGSGHEDYKKTARALIRLSEQTAKPLLVSSSPFSGDITHFTPAQAIINTLSYRNTAALKQAQQLDIAPQPQCRKLTQPQONIKKALAAANPALLAEALHLPPLPA  
HNP

**SEQ ID 2273**

SEQ ID 2273

ATGAAACCTGTTTCCAAACGCAATTTTCGCGACATTTTGC GCGGTTATCGTGTGCGCAATCTTGTGGCGAGTTTTCCTTTTGGCTGGTG CAGAACACCCCTTGCCGAAAACCAATTCACCAAC  
CGCGCACCATCGAAACCCACATTGATGGGCAGCATTTATTTCCGCATTCAAGACACGGGGCGACACCGCGCGCGGAAATCCTGACCGAATGGAAAAACAGCCCGCTCATCGCGCGGTTTA  
CGTCATACAGGGCGACGAGAAAAAGACATCTTAAACCGCTATATCGACAATTTACACCATAGAACCGGCCCGCGCTGTTTTCGCGCCAAACACCCCCATTCCAAACCTTGTCGCGCATCGAATAC  
GACCCTTTTCGCGGAAAGATACCTGCTCTTCATTAAAGGCTGGGACAACCACCGGCACAACGCCTGCCAGCCGCTGTTTATCTCCGGGCTTCGCCCTTCGCCCGATTGGCAGCAATTCA  
TCATCTCTCTCTTCATCATCATCTGTCGGAGCTGCTGATGGCAATATATCTTCGCGGCACATATGCCAAAAACCCATCAGAACTTAGGCAACCGCATGAGAACTTAGGCAACCGCATGGAGCGGAAACGGGACATTTGA  
AACCCGCGCATCTCCCAAAAGTCGACACCGCGAGCAATGTCCTATGTCCTTCGCGCATTTGCGCATTCAAATTCGACAATAATGGCGGAAAACTCGAAAAACTTGTCGCCAAAGAACGTTTACCTACTCCAC  
CAGCTGTTCCCAAGAAATGCGCTCCCGCTTGCCGCTATGCAGGCAATTGTCGGACTGATTAGGCACAGCCCCAAAAACGGGAGCAATATCTCAAACCGCTGGAAGCGGAATGACCCGCA  
TGGATACGCTGGCGGGGAACTGTAAACCTGTCCCGCTCGAAACCTCCAATATGCGCTTTGAAAAAGAAAGCCCTGAAACTCCTGCCCTTCCTGCGGCACCTCGGTAGAGAGACAAACCAAG  
TATCGCCCAAGAAAGGACAGACAGCGTCCGCTCTGTGCGCAGCGAAAAATCCCGAAACACAAACCATCTTGCACACGAAAGCTACCTGTACCGCGCTTCGACAGCAATGACCATCGCGACA  
GCGCTCAACTACAGCCCCGAAGGCAGACCATCTCGATCAACCATCGGACAAGACCAAAACATCGGATATCGACGTTACCGACAGCGCCCGCGGACGAAAGCGCTCCGCGACA  
TCTTCACCGCTTTCTACCGTGCAGATCTCGAGTGCCAGTGCCAAACACCGGAACAGGACTGGGGCTTGCAATTCAGCCCAATATTTATTGAACAGCAGCATTCGGGCAAAATCATCGCCGAAACATCAA  
ACCGAACCGCTTTCGATGCGCTCTATCTCTGCCCAAGAAAAAACCGGGTTTCAAACACGAAAAAGTGCGAAC

SEQ ID 2274

SEQ ID 2274

MKLFQRI FATPFCAVIVCAIFVASPFWLQNTLAENQPNQRRIETITLMGSIISAFKTRGDNGAREILTEWKNSPVSSAVVYVYIGDEKKDILNRYIDNYTIERARLFAANNPHSNLVRLEY  
DRPGEYLFPIKGDWNNHQAQRLPSPLPIGGLPLAPIWHEFIITLSPIIIVGLMAYIILAGNIAKPIRILNGMDRVRANGELETRISQQVDDRRDDELSHLAIQFDKMAEKLKLVAKERYLLH  
HVSHEMRSLPARNQAIVGLIQAQPKREQYLKRLEGELTRMDTLGAGELLTLRSLTSMMALEKESKLPLPLGNLVEDNQSIACKNGQTVALSADGKIPENTITLANESYLTAFDNTVTRN  
AVNYSPEGSTILINI GODEKHWI IDVTNDNGPGVDEMOLPHIFTPAYRADSSANKPGTGLGLALQHIIEQHCCKGKIAENIKPNGLMRPLILPKKKTGPTKESAN

**SEQ ID 2275**

SEQ ID 2275:

ATGAGCCGCGATTACTCGTAGATGACGATGCCCTGCTGACCGAACTGCTGACCGAACTACTGAGCGCCGAAGGTTGAACGTCGCGAGCGTTCCCGACGGGGAAGCAGGCGTACAGGAAATCTCGTAGCGGGCAATACGATGTAGTCTGATTGGATTCCATGATGCCCAAAATGAACGCGCTTGGATGTCCTTGAAAAACGTACGCGCCCGAAGCACCGTCCCATCATCATGCTGACGCCCAAGGCAGACATCGACCGAATCATCGGCTTGGAATGGGTGCGGACGACTATGTCCCCAAACCTTCACACCAACGGGAACTCTTTGGCAGCGCATCAATGCCATCTCTCGCGGAGCAACAACACAGCGGGGAACAGAAACACGACCCCAACAGCATCTCCGTCAGCGATGTCGTCTATACCCCGCCAAACGCCAGGCAATCGCTCAAAGACATGCCGCTCGAAGTGAACGACGACGGAATTCACCTTGCTCGAAGTCTGTATGCGCCATCGCCGAGATGTCGACAAAGAAACCTGTACCGCAAGCTGGCAAAATTCGACCGCAGTATCGACGTACGACATCGACATCGCGCAAGCTGGGCGATGCGCTGATGTCACCAAGCGGACCTTGGGCTACTGTTTGTCAAAAAAC

SEQ ID 2276

MSRVLVDDALLTELLTEYLSAEGLNVRSPVDGEAGVQEILSGQYDVVVLDSMPKMNGLDVLKNVRARSTVPIIMLTAKGDDIDRIITGLEMGADDYVPKPCTPRELLARINAILRRAGE  
CSPFNNA PNSTSVSDVVLVPAKROASVKMDPELFTSTEFNLLGVLMRRAGQGVSKETLSVEALDRKLAKFDRSIDVHSSINRHLGDASLIQTVRGLOGLYFVKN

SEQ ID 2277

SEQ ID 2277  
ATGCAAGACATTGCAAAAACAGCAAAACCGTAGGGAATACGCTATCAAAAACATTGCAGCCGTGTTAAGATAAACTGTCAAACAATCTTTTCAGCCACGCCCGGAACAGGGTCGGG  
CATACCCCTACGAAAAAGAAACACCA

SEQ ID 2278

MODIAKNSKPVGKYAIKKHCSRVLNCQTF SRHARNRVGAYPYKETP



## SEQ ID 2279

ATGTCGCGTGAACGACCGGATCCGGCGCGCGCCGCCGCAAACTGCCGATTTACATCTGCGCTGCTTCTTGGATAGGCATCATCCCTTTAOCCTTCGCACTCAGGCTGAAACCGT  
CGCCCGACTTTTACACGATGCCCGCGCGCGCGCGCGCTGATGTCCTGTGTCTCTACCGCAGGAAAAAGCTGTTGATGTCAAAATCCCGCCATCAGCTTCCTCTGTTTGAAT  
GGCGGATTTTGGTGGCTTCAGGCACGCTGATGAACCTGATTTATCCGGAATGAACGACATCGCTCTTGGGTTTTCATCTTGCTCGCGCTCAGCGCTGGGCGTGAAGAGTTTGGTC  
GCACACTACGACAAGAAGCATCGTTACCTGTTTGCCTGGTGGCTGCTTATCGGCTCCCTGCTTCAATCTGCATGCTGCTATCCAGTTTTCGCGCTGGGAAAAACCCCGCTGCTTC  
AAACATCATCGTTTACAGAGGGCAAGCGTAATCGGACACATCGGGCAGCGCAACACCTCGGACACTACCTCATGTTGGGGCATACTCGCTCCCGCTACCTCAACGACACGAAAAAT  
CCCGCAGCGCTCGCGCAATCTGCTGATTTATGACAGCGCGCTTTTAGGTTTGGTCAATTCGCGCACCATCTTGACCTACATAGCGCCATCGCCCTCATCTCTCTCTGATTTTC  
CGTTCCGACAAATCCACAGACGACGATGCTCGGCATAGCGCAGCGGTAITCTTACCGCGCTGTTCATTTTCCATGAACGCCATPCTGGAACCTTTACAGGCATCCGCTACGAAA  
CTGCCGTGCAACGCGTGCACACGCGGTTTACAGACTTGGCGCGCAAGCGAATGGAATAAGCCCTTGGCGCTTCCAGTCCGCGCGGATTTTCGGGCACGGCTGGAACAGTTTTC  
CCAAACAACTTCTGATCAATGCCGAACAGCACACCATACAGCAACTTCTCAGCACCTTGTTCACCATTCCTCCACACATCATCTCCAACCTCTTCAGAAATGGGGATCAGCGC  
ACGCTTCTGTTGCGCAACCTGCTGACGCGCATTTGCCGGCTGCTGAAACGCTCCCTGACCCCGCATCATCTTCTGCTGTCGCGCTTGCCTCAGTATGTCACAGTATGCTCG  
AATATCTTTGTTGATGCTATTTCTCTATCCCTTCGAGCTGATGCTCTTTCGTGCTCCCGCAGAGGCTTCAGACGGCATCGCTTCAAAAAAGCCCAATCTCGGCATCTAGCCGC  
CTCCGCGCCATATTCGAGGATTCGTCACCTTGGACTGGACATACACCGCGCTGGTAACTCTTTTCCCGCGCGCTGACGACAGTGCCAAAAACCTCAACCGGAAATCAACGAATG  
CGCTATATTTCCGCAACAGCCGATGCTGCTCTTTATGCGGACTTCTCTCTGTAACCTTGGCGCTGCGGAAATACCCGAAACCCAGACTTGGCGGGAAGAACACCCCTCAAGCAC  
TAAATACCGCGCTACTCGGCACCTACCGCATCGCCCTCTACTGATGCGGCAAGGCAAGTTGCAAGAACAAACATGAGTATGCGGCGCAACAGCTCTATTCACCCCTACTGATGCGC  
CGGATACGCGGCAAAATCCGCAAACTGCGCGTATGGGCAACGCTGCTGCCGAACTGCTCAAAGACTGCAAGGCTTCCGCGCGCTCCCGGCATCGGAAACAAACCTTGCAAA

## SEQ ID 2280

MSAETTVSGARPAKLPYIILPCFLWIGIIPFFALRLKPSDFYHDAAGLIVLFLTAGKFLFDVKIPAIISFLFMAAFWWLQARLMNLIYPMNDIASHVPIILLAVSAHACKSLV  
AHYQBERIVTLFANSLILGSLQSCIVVIQFAGWENTPILLQNIIVHRQGVIGHIGQRNHLGHYLMWGLISAYLNGQRKI PAALGAICLMQTVLGLVNSRTILTYIAALILPFWYF  
RSDKSNRRLMGLIAAVFLTALPQF SMNALLETPTGIRYETAVERVANGGFTDLRQSEWNKALAAQSAPIFGHWNFPAQQTFLINAEQHTINDRFLSTLFTSHENILQLLAEMGISG  
TLIWAATLLTGAGLLKRLSTPASLFLCALAVSMCHSMLEYPLWYVFLIPPLMLPLSPAESDGIAPKKAANLILTASAAIPAGLLHLDWYTLRLVNSFSPAADDASARTLNRKINEL  
RYISANSPLHSFYADFSLVNFALPEYPTQWAEBAFLKALKYRYPYSATYRIALYLMRQKVAEKQWNRATQSYYPYLMRYADEIRKLFVWAPLLPELLKDKAPAAAPGHPETKPKCK

## SEQ ID 2281

GTGAACAGACAAACCGCTTACTTCTCTGCTTCTTACGCTGATTCGACTGATTCGCTTATCCCTTCTTGGGAATTTATGATTCGACCGCTTACCGCGCGCGGCTTCGCTGCTCGCGCTCA  
AAGCCCTGCGCTTCTGCTGCGCTTTCAGGTATTTCTAAGAAAAAATCTATACCTACCAATACAGCTCCATCTGCTGTTGATTTTACCTTTCGCGAAGCGCTCATCGCGCTGTTCAACGC  
CTATCCCGCAGAAAAATTTGCGCGCGCTTTCGCGAGTATTCAGATCATCTTCTTCATATCTGCTGCTGCTGCTCAACAAATACAAGGAACAAACATGTCGCG

## SEQ ID 2282

VNRGTAYFLASFLIALIALSLSWELWIAPLRPGGSLWALKALPLCLPLSGILKKIITYYQYSSMLVLIYFAEAVNRLFNAYPAEKICALSAVFSIIFFISCLSFVKYQYKTNVR

## SEQ ID 2283

ATGAATATGCTTGGAGCTTTGGCAAAAGTGGCAGCGTGCAGATGCTGTCGCGCTTTTGGGATTTGTGCGCGATACGGTCAATGCGCGGGCATTCGCGCGGGTATGGCGACGGATGCGT  
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GGCTTTTATCCGCCACGTTGCGGGAATGCTGCTGTTGTGCTGATCTGCTTACC CGCTGGGCATACTTGGCGCGCTTGGGTGATTTATGTTTCCGCGCGCGCTTACCAAAAGCGCG  
GACAAGTTCCAACTTTCACATCAGCGCTGCTCGGATTCAGTTTCTCTATATATTAATGATTTCTTGTCTTCTTGTGCGCTCGATATCAATTCCTACATAGTTCCGGCATTCGCGCT  
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GCGCAAAATTTCTTGGTTATTAACACGATTTTCGCGCTTATCTGCAATCGCGCAGCGTTTATATGATGATTTACGCGACCGCATGATGGAGCTGCGCGCGCGCTGCTGGGGCTGCAC  
TCGGTACAATTTGCTGCGGACTTTGTCCAAACACTCGGCAACCAAGATACGGAACAGTTTTCGCGCTGCTGCACTGGGTTTTCGCGCTGCTGCTGCTGACGCTGCCGCGCGCGCG  
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CTGATTCGCGTGGCGCGGACTGATTTTCGATCTCTGCGCGCTTGGGCTTCCGCTCGCGGCTTCAACACGCGTGGAAAGC

## SEQ ID 2284

MMMLGALAKVGLTMSRVILGVRDVIARAFAGMADAPFVFAFLPNLRRVFAEQAQAFVPIIAEYKETSKEATEAFIRHVAGHLSFVLIVVTALGILAAFPVITYVSAPGFTKDA  
DKPQLSILRLITPPYILLISLSPVGSILNSYHKFGIPAPPTPFLNLSIFVPALFFVYFDPVPTALAWAVFVGILQLGQPLPWLAKLGLKPLKLNFKDAAVNRVMQMAPAILGVSV  
AQISLVINTIPASYLQSGSVSMYADRMELPGVLAALGTILLPTLSKHSANQDTEQFSAI LDWGLRLCHLLTLPAAAGLAVLSFPLVATLPHYREPTLPDAQMTQHALIAYSFLIG  
LIMIKVLASGFYARQNKTPVKIALFTLICQLMNLAFIPLKHAGLSLATIGLACINAGLIFLLRKHGIYRPGRWAAFLAKMLIALAVMCGSLHAAQACLPPFHAHAGGRKAGQLCI  
LIAVGGGLYPASLAALGFRPRHFRVES

## SEQ ID 2285

ATGCGCTCTGAAGCCCCCGCGCACATTAAGGAGCACACCGTGAACACCTTTACTTAGGTTCGGGCGAGCCCGCGGATGGAATCTGACACAGTTGGGCTATCGGGTCTGCAAGCTGC  
CGCGCGCATCGACGAAACCGTTAAAGCCGCGGAAACCGCGCCCTTACGTCCAAAGGATGGCGGAAGAAAAAATCAGCGCGCTTTGACCTCTTTTGGCAACCAACCGCGCAATGCC  
CGATTTCCCGCTGATTACGCGGACACCTGCGTCTTTTCAGACGGCATCATATGGGCAACCTCGCTCCCAAGCCGAAGCAATCGAATTTTAAACCGATTTGTCGCGCAACCAACATACC  
GTCTGACTGCTGCTGCTGCTTATTCGCGGCAACGCTCAAGCGCGCTCCAAACCAACCGCGCTGTTTCAAGCCCTGAGTTTCGGAAGAAATTTCCCGCTATGTCGAAAGCGCGGAAAC  
CGATGGAGAAAGCGGTCCTACGCGGTGCAAGGCATAGGCGGTATCTTTATCAATCTATCGAAGGACGCTTCAGCGGCATATGGGCTGCGCGCTTATGAAACCGTTTCCATGTTGCA  
GGATTTGGGATACCGCCCCCTTATCCGCGCTTAAACCG

## SEQ ID 2286

MPSEAPPHIKETVNTLYLGSPPRMELIQLGYRVVKLPAGIDSTVKAETPAPYVQRMEEKNQAAITLFCFTNGAMPDFPLITADTCVPSDGLILKPRSQABAEFLNRLSGKHQHT  
VLTAVCIHRYGRKTSRVQYTNRVKPLSSEISAYVQSGEPMEKAGAYAVQIGSIGIPIQISBGSFSGIMGLPVYETVSMQLDLGYRPLSLAKP

## SEQ ID 2287

GTGTCGGAACACAAACGAAACAAACCGTCCAAACCGCTTGTGGAACACCTCATCGAGCTACGCGCGCGCTGATGTTGGATGGTTGTGCGCATTCGCTGCTTTTTTGGCATGATCGCGT  
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GGCGCGCTTTTGGTTTCACTGCGCATACGCTTACCAAACTCGGCGATTGTCGCGCGCGCGCTTACCAAAACGAAACCGCTGATTCAGCGCGCTGCTCTCTCCAGCGTCAAGCTG  
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TCTTAGGTATGCTGCTGCTGCTGCGCACGCAATTTGAAGTGCCATCGTCTCATCTGTTAAACCAAAATCGCGCGAGTCAACGACGAGCAGCTCAACACGCGCGCGCTTATGCTATGTT  
CGGCGCTTTTGGCTGCGCGCATCATCAACGCGCGGACATTAATTTCTAGACCTGCTTGCATTCCTGATTCCTCTTATACGAGCGCGCATTTGGTTGCGACGCTCTTCTACTTCA  
CGTTCAGAACAGATGGCGACATACAGCGCGCTGCAAAAAAC

## SEQ ID 2288

VSETQNEQTVQPLVEHLIELRRRLMWNVVGILVCFQGMPPAQQLYFTFIADPLMANLPKDTSMIATDVIAFFFPVKVTLMAAFLVSLPHTLYQINAFVAPALYQNEKRLITPLVLSVSL  
PFIHAFAYFLVFPVIFKFLAGVTPVGVNMTDIDKXLSFLLGMFVAFGTAPEVPIVVILLTKIGAVTTBQLKHARPYVIVGAFVVAIVTPPDIIISQTLIAIPLILLVEAGINWGRFPFP  
RSEQDGDIOPPAKT

## SEQ ID 2289

ATGTTTGATTTTCGGTTTGGGCGAGCTGATTTTGTGCGCATTTATCGCCCTGATTGTCTTGGTCCAGAACGCTGCCGAAGCCGCGCACTGCCGACGGCTTATCGGCAGGCTGCAAC  
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TACGGATATGCAGAACAGCTTGCACGACATTTCCGACGGTCTGAAGCCTTGGGAAACCTGCCCGAACAGCGCTGCCGATTTCCGTGTGATGAAACCGCAATCCCTTCCCGAT  
ACGGCAAAACACCGTATTCAGACGGCATTTCCGACGTTATGCCGTCTGAACGTTCCGATCTTCCGCCGAAACCTTGGGACGACAGGCAAAACCGGCACTACAGCCGAACTCCGGAACCG  
ACAAAGACCGCGCATGGCGGAATACCTGACTGCTTCTGCCGCCGACCTGTCTGACAGCGCTGGAAGTCAGCTATATCGATACTGCTGTGAAAGCGCTTCCGACACCACTTCCCT  
GCGCAAAACAGCAATAAACCGCAACCGCATTTCTGTCGAAACACCGCCCAAAACGAAATTTGGCGCTCCGTAAATCA

## SEQ ID 2290

MFDPLGELIFVGIILIVLPERLPEAARTAGRLIGRLQRFVGSVKQELDTQIELELRKVQAFEAQAQVRDSLKETITDMQNSLHDISDLKPWEKLEPQRTPADPGVDENGNIPLD  
TANTVSDGIDSVMPSERSDTSAETLGDURQGTSTAEPAETDKDRAWEYLTASAAAPVQAVEVSVIDTAVETPPVHTTSLRQALNRKRDRPRKRAKPLKLRKKS

## SEQ ID 2291

ATGGGCACTTTTCTCTGACGCACTGGATTATCGTACTGATTATCGTCGTTTGTATTTGCGCACCAAAAAATTGCGCAACGCTCGGCAAGACCTCGGCGGTGCGGTTTATGACTTCAAC  
AGGGGCTGAACGAAGCACAGCGCAAGAACGCCAAAAAGCAGATGTATTCAGACACAAAAAGACGAAGACAAAGCA

## SEQ ID 2292

MGSFSLTHWILVLLIVLIFGKTLRNVRDLGGAVHDFKQGLNEGTDGKEAQKDDVIEHKKDEKA

## SEQ ID 2293

GTGTCGTATACATCGTCTTTTGGGGTCTTTGCGCTCTGTGCTTCGTTACGCCCTGTTTGAAGTCATGAACCGCACCGCGAGGTCTTTGCCGAGTTCGCGCAATTTTGGTGCCG  
AATATCAAAACGACGATAATCAGTACGATAATCCAGTCCGTCAGAGAAAACTGCCATGATGTATCTTAAAGTAAGTAT

## SEQ ID 2294

VFDYIVFLGFFAVCAFVQPLFEVMNRTAEVFAADVAQFFGAETQNDNQYDNPVRQRKTAHDVSLSKY

## SEQ ID 2295

GTGCTTTTTCAGACGGCAACGGAGCCGTTATGGACAACGTATTTTCTGCAAAATCGCCGCCAAGAGATTCCGGCGCAACCGCTCTATGAAGACGGCGAAATGGTTTGTTCAGAGCA  
TCAACCCCGCCGCTCTTACGTCGACAGCTCTCTGCAACAAAGTCCATTTGATTCTGTGCGACACCGCGCGCGCAACATCAGCCCTTTTGGGAAAAATGATGCTGAAAGTTCCCGAAAT  
CGCAAAAGCTTCGGGACTGACCGACGGTTTCAAAACCTTATCAATACCGGCAAGGCGCGGACAGAGGCTTCCACCTGCATATACACATCATGGGACACCCGTA

## SEQ ID 2296

VLFSDGNAGVNDNCIFCKIAAKEIPAQTVYEDGEMVCFKDLNPAAPLHLLLIIPKVHFDLSLAHAPEHQFLILGKMLKVPEIAKASGLTDGFKTLINTGKGGQEVFHLHIHIMGTFV

## SEQ ID 2297

TTGCCCGAGAGCAGCCGTTTACCTTATCATTCGCAACAAACAGAAACAAAGGAAAAATCATGGGAGATTCCGTACTATCCGCCATCCAAACAACTTATACAGCGCAAACTCGCCG  
ACCGTCCGAATCTTACGTCGACAGCTCTCTGCAACAAAGGCGAGGACAAAAATCCTAAAAAAGTGAATGAAGAAGCGGGCGAAGTGTGTATGGCATCCAAAGACAAAGACCCGTCACCT  
GGTTACGAAGTTCGCGACTTATGTTCCACACCATGATCTTCTGACACACCCAGCACTGAAGCGGAAGACGTATTGGACGAATTTCCCGCGCTCAGGGGCTGTGCGGGCTGCGCGAA  
AAGCGCGCGTACAGAACTC

## SEQ ID 2298

LPSSRLAYHSEQTETNRRKIMGDSVLSAIQQTIIQRKSADPSESYVAQLLHKGEKILKKVIEEAGEVLMASDKDKPSHLVYEADVLWFHTMILLTHDLKAEDVLDLSRRQGLSLAE  
KAARTES

## SEQ ID 2299

TTGTTAATCCACTATATTGTCCGGCATGGCCAGCTTAACCTTTAAGCCGCTGCTTTCCGCAACCGACCGCTATCAGCGGCAAAATCCATCAGCGAAAGCGCTCGACAAGGCATCGGCAACC  
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CGTCTGTCAAAACGAGACTTTGCCGGAAGCGGACCCGTTTACGGGTTTCTTCAAGCTTAATCTCCGCGCGGCTTCCGATCGGAGCGGCGCAAAATATTCGGCATACAGTTTCCCAACAG  
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## SEQ ID 2300

LLIHYIVRHGQPNFKPPAFGNRPYQRQIHGKRRRQIGNRRIIRHYAHAFITRRTHAGSRIBQMKPARFVHRPIAARSCKRLVFRDICIQHAFVVRIDADADIPHPPAVCIKPPDFAH  
IDQRGRHVSVCFKQRNNLVRDIALRDAVQGTHTLFGKTDPTVVKRDFAEADPPQGLHAILRRFRIGTGGKIIGIQPQRLNRRIERAFQRVNIARLNSKKSGAGSEVR

## SEQ ID 2301

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CGGCAAGCACAACGACTTGAAGAACTCGGCTACACCGCCGCCACACACCTTCTTTGAAATGATGGGCAACTTCTCTTCCGCGATTTACTTCAACGCGACGCGATCCACTTCCGTTGG  
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CGTTCAATGAGAAACCCAGCTGAAAGTTATCGCGACACATCCGCTCTGCTCATCTCTGATTCGACAGCGGCTATTGCTTCCAAAGAGGACGCGGCTACGTATTGCGCGCAT  
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CAACGCCGTGATTCTTTTAGCGGCAGTAAACGAGGTAAGTCTCCCTGTGTCGCGCGCGGTATCCAAAGCCCTGACCGGAAAAGTCAAAGCAGGAGATCTGGTTAAATTTGACGCCGAACAA  
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**SEQ ID 2302**

MTRHLRDLEKIMKTSSELQKPLAFFETKGHTVVRSSSLVPHDDPTLLFTNAGNQPKDVLFGDKRPYSRATTAQRCVRAGKHNDELNVGYTARHHTFFEMGNPSPFGDYFKRDAIHPAH  
EFLTSPFWLNI PKDKILLATVYAEDDEAYNIWLNIEIGMPSERIVRI GDNKGAKYASDNFWMGDTGPGPCSEIFPDHKGREIWGGIPGSPPEEDGRDWIETWNCVFWQPNRDEQGNMNPILPKP  
SVDTGMGLERMAAVWQHVSNIYEDILFQDILLKAVARETGAPSPMEEPSLKVIA DHIRSCSFLIADGVLP SNEGGRGYVLARIIRRAVRHGYKLGQSKFFPHKLWADVLWQEGGAYPELKEKK  
AQITEALKNEESRFAQTLETGHALLENALAKGKKTGGELIIPKLYDTGYPGYDILTADICRENI EPDEAGFEREMEAQARARAAQSFKANAQLPYDQDTEFGYSERQTESKVLALYKD  
GEQVVELNBGDSGAVVIDFPFYAESGGQVGDVGYIFAGENRFVYRDTPQKIAAEQPGVQVTSGRLLKVGSDITAKVDDEIRNANMRNHSATHLMKHALADVLGGHVQKGSVLTAESTF  
DI SEHQAVTAEELAEVRRVNEAILANVA VNAATMSMEDAQRTDAMMLFGEKYGVDEVRVLQIBGSGFLKCGTHVSRTDGLPKIISBGGLAAGVRIIEATLGNALNKWAQBERLVEDI  
IABTKAQTEKDVLLAKIQAGAAHAKALEKELARAKALAVHAGAKILLDDAKDLGAAKLVAQIGBADAALREFVTVIDTGSDISNVTILAAVNEGKVSICAGVSKALTGVKAGDLVFAAEQ  
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**SEQ ID 2303**

ATGAAATGCCGTACCGATCCGGACAACAACCGATGCCGCACCCCTGCGGGCAGGCTTGGCACTCTGAAAGGTTTCAGCGGGCATTTTTATTGGAAAGGCTTTTTTTTGCACCCGCCCTACACA  
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CHCAAATGATGTGAAAAACCGCTTACCGGACAAGCCGCATCAAAATGTCGGGCAAAATGGAGCAATTCAGCGGCAACAAGTCGGATTGGCAGATTAGACCGATACAAACCCAAAGGGCGGACG  
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**SEQ ID 2304**

MMFYRSGQPMMPHAGRLRLTKSGGGIFGLRFPATALLKAVFCVTRTIIAACHROGRMLPLKFPQPRRSVILKDFRGYKEPEMVKKRPVVVLIARNRHNGKLVTWVPLSSTPEVFLADCH  
HMSSENPLDPKPHICRAKCDMTATUGLARLDRYKPKGRDRCPII SEEDFOAVKTVAKAPKLY

**SEQ ID 2305**

ATGAAGTACGTCGCGTTATTTTTCTCGGCACGGCACTGCGCGGCACCTCAAGCGCGCGCTGCCGAATGGTTCAAATCGAAGGCGGCAGCTACCGCCCGCTTTATCTGAAAAAAGATACCG  
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 AACTTGGGCTTCCGCTGCGCAACCGCA

SEQ ID 2306

MXYVRLFFLGTALAGTQAAAEAMVQIEGGSYRPLYLKDKTGLIKWKVPFKLDKYPVITNAEAFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVNTISWFAANAYCAA  
 QGKRLPTIDEWEPAGLASATQKNGSNEPGYNRTILLDWYADGGRKGLHDVGKDRPNYWGVIYDHGLIWEHTEDFNSLLSSGNANAQMFPCSGASVSGSDSSNYAFLRYGIRTSLSQSKYVLH  
 NLGPRCASR

**SEQ ID 2307**

TTGTGCTCTAAATCCGCGCTTTTGTGTTTCAGGATTAAGTCGATACAATCATCACCCAAATACTATGTTTGTTTTCTTTTCTCTGCGAGAGGTTTTTATCCTTTGCAAGAAATAAAAAATC  
AAAACAAATCATGTCTTTGTTTGT

**SEQ ID 2308**

LCLNPAFCVSGLSRYNHPNTMFVFFSLARGFYPLQRIKNQNKLIIVVC

SEQ ID 2309

TTGCGGTTTCGTTGGAAAAATGCGGCTCGAGCGTTTCAGACGGCATTGTGCTGTTGGCAAATGTAATTTGCTTACAGGTTTGGATTACAAATAATTTTAAACGGCGGATTCGTTGTTGGAATC  
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AAGC

SEQ ID 2310

LRFGVKCRRLSVDGICAVANVICLQVWHNNFNGGFVVVDQTLFAFGNQFVQLDALGDEGEFVDFAFFDQDGFGRVVAVGNRAAHIQFPHHDADVDDGGGVAPDGYDNQVGGGFAGFDQS  
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DGDFFGQAAAAAQADKVHVFGEVVAAAFAGRYVADVDVGFHDHDLADFNVHFAFDGINHAGELVSHRYGRGLAGNRMMTAGRDENRAFHKFPVQGTADAAPGDIDADGAGDGRFGDV  
FDADVAFVVKTCFCHNAPCFQVGMPSSESSRRRLKNEHREEA

**SEQ ID 2311**

TTGGGTTTCGGATGTCGAAGGAAGGGAATTTTGCAAGGCTCAGTTTGTAGTAAAAATATCTAAACAGATTCAATCGGAAGCGGTACGGCTTCTTCACGCCATTCOCATTTCAACGGCCGCTGCTAGATTACAGCGCATTOCTACTTGAAAACAAGGAGCGTTACAAATGAAAGCAGCAGGTTTTCACAAAGGCGCATCTCGCATCGGAAGACATCCCCGAAACGACCGCTGCCCCCGGCAACCGTCGGCATCAATGTCGCCCTGCTGTCGGCATCTGCGGTACCGACCTGCAACGAATTTATGGAAGGCCCGGATTTTCATCCCCCCTTCGCGTCATCCGCATCCGATTTCCGGCGAGTCCGGCCCCGTAACGATGGGACACGAGTCTCCCGCGTGTTTATGCCGTCGGCGAGGCGTGGACAGCATATAAGGTCGGCCAAACAGCTCGTGTGCGAACCCTATCATCTCCGCGACAGCTACCGACCGCGAAGCAGATACCACTCTCCAAAGCATGACTTTATCGGCTTGGCGGCTCCGGCGGCGGCTGTCCGAAAAATATCGGCTGCGGTCATCCGATTCGATCAAGATTTCCGACAAAATCCCGTTGGAATCAAGCTGCTTTGATTGAAACCTCTGCTGTGCGGACACCAACGCTATGTATCGCAGCGCCGCGAAAGCAGCGATGTCGCATTTGCTGGCGGGCGCAGGCCGATCGGTTGCTGTGTGGCCCGCTGTGTAAGGCCAAAGGCATCAAAGTCATCATTTACCGAGTTGAGTAAAGCAGCGAAAGACAAAGCCCGGAATCCGGCGTTGCGGACTACATCTCTGACCCGTCGGAATGTCGATGTTGTGGAAGAGTGAAAAAATCTGACCAAGCGCGAAGCGCTGAGCTGGCGTTGCGAATGTACACAGCGTGAACAAAGTGTGGAATCTTTGGTCGAAGCTGCAAAACCGCGCCCAACTTGGTTATCTGATTCATCTGGAGCCACCCCGCCACCGTCAACGTCCACAGCGCTCGTGATGAAAGAACTGGATGTGCGCGGCACGATTCGCTACTGCAACGACACCGGGAAACCATCAACTGGTTCGAAGAAGGCAAAATCAACCTCGAAACCTTCTATCACCCAGCGCATCAAGCTGGACAACTGGTTTCCGAAGGCTTCGAGCGCTTGATCCACAAACAGGAATCCGCGGTTAAAAATATTTGTCGATCAAACTCTG

**SEQ ID 2313**

**SEQ ID 2314**

**SEQ ID 2315**

**SEQ ID 2316**

SEQ ID 2317

SEQ ID 2318

**SEQ ID 2319**

SEQ ID 2320

SEQ ID 2321

**SEQ ID 2322**

SEQ ID 2323

SEQ ID 2324

SECRET  
REF ID: A66541

SEQ ID 2325

TTGTTCAAAATGCGCTTATATTTGGATTGTTAGAATGAATACTAAAAACAGAGTTACAAAAAAGCTTTTAGAAGAGGATATATCAACTTTAAAGAAACACTAAATCGTGTAGATGCTCTTCTC  
CAAGATATGACGTAGCATTCGAACCTCCTATTGTCGTCGATGGTTAATTGCAACAACTAAATATTTCTCGCAAAAGAAATAGGTTTAACTATAGAAATGCGCACTCTTGATACAAAGTTT  
GGTATTGTAAAAAATGTCAACCTTAGAGAAATAAAGTTAAATTTTATAGTAGATTAAACAAATTCAGGACAAGCGCGAGCGCAGACAGTACAATAAGTACGGCAAGCGAGGCAAGCGC  
GTACCGGTT



## SEQ ID 2326

LPKMLIPWIRVMTKTELQKLLEEDISTLKETLIRVDALPFRYVRSIATPIVRRLIDKQLANILAKEIGLTIELPILDTSLVPEKSLTENKVNPFYSRLTKIRTRRAADSTNSTARRGHA  
VPV

## SEQ ID 2327

TTGTGGAACCTGATGCCGATTATTTTCCGCCCGTCCCGATCGCGAAACGCCCGCGGAGAATAGCGTGAAGGAAACCTGAAACGGGTCCGCTTCGGCAAAAGTCTCGCTTTGACGACCGTG  
AAATCCGTTTTCGCAAAAGGGTATGGGTTTGTCTTGAACCGGCATCGCGCAAGGTATATACAGGACAGAGTTGTTGCCGTGCTTAAAGCAAAACGAGATGCTCGCCGCGCTGGTCGATAT  
GGCGGAAATCAGGGGTTGATACAAACCGCAGCGGATGTGAATGTCCGCATCCGCAATCCGGACGACGAGAAGGCGGTGTGGCAAAATATCAGATGAAAGCAAGGCGTTTGCCTACT  
TCGGCGCGCTTGTGGGACGGTGTGACAAAGCGCGGCGGCTTACCCATTTGTTGATTCGCGGCAACCGCGGTGATACCGCGGTATATAAAGCATGAGCGTAATGGCGATGATCGCGCG  
TTGCCGATGCTTGTGCGCGGCTTTCCGTGATGATTTCGCGTGATACGTTGCGTTCGCGAAAGCAGGCGCTTAAAGTTAGGCTGGCCATGCGCGCAATATAGTGGAT

## SEQ ID 2328

LMKLYADYFAARPDATPPENSVKETLKRVPFGKVSFDDREIRPAEKGMGLSLNGIAQGYITDKVVALLKANGVPAALVIMGEIRGPDITNGRMNNGVIRNPDDEGVLANITKDKAFAP  
SGGYTVMKAGRLTHLFDPRGTVPYKSHSVMDADDAVADALSTAFVMDLPIRSVARSRLKVRILAMPDNIIVD

## SEQ ID 2329

TTGGAACCCACCCCTTCGGTGGTGTGCGAATCNGGCTATTTTCAAGAGGCAAAACCCCTCCCTGCCAGGCAAGACGAAAGGCGAGCATCTGAAATATGCCGCCCTCGGTGCGGAACAT  
GGTCAAGCCCTTCGGTGGATTCAAACCAAGGTGCCGATTCGGGCTTTCCGATCGCGCTTGTGCGCACAAATCAATCGACTTTTGGCGCAATCGCATTCGCTTCCACTTCGACCTCGAT  
TTTTGTACCTGTGCGATATCCAGGTAAAAACGTTCGCGGACTCTGGTTACCTTACCTTGAAACCTGCCCGCAAGACCACTTTTGTGCGCGGCTTCAAGCGCGCAAGCATTCGC

## SEQ ID 2330

LEPHEFGVGIXLFPQKRNPSLPKTERQHPYALRVGTWSSRLLEFKTKRIRAFPMRLVGTNQSTFAAIALRSTSTSLFVPCPISTVKNCPTLVTLPLKPAARTTSLPAPKAASIA

## SEQ ID 2331

ATGATGAACCGTTATCTTTATGGAATATCTGCTGATTGTGTTCACGATTGCGGTTGCCGAGTGTATTCGCTGCCAACCTATTCGGCGAAACGCCCGCGCTGCAGGTATCGAACCAAC  
GACAAAGCATCATCATCAACGAACAGACTCAATCCAAAGTGGATGCTGCGCTGAAAACGCCGGGCACTTCAGACCGACGGGATGTTGTTGTGTGATTAFTCACTGAAAGTGCCTTTCAAAGA  
CACAGAAACCGAGCTTAAAGCGCGGACGTTATCGAAACACTTTGGGCGAAGGTATATTACGCGCTCAACCTGTGCGGACAGCGCCGAAATGATGGCGAAATCAAAGCAATCCG  
ATGTTTTTGGGTTTGGACCTGCGCGCGCGCGTGCATTTACCATGCGAGTGCATATGAAAGCCGCGATGCAGAAACGTTTGAAGCTTATTCGGCGGACATCGCGCGGAACTGCGCGGTG  
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AAATTCAGAAAGCAGCAATATCGTCTTGACGCTTTTCGGAAGAGCGGTGAATAAAGTACGATCAGATGCGGTGAAGCAAAACATCACTACATGCATACCGGTGAACGAAATGGGTGTG  
GCAGAGCCGATTATCAACAGTCAAGTTTGGACCGCATTTGTGTACAGTTTCCCGCGTGCAGAGTACTGCCAAGCGAAAGACATCATCGCGGTACCGGACTTTTGAAGTCCCGCATGG  
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GACCGCGGACAACATCAACGATCGCAACCGAGTTTCGACCAAAATGGGCGCACTGCGCTGAGTCTGAGCTTGGACAGCGCGGCGGCGAGCATTTTGGCGAACTGACTGCCGCAATGTC  
GGCAACGCGATGGCGATGTTTGTATCGACCAAGGAAATCCGAGGTTGTAAACCGCACCGGTTATTCGCTACTGCCATTAACCGCGGAGCGCTGGAAATTTCCGGAAGCATGACGACAGCG  
AAGCCAACGATACGCTTTGCTGTGCGTTCGCGGTTCTTTCGCGCACCGATCGAGATTGTGCAAGAACGTACCATCGGTGCGTCTTTGGGTAAAGGAGAACATCGAAAGGCTTCCATTC  
GACTTTATGGGGTTTGGCATCGTTGCTGCAATCATGGTGGTTTATTACCGCTGATGGGTTTCTTTCTACTATGCAATTGAGTGCCAAACATACATCTGCTTAATCGGTATTTGCTGCGC  
ATGCAAGCAACGTTGAGCTTACCGGTATGGCCGCGCTGCGGTTGACTTTGGGTATGGCAATCGACTCCCAAGCTTTGATTAACGAAGCATTCGAGAGGAATTCGCTCGCGGCGTGGCG  
CGCAGCAGGCAATCAATCTCGTTTCCAAACGCGATGGCGGACCATTTGTTGATTGCAACCTGACTTCGCTGATTCGCGGTATCGCGCTTTTGGTATTCGCTCGCGGTAAGAGGTTT  
TGCGCTGATACATGCTTGGGTATTCGACTTCGATGATTCGCTGCTGCTGATTCGCTGCGTGGTCAATCTGTGTAACGCGCGCGCGCAATTCGAGAAATTTCCATCGGTGCG  
GTATGGAACCTGAAGCGGAACTCGCGCAGGTAAAGG

## SEQ ID 2332

MNRYPILWKYLLIVFTIAVAAYSLPNLFGETPAVQVSTNRQAIINEQTSKVDAAALKNAGIQTGDMFVVDNSLKVRFKDTETQLKARDVIENTLGEYITAINLLADSPENNAKIKANP  
MPLGLDLRGVHPTMVDKMAAMQRTTFERYSGDIRRELREKIRSGTVRQENSLTVPLQDAGDVQKALPQLLKLFPBATLNEGSNIIVL/LSSEAVNKVRSDAVKQNTTLNHRVNELGV  
ABPIIQSGSLDRIVQVLPVQDTAKADIIIGRTATLEVIMVEDDPAKLREALGENVPFSGYELLSSGGEHPETLLISKQVELTGDNDINDAQPSFQMGAPAVSLSDSAGGSIFGELTAAIV  
GRMAWVLIIDQKSEVVTAIVRTAITGGRVEISGEMTAEANDTSLLRAGSLAAMFQIVERTIGPSLGKENIEKGFHSTLWGAIVAAFMVYVYRLMGFFSTIALSANILFLIGILSA  
MQATLTLPGMAALALTGMAIDSNVILINERIRELRAGVPQQAINLGFQHWATIVDSNLSLILAGIALLVFGSGPVRGFAVVRCLGILLFSMYSSVVVPRALVNLWYGRRRKLQNLISGA  
VWKPEAETAAGKE

## SEQ ID 2333

ATGGAACCTCTTAAAAATCAAAACCGGATATTCCTGTTATGAGTACGCGAAACTGACAACTTCATTTGTTGGTTACCTTTATTCGCCCGCTATTCTTTTGTGTTGCCAGAGGCTGAAAT  
TCTCTGTGCAATTTACCGCGGTACGGTAATGGAAGTCAATATCAGCAGGGTCCGGATGTCAATAAGATGCGCGAAGCGCTCGATACGCTGAAATGGGTGATGACAGGTTCAAGCAT  
GGGTACGAACAAACATCATGATCCGCTGCCGAACAAAGAGGTGTACTTCCGACAGTTGTCCAATCAGGTTATGGATTGCTGAAAAAGACAGTCCCGAGCTTACTTTGCCCA  
GTCAATTTATCGCCCGCAAGTTCGGTGAAGATTTGTAATAATGGATTGATGCTTTAGGTTTGTGCTTATCGGCATCATTTATACCTGTGATGCGGTTTCGAATGGCGTTTTCGCG  
TATCTGCCATATTCGCAATATGACGACATCGGATTTATTCGCGCTGCTTTGCTTCTTCCAATGGGAATTTTCGCTGACCGCTTCGGCAGGTATCTTGGCGTATTTGGCTATTCTGT  
GAACGAATCCGCTGCTGCTGACCGTATCCGTGAAATTTCCGCAAGCCCGGATGCGCGGACATACCGTCCGGAAGTCATTGACAACCGGATTAACCGCAACGATGAGCGCGACCATC  
ATTACCAACGCTTCGACCGAGGCGATGTTGTTCTGATGCTGCTGCTGCGCGGTGCAAGCTTTCGACCGGCTTTCATGCGCACTGACCATCGGTATCGGTTCGCGCATCTACTCTTCGCTAT  
TGGTTCGACCGCGCTCTTGTGATGTTTCGCTTTCGAGCGCGCAATATCGCAAGGAAGCGAAACAGAGGAAGAAATGTTGCT

## SEQ ID 2334

MELFKIKRDIIPMSYGLKLTFFISLVTFIAVFFLVARGLNFSVEFTGGTVMEVQYQOQADVNMKRRERLDLTKMGDVQVQALGTNKHIMIRLPNKEGVTSAQLSNQVMDLLKIDSPDVTLRQ  
VEFIGPVQGEELVNWMLMALGFVVIGIIYLSMRFEWFAVSAIIANMHDIVIIIGCPAFFQWEPFSLFVLGILAVLGYSVNESVVVFDRIENFRKPAHRGHTVPEVIDNAITATHSRTI  
ITHGSTAMVVSMLVFGAALHGFMAALTIGIVPGIYSSVLVASPLLLMPLGSLRDLNLAKEARQKEIVV

## SEQ ID 2335

TTGCCGTTGTGAGGCTTGGCAAACTTGTCCGAATCCCAATTTGGGGTCTTTTATTTTTCGGAGTTTTTCATATATGCACTGACCGTAGAACAAGCAAAATCGTTAAAGATTTCC  
AAGCTAAAGAGCGGACACCGGCTCTTCTGAAGTACAAGTTGCCGTGTGACTTTCCGATCAACGATCTGACCCCGCACTTCAAAGCCAAACCCCAAGACCCACAGCGGTGCGCGCT  
GTTGAAATGGTCAGCAACGCGCGCGCTGTTCGCTTATTTGCGCGTACCCAGCGCGGATACGATTCGCGCGTGTGATTACCGCTTGGGTCTGCGCTAA

## SEQ ID 2336

LPLSRLKLVRIFFGVLFIFRSFSTHALTVQKAQIVKDFQRKEGDTGSSEVQVALLTFRINDLTPHPKANPKDHSRRGLLKMVSQRRRLAYLRRTPDTPYRALITRLGLRK

## SEQ ID 2337

ATGGCTGGTGGAGTTTATTTAGCGGAAAAATTTATAGCCCTATATATCATTCATCACAAGAAATTTTCGTTGAACCAATAATCTATGCTGAACAAATAATTTTATGCTGCTGAA  
AATTTTTAACTTTAAACGAGTTTTCATATGGAATATTTTAAATGATGATCAGATAATTAATTTTATCCAAATAAAGAGGGGAGTACGTTTGTATAAAATTAAGATAATATAA  
AATTTGGCAAGTGTCTATAGAAAGCAGCAAAATTTTAAACTCGGTAATCCATATAAT

## SEQ ID 2338

MAGGVYLGKKIISPIYHSSQEFSGRPIIYAETNIIICPAEKFLTKRVPHNGNIPNNQIITFLSNQGGVRFDKNYDKYKTWQVAIEKAANFLKGNPNH

**SEQ ID 2340**

**SEQ ID 2341**

**SEQ ID 2342**

**SEQ ID 2343**

**SEQ ID 2344**

**SEQ ID 2345**

**SEQ ID 2346**

**SEQ ID 2347**

**SEQ ID 2348**

**SEQ ID 2349**

**SEQ ID 2350**

**SEQ ID 2351**

SEQ ID 2352

SEQ ID 2353

ATGCGAAGATCCAAATTATCTGTGGTCTTGAAACTGATGTTGGCACTATCGCTGGCGGTTTCGTATATCCCGCTGGTGTGTTTTGGTGCACTATTTCGTTCACGAAGATCCAAACTGTTGTACCG  
TTTGGGGCGGCTTTTCGACCAAGTGGTACGGCGCAATTGCTGGAAACGACACCAATTTTGGAAGCGCTTGGCTGTGCGCTGCGGATTTGCCGTTGTGCTTGTGCTTGGCGCGCTCGTTTGTGG  
CAGCTTGC CGGGCTATGCGATGCGCGGTATCAAAACGCTTTCGCGGCAGCAAGCTGTTTTCGCGGATGATTTCCGCGGCCATGGTTCATGCCGACGTGATACCGGTCTGTCTATGCTGCTG  
CTGATATTACAGTGCAGATATTTTTTCGAGGGCAGCAAGATGGTTGCAACATCTCTACTTCGATCGCGGGCTTTTTCACCAATCTTCTCCGACATACGACGCTGTGCATGGATACATATTACCG  
TTGTGATCCCGTTCGCGGCTGGTGCAGCTTGACCACTGCGCTCGAAGAACCGCAATGCACTTGGCGCGGCTGCGCTCGAATAATCTTTTGTGATCACTTGGCTTGTGATGGCCCTGGCCAT  
TGTCTCAGGCTTCTCATCTCGGCATTAACCTGTGCTTTGGATGATTGTGTAATTAACCTCATTTCTCTCGGCGCCGCTGTCAATCCATTTGCCGCAAGTTATTTTCTCCAAGATCAAGTTGGGT



CTCGATCCTCAGATGAATGTCTTGCAACCATCTGATCGGCATCATCGGAACATTGGTCATCATCTCAATTATTGGATGATGAGCAGGCAACCAAGCGCAACCGAGAAGCGGCAGAAG  
CCTACCGCCAAGAAAAATTGGCTGCCGAGAAAGCAAAAT

## SEQ ID 2354

MQKSKLSWFLKLMALSLAPLYIPLVVLVIYSFNESKLVTVWGGFSTKHYGALLENDTILEAAWLSLRIAVVSSLAAVVIGTLAGYAMARIKFRGSTLFAGMISAPMHPDVTITGLSHELL  
LIIQVQIFLQGSSEWLQHLVYFDRGFTTIFLGHITLCMAYITVIRSLVELDQSLREAAAMDLAGRPLKIFVITLPLIAPAIASGFLIGITLSDLDLVTISPLSGPGSSTLPQVITPSKIKLG  
LDPQMNVLATILIGITLVIIVNYMMRQATKRNREABAYRQELAAERAN

## SEQ ID 2355

ATGAAGATAACACACTGCAAAATTAAGAAAGAGTACAGAAAGAACCGCTCGTCTTTGTACCGGAAAGTTACCGCCCGTCTCGCCCGCATATTTTGGGTATCCATCCCGATTCCGCGG  
CACTGTTTACCGTAAATCCGACGGTTACCAACCATCGTTTGGCTTGGCTGCGCATGAGGTTTTCGGGGGCCCCCGCGGGCGGGCGGAAGCTATTTCGGCGGACCGCGTAAAGGCAG  
ACGCGGTGCGCGCGCGGAGAAAGCGGTGTCTTCGGCATTCGAAACGCAACGGCGGCGCTATACCGTTGCGCGGACAAATGCGAGCGCTGAAACGTTGCTCCCTGCCGTCAAAAAG  
AAAATCATGCCGGACGGTATTGTTTATGCCGATAGCCCGGCGCGCGGCAAGTTGACGCGCGGCGGTTTTACCGGTTGCGCGCATCAACCGGTTCCAAGGAATTTGCAGACCGTCGGAAC  
ACATTAACGGCATTTGGGAATTTTGAATCAGGCAAAACCGCGCTTGGCAAAATACAACGGAATCGATCGTAAACCTTTCCCGCGGTGTGTGAGGGAATCCGAATTTGATTTAACTTCGG  
CACACCGTCCCGGACGCTAAAAATCTCGCGGATTTGGTGTGAAT

## SEQ ID 2356

MKI THCKLKEVQKEPLRSFVPEVTARSAADILGIHPDAAALFYRKIRTVNHRLLAAADEVFGGPGAGPGGSGYFGRRRKRRRGAAGKAVVFGIPKRNGRAYTVAADNAEPETLLPAVKR  
KIMPDGIVYADSPGRSKLDAGGFTRCRINRSKEFADRRNHINGIGNFWQAKRALRKYNGIDRKPFPPLLRCEFRPNFPGTSPRQLKILRDHCGI

## SEQ ID 2357

ATGCGCCACGCTCTCGACAAACGGTACGGACAATCAGACCGCACCGGCTACGGCTACCGCTATTCGGTTATCAGATGCGTTTGTACTTGGGCAAGGTTTTCCGCTGCTGACGACCA  
AAAAGCTGCATTTCCGCTCGATAATCCAGAGCTGCTTTGGTTCCCTCAAGGCGGATACCAATATCAAAATACCTGAAGGATAAACAATGTTTCCATTGGGACGAGTGGCGGACGAAAAACGG  
CGACTTGGGCGCGGTTTACGGCTACCAATGGCGCAGCTGGCGCGCGCGGAGCGGAGCATATCGCAAAATCGCCAATGTGTGGGAACAAATTAAGAAAAACCCGCACTCGCGCGCGCTG  
ATTGTGTGCGCGGTGAATCCGCGCTTGTGTGATGAGATGGCTTGGCGCGCTGCCACGCGCTGTTCAGTTTACGTTGCGGACGCGAACTGTCTCCGACGCTTACCGAGCTAGTGTGAG  
ATAATTTCCCTGGTGTGCCGTTAATATTTGCCAGCTACGCGCTGTTCAGATGATGATGCGCAAGTGTGCGGCGTGGAGGCGGCGGAGTTTGTCCATACGTTTGGCGACGCGCATTTGT  
CGTAACCATTTTGAACAGGCGCGCATTTGAGTGTGAACGCGAACCGCGCGCTTGCCTGTGATGAAATCAATCTGAAAGTCAAGGATTTGTTCCTTCAAGTTTGAAGATTTGAGATTG  
GAAGGCTACGATCCGATCCGACATCAAGCGCGTAGTGTGCGTT

## SEQ ID 2358

MKHVLDNGFDKSDRTGTGTSFVGYQMRFDLKGFPFLITKHLHLSI IHELLWFLKGDITWIKYLDKNVSIWDEWADENGDLGFPVYGYQWRSWPAFDRHIDQIANVVEQIKKNPDSRRL  
IVSANNPALVDEMALPCHALPQFVYVADGKLSQLYQRSADIFLGVFFNIASYALLITMMAQVCGLEAGFVHTFGDAHLVYRNFHQAALQLEREPFALPVNKINPEVKDLFAKFEDEFEL  
BGYDPHPHIKAVVSV

## SEQ ID 2359

ATGACTGGGTGAGCTGTTTTTTTCAACCGATTTTCTGTTTGGACGATATGGCCCGCAGCTGCTATCATTCCTCGCGGAAATATACCCGATAAAGCAAAACACAATGATTCGCGCTGATT  
TTCAAGAATATCTGCTCTTATTTAGTTTCGGTTAATCCGCATAGCTTTATCCGAAATCCCAATGCGCTGTGAAAGCGGAAACCTGCATTTATCGGCGCGGTTTGGAGCGGTTGTG  
TACCGCATTTGCCCTGCGCGGAACACGGACATGAAGCCGTCGTTTGGAAAGCCGACGATTCGCTTGGCGCGCTCGCGGAGGAGTGGCGGGCAGGTTATCAGCGACTACCGCTGCGGTATG  
GGGAAATTTGAAACAGGTCGCGCTTGGAGCAGCGCAATGTTTGGCAACAGCTTTTGCAGCGGCTGCAATGTTGAGCAACGCGCTCCGCAAAATCATCGATTGCGATTGCGCAGC  
GGGTTATGCCACGCTTGGCGCTCGTCCGAGCATTTGGAAAGAGTTGCGAGCTGGCATGAACACGCCCAACCGCATTTACGTTGCGAGTCATTATCACTTTGGGATAAAGCCGAGTTGAA  
ACAGCAGCTTGACAGCGATATGATACCAAGCGCGCAGATTCGATCCCTTGTTCGGGCACTTCATCCGCTCAATTACACGTTGGTGTGTCCAGCGCGCTGCGGAAGCGCGCGCGCATTT  
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ACCGCATATTTCCGCGCTTTGGAAACGCAAGCGGATTGCGCTCAGCAGCTTTATTTATTTGCCACCGAACCTTTGGCGCGCGCACAAAAGGGCTTATCCGCAACAATATGGCAGTATGCGACAA  
CGGCATATTTGGATTATTTACCGCTCAGCGCGGACGCGGAGCTTTTTCGGCGGTGAAGGATAACGAATTTATCGCAATCTCGCGCTATGACCGAGCTTTGCGCGCAAGATATGCTT  
AAAGTTTTCGCGAGCTTGGCGATTTAGAAATCGAATATTCGTGGGCGGGAGTGGCATATACCGCAACCTTTGTCCCGCATTTGCGAGCTTTGACCTCGAATGTTTTTATACGCAAG  
GTTATTTCCGCGCAGCGGATGGGATAACGGCGCATTTGACGCTGCGGCTTGGCGAGCAATTTAGGGGACGAATGCGCTGAAACCGTTTGAACAGTTGTGCCAGCGGAATATTATCT  
GCAACCGTTTTTGCAGCAACTCGGTTCTTCTCGCGCTCGAAATATTATCAGTGAAGACAGCGCT

## SEQ ID 2360

HTGSACFSTDFLPGRYPTVCIIPSENIIPDKANTWIRPQFYLEPSYFSSVNPHTVYPKLCRLKAETCIIGGSLGLCTALPLAEHGHZAVLEAARI GFGASGRSGGQVLSIDYACGH  
GEIEKQVGLBQAFWQSSQLQAVELVDERVRKHAIDCWQGRYATVAVRPQHEEELQWHEHAQRHYGASHYQLWDKAEKQQQLDSMYPQGAQFPDPLSGHLHPLIYTLGVASAAAEAGAI  
FQSPMTRIEPYQNGMLVYTPGSEVECKNVVYVNTYVGLNPIPRPLERKAIASVTFIATEPLGARTKGLIRNMNAVCDNRHILDYRISADGRLLFGGCKNEFIDNPARMTLVRQDML  
KVFPLADVRLISYSWGBCDITANLVPHFGRITSNVYTYGYSGHMAITGIAGLAVAEAILGDECRKLPFEQLCPNIILQPPRLRLKLSFLGSKYQWDRSR

## SEQ ID 2361

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CGCGCTCAATTCGGGCGATACCGCTGGGTGATGACTGCGGCTGCTTGTACTGTTGATGACGCTTCCCGGCTGCGCTTATTTCTACCGCGGTATGGTGGGAAAAAACCTGCTCTCG  
ACGATGATGCACAGCTTTTCCATCGGACATTTGGTGGCATCTTTGGGTGCGCGTGGCTATTCCTTTGCGGCTTACGCGCGGAAATGCTTTATCGGCGGTTTGGGCGCGCTATTTTAA  
CGGGATGCGATAGACGCTGCGGCACGGATGCTGACCGTGTGCGCCAAATGCGCGGACTGTTCCCGAACCGGATTTATGTTTTTTCAGATGACGCTTTGCCATTATTTGACGCTGCCATTAT  
TACGCGCGGCTTTGCCAAACGAATGAAATATTCGCAATGATGCTGTTTTCGGGCATATGTTTTTATTTGTTTATGTTGCGGCGCGCATTTGGTGTGGGCGCGGCTTATGAGCAAG  
GGCGGCTATTGGATTATGCGGCGGTACGGTGTGCACATCAATCCCGGTATCGCGGACTGCTGCGCGCTTGGTTTTGGCGAGGCGATAGGCTACGGCGCGGAGGCGATGCTCCCG  
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GTCGGCGTATTTCGCGCGGCGGAGCTGGCTTGCCTGCGAGAAAAAGCGGACACAAACCTTCTGCTTTGGGCTGGCTTCCGCGCGCATTTTCGCGCATCACCTCGCGCGC  
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TACACGGATTTCGGCGGCTGGTAGCGGAATATGACCGGCTCTTTTTCGCAACCGCATTTTTCGGCGGATGCGGCGAGTTTGGCAGCAGTTGTGGATACAGTAAAGACGGGTTTAT  
TATGCGCGCATACAGCGGCTGATGATGTTGGCGATTTTGAAGGCTGTGGGAAAAATCTGCGCGGCTGCGCGCTGCGCAAGGATGTGCAACGCGAAGGTTTGGATCTGAATATCCAGCGC  
GAACAGTGGAA

## SEQ ID 2362

MRYHIQTRDLFHAQGGTSAKSPRRSGRACAHQAPPTPFRKTGPTIKETLIKMKHIIWAASLLFASLSAEPLNWMKPYSAVNSGDTAWVHTAAALVLMTLPLGLATFYGNVRKKNLS  
TMMSFSIATLVGILWVAVGYSIAFTPGNAFIGLGRVFLSGMIDAAARMLTVSPNATVPEVPMFPFQMTFAIISTAIITGAFERMKYSAMMLFSGINFLVYVPGHWWGGGFNSK  
GGVLDIYAGTGVHINAGIAGLVAALVLRRI GYGREAMPNHNAMTLI GAAMLNFGWFGPNAGSALAADAAGMAMAVTVQSAVPGAAGWLAKEKIAHGKPSALGLASGAVSGLVITPAA  
GFTGPSGAAAGITLAAACFVSVTVVKHKLRYDSDLDFGIHFGGLVGGILTGIFPINKIFGGDAAVWQQLNIQVKGDFMAAYSGIASHAILKAVGKICGGLRVGKDVREGLDLNIRG  
EHVE

**SEQ ID 2363**

SEQ ID 2363  
TTGAATATGGAATATCGCATCTTATCCCTTGCCCCCGTTGTCCGGCGGGAGGATTATCTTAGGGGGCGCATATGCGGGCGTATGCATTGTCAACAATTTACTGTAGGAAATATACAG  
AGGTTTGGGGCATAAGTCAAAGATGTGTGACAATATTTTATTTTA

**SEQ ID 2364**

LNMEISHPIPCPRCPAGGFILRRRICGRMDCQQFTVGKYTEVWAI SQKIVDNIFIL

**SEQ ID 2365**

SEQ ID 2365  
TTGCAAAACCGGCTCGAACGCATCCCTACCGCAATGAAAACGATGCGGGAACTTGATTCAAGGTTGCGCCGAACCGCGCCCATTTTTGTATAAATTTTATTTTTTATTTCCAATTAGAA  
ATTTT

**SEQ ID 2366**

LQNRLEIPTGNEENRCGNLIQGCAEPRPFLYKFYFLFPINP

**SEQ ID 2367**

SEQ ID 2367

TTGACACCCGACGCGCGGACTGCTTCAAAATCCCCCTCTCCGAGCAACGGCAACAGTCAGCTTCTCTTTTCAGACGGCATCCACCCGCTCTTTTCCCTTTCATATATATCAATTTGATTA  
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GATGATGAAAAAAGCGAGGGTTTTACTGTCTCGGCACGCTCGAAATCTTGCCCGACGGCTTCGGCTTCTCCGAGCGCGGACACGTCCTATCTTGGCGGCCCGGACGACATCTATGTCT  
TCGCCACTCAAATCCGCGCTTCAACCTGCATACGGGCGACACCATCGAAGGCAGCGCTGCGCGCTCCCCAAAGACAAACGAAACGCTATTTTGGCTTGGTCAGACTGGATTCCATCAATGGCG  
ACCAACCCGGAAGTATGCGGCCATAAAATCTGTTTGAACAACTGACCCCGCTGTTTCCGACCGAAGCAGTTCGAAAGCTGGAACTGTGAACCGGCATTTAAAGTCGGAAGAAAACCTGACCGGACGCGCCAT  
GCACTGATGCTTTCGCCCATGCGCAAGGTCAGCGCGCTCTTGGTGTGCGCCGCAAAATCGGTGTAAGCCGTGATGCTGCAAAACATTTGCCACGCGGTTACCGCAAACTATCCTGAAGTC  
CGAATCATGTCTCTTCTGTTGACGCAACGCCGCCGAAGAAGTAAACGAAATGAGCCGTTCCGTCGAGGTTGAAGTAGTCTCTCACTTTGACGAAACCGCGCCAAACGCCACGTCCTCAAGTGTG  
CCGAAATGGTGCTTGA AAAAGCCAAAGCGTATGTGTGAACACAAAAAGACGTGTGCATCTGTCTGATTCGATATACCCGCCCTTGCCCGCGCCCTACAAATCCGTCGTCGCCCTCGCGGCAAC  
AATCTCGACGCGCGGTGTGCATGCCAAGCGCGTCACCGCCCCAAACGTTTCTTCTGGTGTCCGCGCGCAACGCTGGAAGAATAGGCGGTTGCTGTACCAATATCGCCGACCGATTTGGTTGAAC  
GGCAGCGGTATGGACGATGTGATTTACGAAGAATCAAGGTACCGGCATATGAAATGCGACTCGACCGCGGTGCGGCGGAAGAACGCGCTCTCCCGGCCATCAACATCAACAAATCCG  
GCACGCGCGCGCAAGAGACTGCTTGTGCGCAACGACCATCAAGTTCACCGCTATGTGGTTTGAATTCGCGCAAGTTCTGTACCCGATGGACGAAATCGAAGCTACCGAGTTCTTAAACGGAAAAATCAA  
AGCATCTAAAAATAATGATGATTTCTTTGAACTGATGCGCGGAAAA

**SEQ ID 2368**

SEQ ID 2368  
LPTTRRLPTTPPSPSNRQSSASSFRHRPPVFSFLFYISLIMHVSELQTLHIKSLLELAEEHGIENANRFRKQDLVFAIVRQMMKKGEGFTCSOTLEILPDGFGFLRSADTSTYLAGPDDIYV  
SPTQIRRRFNLHGTDTIEGSRVRPKDNERKYPALVRLDSINGDHPEVCRHKILPENLTPLPFTPQKLKLERDKSEENLTGRAIDLSPIGKQRALLVAPPKIGKTVMLQNAHAYTANYEV  
ELIVLLIDERPEEFTMSRSGVRGEVSVSTFDEPAQRHVQVAEMVLEAKRMVEHKDVILLDSITRLRAYNTVVPASGKITGGVDANALHRPKRFGAARNVEEGSSLTIATATVET  
GSRMDVITYEEFKGTGNMELHLDRRMAEKRLFPAININKSGTRREELLVNDQLQRMWLRKFLHPMDEIATEPLNGKIKASKNNDFFELMRGK

**SEQ ID 2369**

SEQ ID 2369  
TTGTTGGCAATTTACGCCCTTTTTCACAGCAAAGCAGGCGTGAAAACAAAATATCTTGATTGGAATCAAAAAATCTAGTTTAACACTACT

**SEQ ID 2370**

LLAISALFHKSRRNKILLIGIKSSLT

**SEQ ID 2371**

SEQ ID 2371  
ACGGTTTGATGCTCAATAATCCCCCTTTCCCCGGACAAATACGGAACACGACATGACCGACATCCTCAATAAAATCCTTCCACCAAGGCACAGGAATTCGGCCCCA

**SEQ ID 2372**

TV\*C\*YSPFPRNTTEHDMTDILNKILATKAQEVAAQ

**SEQ ID 2373**

GTGGGAATCCAGGATGCAGGGGAAACCGTTTTATCCGATAAGTTTTTCGCACCGAAAGGTCGGATTCCCGCCTTATATGATGCGCTCTACGCGGGAATGALGGGATT

**SEQ ID 2374**

VGIODAGETVLSDKFSHRKVWIPALYDALYAGNFTGF

**SEQ ID 2375**

SEQ ID 2375

TTGGACACACAAATGGCCGACAACTACGTAATCTGGTTTGAAACCTCGCGTATGACAGATGTTGAACCGGTGGCGGTAAAAACGCCTCGCTGGCGGAAATGATCAGTCAACTGACCGAA  
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TTCCGAACTGGCACGCGCTCGGCAAAAGAGTCGTCATTTTGGACACGCCCTTCCCGGAACAGCTCGATGCCGAAATCGAAGCGGCATGGAACAAAATGATTACCGATGCCGACGGC  
CGCGACATTTTCGTTTCGCGTACGCTCTTTCCGCAACCGCCGAAGACCTGCCCGACGCATCATTTTGGCGGCAACAGGAAACCTTCTCTGAATATCAATGGCTTGGATTAACGTTAAAAAAGCGA  
TCGGCCACGCTGGTTTGGCTTCCCTGTACAAACGACCGGCCATTTCTTACCGGCTCCACAAAGGCTCGAACACGACATCGTCGCCCTTTCCGCCCGCGCTTCAACGCATGGTGGCTTCGACAG  
CGCGCATCAGGTGTGATGTTTCAACCTCGACACCGAATCGCGCTACAACCAAGTCGCTTTTGTACTCTCTTACGGTCTGGCGGAAAAAGTCTGTACCAAGCGCGGTCAACCCGGAGAA  
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ACGTGGAAGTCCCCGAAGAGACCCGAACCGCTTCTCCATTACCGACGAAGAAATCACCAGTTGGCACACTACGCGCTGAAACCATCGACATTCGAAACACACTACGCGCGCCGATGGATATCGAATG  
GGGACGCGACGGCCTGGACGGCAAACTCTACATCTCGCAAGCCGCCCGGAAACCGTCAAAATCCCAAGAAAGACGCGCGCAACCTCGCGCGCTACGCCATCAACGGCGAAAAAACCGCT  
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TCGGCATCCACCCGAAAGCCTTGTGGAAATTTGACAAACAGACGACGAACCTGAAAGCGGAAATTTATCCGCGCATCGCGGTTCAGCACTCCCTCTGCACTCTACGTGTGATATAAAATCGC  
CGAAGCGTGGCAACGCTTTCGCGCATCGGTTTATCGCGGTAAAACCATCGTCCGTATGTCCGACTTCAAACTCAACGATACGCCAACTGGTTCGCGCGAGGTATATCGAACCGCATGAA  
GAAAACCCGATGTTGGGCTTCCGTGTTGCGGCGGCTTATGTGTCGAGAGCTTCAAAGACTTTTCGCGCTGGAATTCGAAAGCTTGAACCGGCTTGAACGCGGCAAAAACGGCCTGCGCTGATTGATGTGCGAGCT  
TCGAAATCATGATTCCGTTCTGTCGCACTTTGGCGGAAGCGGAAGCATGGTTTAAAGCATTTGAAGCAAAAAACGGCTTGAACGCGGCAAAAACGGCCTGCGCTGATTGATGTGCGAGCT  
GCCGAGCAACCGGTTATTTGGCGGAACCAATCTCTGCAATACTTTCGACGGCTTCTCCATCGGCTCGAACGACATGACCCAGCTGACCTCGGCTCGACCGAGACAGCGGCTTGTGTGCGAA  
TCGTTTGAACACGCAACCTCGCGCTCAAAGTGATGCTGCATCTTGCCATCTCGGCTGCCGCAAGCAGAACAAATATGTCGGTATCTCGGCTCAAGTTCGCTCCGACCATCCGGACTTTG  
CCAAATGGCTGGTTGGAGAAGGCATCGAAAGCGTGTCTCTGAACCCGGATACCGTCTCGAACTTGGCTGTATTTGGCGAATGAATTTGAACAAA

SEQ ID 2376

SEQ ID 2376

LDTQMADNYTVTFENLRMTDVERVGGKNASLGEIMSQLTEKGVRVPGGFATTADYAPRALAHNGLNERISAAALAKLDVEDVSELARVGKEIRQWILDTFFPEQLDAETAEAWNKMITDADG  
ADISVAVRSSATAEDLPDASAPAGQETFLVINGLNDVVKAMRHVFASLYNDRATSYRVHKGFHEIDIVALSAGVQRMVRSDSGASGVMTLDTSESGYNQVVPVTSYGLGENVVQGAVPDE  
FVVPKPTLKAGKPAILRKTMGSKHKIMTPTDKAEAGKSVTVNEVPEEDRNRFSITDEKITELAHYALTIEKHGRPMDEIWRDGLDGLKLYILQARPETVKSQECSRNLRARYALNGKTV  
LCEBAPQKVGQVQKQVRLIKDASEMDSVEAGDLVLTDMTPDPWEVPVKRASAVITNRGGRTCHAAIARELGIPAVVCGGNATELLENQGEVTVSCAEGDTGFITYAGLLDVQITDVALNN  
KPRAPVYVMNNQVNNPELAFSFAANLPSEGIGLARMEFITNRQIGITHPKALLFQKQDELKABIIIRRIAGTASPVDFVYDKIABGVATLAASVYPRKTIIVRMSDFKSNEYANLVGGSVYKEPHE

ENPMLGFRGAARYVAESFKDCFALECKALKRVRDEHGLTNVEIMIPFVRTLGEABAVVKALKENGLERKNGRLIMMCELPNSNAVLAEQFLQYDFGSIGSNDHQTULTGLDRDSGLVSE  
SPDERNPAYKVMHLALISACRQNKYVIGICGQPSDHPDAKWLVBGEGISVSLNPDVVIETWLYLANELNK

## SEQ ID 2377

TGTGCGGCATTTGTGTGTCATCCAAATATGTTAAAAAGAAACAAATCCGCTGCTTATTTTAAAGCGATTGTTCCGCCGTGTACAGTTTATCTGTCCGGACAAACCGCTGGCGC  
GTCTGAAAAATAGCGGGTTCGGCTGTGTAGCGGTGTAACCGATGGCAGGCATATGTTTTCGGGTATTCCTTTGTAAACAGATGGTTTGAATAGGTAAATGTTTATGCCGT  
ATTTTTCCTGTTCTTTTTCGGAATTTTATTT

## SEQ ID 2378

LSAICVSNPKYKETNPPLAYFKRFVPLSRFYLSCQPLRLKNSGFRICSLKPHAGILFFSGISFVKQVNLNRMFYAVFPLFLFFGILP

## SEQ ID 2379

ATGAAGATAACACACTGCAAAATTAAGAAAGAAAGTACAAAAAGAACCGCTCCGTTCTTTGTACCGGAAGTTACCGCCGTTCTGCCGCCGATATTTGGGTATCCATCCCGATTCCGGCG  
CACTGTTTTCACGTAAATCCGCACGGTGTCCCAACCATCGTTTGCCCTTGCGTGCAGTGAAGTTTTCGAGGGCCCCCGCGGCCGCGCAAGCTGTTTCGGCGTACCGCGTAAAGCGAG  
ACGCGGTCCGCGCGCGGAGGAAAGCGGTGTCTTCGGCATTCGAAACGCAACGGCGGGCTATACCGTTGCCCGGACGATGCCGAGCTGAACGTTACCCCTGCCGTCAAAAAG  
AAAATCATGCCGCGGATTTGTTTATGCCGATAGCCCGGCGAGCGCGGCAAGTCGAGCGCGGGCGGTTTACCGTTGCCCGCATCAACCGTTCCAGGAATTTGCAGACCGTCCGAACC  
ACATTAAACGGCATTTGGGAATTTTGAATCAGGCAAAACCGCCTTCGCGAAATACACCGGAATCGATCGTAAACCTTTTCCCGCGTTCTTGAGGGAATCCGAATTCGACTTAACTTCGG  
CACACCGTCCCGGACGCTAAAAATCTCGCGGATCGGTGCGAATTT

## SEQ ID 2380

MXITHCKLKEVQKEPLRSFVPEVARSADILGIHPSAALFYRKIRTVANHRLALAADEVPEGPAGPGASCVPVRRKGRGRGAAGKAVVFGIPKNGRAYTVAADAEPELPPAVK  
KIMPDGIVYADSPGSRGKSDAGGTRCKINRSKEPADRRNHINGIGNFWQAKRALRKYNGIDRKPFPPLRECEFRINFGTSPRQLKILDRDGI

## SEQ ID 2381

GTGGTGAGAAAGTCAATCGGAGCGCGCAGGAAACGGTCAGCGTCCGATTGCGTTTGTACGCGTGGTTGATGACGAAATCCGCCGATTATTAAGGGCGCGATGCTTTTCAGATTAAAT  
TCTTTGAGACTTTTTCGGCATGTTGAGAGGAACCTCAATACCGAAGCAACGGTATCCGGCAGGGGATCAAGTATCGGCAATACGAAGCGTTACGATGCGGTATGGAGCGGTCAA  
TTTTCTTTTGAACCATGATGACGGGTTCAGCGATAAGAACCTTCAGGAGCGGATGTGATTCTGATGGGCGTGTCCCGTTTCGGGCAAAACCGACCTGCCCTGATCTGCGGTTCGAATAC  
GGTATCCGTCGCGCAAACTATCCGCTGATTCCCGACGATTGGAATCGCGCATCTGCGCGTATGTTCAAGCGGTATAAGACAAACTGTTTCGGGTGACTATCCAGCCGGAACGTTTGC  
AGGCCATCCGTGAGAAACCGCCCGAATTCGGCTTATGCGCGCATGACACCTGCGCGACGGAAGTGGCGGACGCGCAGAGTATGTTACAGCGCATGCAATTCGGTTTCGAATACGAC  
GGACAAGTCCGTTGAGGAATCGCGGTACACATCTTCAAGCGTCAAGCTCAAAACGCGAGTTT

## SEQ ID 2382

VVEKVNRSQENQRIAPVSVVDDEIRRIKIGADAFQINFFETFLGLEKEINTEATVSGQGHSTGNFKRYDARHEAVNFSLNHDDGVSVDKMLQADVILMGVSRSGRTPTCLYLALQY  
GIRAAATPLIPDDLESADLPRMVKPKDKLFGTLIQPERLQATRQERRPNSAYARIDTCRSEVADAQSMFRRHGIPFANTDKSVEELAVHLLQACKLKRFP

## SEQ ID 2383

ATGGCGTTTGAACGACGATTGCCAACTGGTTCAGCAAGCCCTCGCCGATATCTCGGCAGTCAGACCGGTGCGGTCCGAAATATAAAACACTTGGCGCGGACTGCTCATCACCCCTCC  
TTAATACAGATAAAATATCATCA

## SEQ ID 2384

MAFERQIAKLVQSLADILGSQTGAVGNIKHLARTAHPLKRYIKISS

## SEQ ID 2385

ATGCCGCTGTAACCTTTTCGCCGACTTTATAAAAAAGGAAACACATGATACAAAGCCGATTGTTTCGACCTCGACGCGACGCTCGCCGACACCGCCCTAGACCTCGCGCGGCACTCA  
ACACCCAACTCGCCCGCCACGGACTGCCCGGAAAGCATGAGCAAAATCCGACCCCAAGCCAGCCGCGCGGAGGATTGCTCAAACCTCGCGCGGACATCAGCGCCGAAACACCCCGA  
CTATACCGCATGCGCGACCGGAATATCTGGAGGAATACGACAGCCGCTACGCCCAAGACACCACTCTCTTCGACGGCGTGAACGAATCATCGCGCACTCGACAGCGCGCATCAATGG  
GGCATCATCAACCAAAACCCATCGCGCTTCACCGCAAACTCGTTCCAACTCGGATTCGCGGTTCGCGCGCGCACCGTCTGACGGCGGACACTCGCGCGGAAACCAACCCGACATCA  
AACCCATGCTGCGACCGCTCGCGGAAATCCACCGCGACCGGCAACACACCTCTACGTCGCGGACGCGGAAACGCGACATCCAAAGCCGCGACGCGCGGTATGAAAACCGCTTCGCGCGA  
ATGGGGCTATATTTCCGATGAAGACGATACCGGCTCATGGCAGCGGATTTCCACATCCGCGACCGCGCTCGATCTGCTCGAATGCTTGGAACAAATACAGCC

## SEQ ID 2386

MPSETPRPALYKKGKHMIAVLFDLDGTLADTALDGLGALNTQLARHGLPEKSMDEIRTAQSHGAAGLLKLGANITPEHPDYTAWRTEYLEEYDSRYAQDTTFLFDGVNELIAELDRRGIRW  
GIITNKPMPRTDRLVPLKGFVAPPATVVSVDTCGEKPSIKPMLHACGKIHADPQHTLVGDAERDIQAGRNAGMKTVLAENWYISDEDDTGSWQADFHINTPLDLLECLDKIQP

## SEQ ID 2387

ATGAACCCCGATATTTATGCTTTGCCGGAACCGCCCTGCTTTCCGGCGACCCCGATGAAAAAGGACGGCTGACGGATGAGCGTTTTCGCCCGCTTCAAAATCGCGGACGGGCGGAGGCA  
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GATTACGCATATCGAGTTCACCGCGCTCAATCTGGCTTTGACGCGGCATACCGTTTCGCGACGCTGCCGTTTCAGTTTGTCCGCGACTGGGTGAAGTGGCGAAGGAGGAGGTATCCAC  
TTCGCCCTGTGTCCGCGACAGATTGCGCGCTTTCCGCTTCGATTACGGCAGTTTCGAGGCGCAACACCATTTGTGGGATATGGCGTACAAAAACCGCTACGACCCGCTGTTGCGTATGCGGT  
TGGTACCGCGCGTGTGGAGGCGCGGCGATGACGCTTATGCCGGGATACCGCGAAGGTGAGCAGCGCGCGGATTCCGCAACCTCGCGCGTGTGGACATCATTTACCGCGGAGGAAGT  
GGGACAGCTGCGCATCGCGCAACCGGTGTGATCAACACCTCTCGCGGAAACCGGTTTGAACCTGTGCCCTGTTCCGCGCTGATTGCGCGCTTACGATATGTTATCTTCCCGCGCTAT  
GTGAACATCGAAGCGCGGCAAAAGCGGCTTCAGCCGCTTCGAATTTGGATATGTTGGAAGATTTTCAGGACGGGTTTGAACAAATTAACATCGCGCT

## SEQ ID 2388

MNPDIYALPERALLSGDPDEKGRITDEFAAVQNADGAENAPPADFPFRAGRPDTPVLVAPSQITPRKMTAEGYAAMLHAITHIEFNAVNLALDAAYRFTLPPQFVRDHWKVAKEEVH  
FRLVDRDLRAFPGFDYGSFEAHNLMDMAYKTAYDPLLRMLVPRVLEARGLDVMPGIRAKVBQRGDSATCGVLDITYRDEVGHVAGNRYQHLRCRERGLEPVALFRSLIARYDRTIFRGY  
VNIERAREKAGFSRFLDMLDFFEQGLKQKHAV

## SEQ ID 2389

ATGTTTATTTTGTTCAAACCTGCTCGAAATCTTCCAAACATATCCAAATCGAAGCGGCTGAAGCCCGCTTTTTCGCCGCTTCGATGTTACATAGCCCGGAAGATAACAATATCGTAA  
CGGGCAATCAGACTCGGGAACAGGGCGACAGGTTCCAAACCGGCTTCGCGGACAGGTTGTGATACCAACCGGTTGCCGATGCGGACGTTGCCACTTCTCGCGGTAAATGATGTCCAACA  
CGCCGAGGTTGCGGAATCGCGCGCTGCTCCACCTTCCGCGGATCCCGGCAATAGCTTCAGTTCGCGCGCTCCAAACGCGGGTACCAACGCGGATACGCAACAGCGGGTCTGAGGC  
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ACCCAGTCGCGGCAAACTGAAACGCGAGCGTGGGAAACGGTATGCCGCTTCCAAAGCCAGATTGACGCGGTTGAACCTGATATCGGTAATCGCGTGCAGCATCGCGCATAGCCTTCTG  
CCGTGTTTATTTTTCGCGGGGTCACTTCGAGGCGCGCAACAAACAGCGGTTTCGCGCGCTCCCGCGCGGGGAAAGTCCGCGCGCGCGCTTTCCTTCGCGCGCTTCGCAATTTGAAC  
GCGCGCAACCGCTCATCCGTGACCGCTCTTTTTCATCGGGGTGCGCCGAAACGAGCGCGGTTCCGCGCAAGCATAAATATCGGGGTTCTCATCAAGTCCCGCGTGTTCGGAACGAA  
TATTA

## SEQ ID 2390

MFILFQTLLEIFQHIQFEAAEARFFPRFDVHIAEDKHIVTGNQTAEGQDRFPQTAFAAEVLIPVADGDVSHFVAVNDVQHAAGCRIAALLHLRAVPRHNVQSAQLHARYQRHTQORVVG  
GPRVHIPQMVRLLEAVIAESAQSAHQAQVHLLLRHFHFPVADKLKQRAETVCRVQSQIDGVELDMNRNVQHRRIAFCRVHFARGQLRGRDNRVRPRAGEVRRRRVCLRPVRLN  
GGKRLIRQSPFFIGVARQGAFRQSINIGVHLKSAVFGKRL

## SEQ ID 2391

TTGAAAGGCGAGCGTGGCGCGCTGCTTTTCCGAGCGGTCAAAAAATCAGCCCTCGGAAAAACGGGTTTGCAAAATGCAAAACCGCCG

## SEQ ID 2392

LGQRGAPAFSERSKSLGKRLQVNRFP

## SEQ ID 2393

TTGTCGGTACTGACGACGAACCTTATTCGAAGGTTGCCCCGAATACCTCAACAGCGCGCGAAGCCGTATTGCTGCCCGTCTGCGCAAAGACTTCATCATCGACGAATACCAGGTTT  
ATCAGGCGCGCGCATGGGGGCGGATGCCGTCTGCTGATTGCCGCCGCACTGGAACAGGGACAATTGGAACGCTTTGAGGCGCTGCGCGCAAGAAATGGGCATGACCGCTCTGCTCGAGCT  
GCACGACGAAACCGAATTGGAATAATGCCGCAACCTGACACGCCGCTGTGGGGCGTAACAACCGCAACCTGCGGACTTTTGAAGTCTCCCTCGACCAAAACCGCTGCTGCTGCTGCCCGCG  
CTGGAAGCAAACCGCTGTTTACCGAAGCGGCATTACAGGCAAGCGGATGTGAATTTATGCGGGCGCGCGCGTGCATACCTTCCTGATCGGCGAAACGTTTATGCTGCGCGACGATA  
TTGGGCGGGAAGTGGCAAACTCTTC

## SEQ ID 2394

LSVLTDEPYFGSPYLKQAREAVLLFVLKDFIIDYQVYQARAWGADAVLLIAALEBQQLERPEALAHLELGMTVLELHDETELEKCRNLITPLGVNRRNLRTFEVSLDQTLSLPLA  
LEGRTVVTESGITGKADVEFMARGVHTFLIGETFMRRADDIGAEEVKLF

## SEQ ID 2395

ATGCCAAGCCTAATTTTGCACAAAATGTTGACATTATTTTCCCATATTTTCGATATATGATGTTTATGCGGATAATCAACCAATAATCATAAAT

## SEQ ID 2396

MPSLILHLKLLTLFPYPRYMFADNQPILIN

## SEQ ID 2397

TTGGAAAGCAGAAACTGCTCCGCGCTTATTTCCCGCAGAGGAGGAATCTGAACACGTCGCTAGGGAACCTATATCCCGTCATTCCACGAAAGTGGGAATCCAGGATGCAGGGGAAAC  
GTTTTATCCGA

## SEQ ID 2398

LEKQKLLRRYSREGRNLNTSVGKPLSRHSHEGPNPGCRNRFIR

## SEQ ID 2399

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CCAACGCGCATGATTATGTCGGGGCAACGCCAAACGCAACAACGCCGGCTACCAATACATCCGCATCGGCTTCAAGGCGCGCAACCTCGCCCGCATGACGCTTAAAGACAGCTTCGCGCAA  
CCAAACCTCCATCAGTTTTCGCGCGTTTGAATACCAATCCCAACTCTCGCGCGCGCGTTCAAGTTTACCCCGCCCAAGCGCTGACGCTTTGAGCAAC

## SEQ ID 2400

KYTARNAARMIVLPRRYFAPHPRSQKIMMKPHNLPQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHGTFKILRPLFKWEYTLPLRYQTIVGDQTVWLYD  
VDLAQVTKSSQDAIGSPAILSNKTALESSTYTLKEDGSSNGIDYVRATPKRNNAGYQYTRIGFKGNLAAMQLKDSFGNQTSLISFGGLNTNPLSRGAFKPTPPKGVVDVLSH

## SEQ ID 2401

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CAACATCGTAGAGCAACCGGTTTACCGTCCGCGCAATAGTCTGTCTGTAGGGCAAGGTATTCCCATTTGAAGAGGCGCGGCGCAGGATTTGAACGCTGCCGTGCGCGGTTTGGGT  
TTCTTTTGTCTTTGAGCGGTTTGGGTGAAGTCTGCCGTGATACCGTCCGCGCATCTGTTGAATTGCTTTGAGCGCGCTTCAACCGCGCCGCTGTCGCGAAGCGAGCGCGGACGGTCAGGAG  
CAAACGCGGAGGAATGGAACAGGTTGTGCGGTTTCACTAATATTTCCTCTGTGCGGATGGGTGCGCGCAAGATATCGCGCGGCAAAACATCATACGCGCGCGGTACGCGCGGTTT  
GCATTTTGAACACCGGCTTTCCGAGGCGTGAATTTTTTGACCGCTCGGAAAAAGCAGGCGCGCCACGCTGCCCTTTCAATTTGTGCGCGCTTATAGTGAAT

## SEQ ID 2402

LVAEAVFKLHGGEVAFAFADADVLVAGVVAFERPCHIIDAVERTVLFQRTAFEGGFVRQDGGGAAADGLVLGRHLQINIVEPNGLFVADNLSVQSVFPPEBARAQDFERAVRGLG  
FLFALDGLGEAAADTVGIVVELLERVHRARLCSDGCGGANGRELEQVVRPHYFSLSGWVNRKVSARQNNHTGVTGGLHFANRVFRGLIFLTARKQARHAALSTIVCRIVD

## SEQ ID 2403

TTGCGCCTTGGTGCAAGCAAGTTTGCATTAAACCGCAAAACAGCGGGGCGCAACCGTTAATTTTACCGGATTTGCCGTTCCGTTGCCCGATCGCGCGATAATCGCGGACATTGTTCCGC  
CTGCG

## SEQ ID 2404

LALGAARFALNGKNSRGATVNFHGFVPLEDRPIMRDIVPPA

## SEQ ID 2405

ATGCAAGCGCGCGCTCCGCTCCCTGCAATGTTTATTTTGAACGAAAGGTGCAAAACCATGAAAAAAACACTGGTGGGCGCAATCTGAGCCTTGCTTGACTGCGTGGCGCGCGGAA  
GCGATACCGCGCGCCCAACCCCTCCGCCAAGCCGGAACCACTGGGCAAACTCAACATCTACCACTGGTCCGATATGTCGATCCCGAAACCGTCCGCGCCTTTGAAAAAGAAAC  
CGGCATTAAAGATGCGTTCGCACTATTACGACAGCAACGAAACACTGGAGGCAAAAGTCTGACCGGCAAAATCCGCTACGACCTGACCGCGCGCTCCATCGCCAAACGTCGCGCGGCAATC  
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## SEQ ID 2406

MQARPSLQCLFLINERSKTMKKTLVAAILSLALTACGGSDTAQTPSAKPEAEQSKGLINYNVDYVDPETVAPEKETGIRHSDDYDSNETLEAKVLTKSGSYDLTAPSIANVGRQI  
KAGAYQKIDKAQIPHYGNLDKLLKMEAVDPGNETAVPYFWGINTLAINTRVQKALGTDLKLPENEDLVFKPEYTKLSCGISYFDSAIEQIPLALHYLKGDPNSENPEIDKAAVDMH  
KAVRGDVKRFSSSGYIDDMAAGNLCAAIGYGDNLIAKTRAEEAANGVEIKVLTPKTVGVGVNDSFMIIPRDAQNVANAHRYIDYTLRPEVAARKNSFVTPYAPASREARELMDKEYTSDASI  
FPTKELMEKSFVSPKSAESVKGVLWQGLKAGK

## SEQ ID 2407

ATGAATTTAAGTATTGCTGCTTATTTATAATGTCGAAAGTTATTTGGAAGCGGTGTTAAATCTATAGAACCTATATTAAGTAATGAAATGTCGAACCTATTCTTGTGAATGACGGGT  
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AAATTTCCGGGTCGGCGTGGGAATAAGATTATAAAAAGAGAAATGATTATTAGAGAAAAACCTGTTTTTGAAGGGAATTTATCTGAAGATATTGAATGGTCAATGAGGTTATTTAATGC  
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AAGAAGGGCATATCATTTAAGGTTTATGCTGTTAAAGTCCATAAGCTGATATATAGCTGATATCCGATAATCACATTATTCGGGTCGATATTACAGGCAGGATTTTAAAGCAAT  
CAGGGGAATATT

## SEQ ID 2408

MNLSTVVPIYNVESYLEACINSIEPTILSNENVELLIVNDGSKDGSIEDICYKIDKLSNKHQTPNFKYITQDNQGLSEARNFNGIKNSNGKYAFIDSDDFINCVLLDFLGKDDSDHFDV  
FLNAVYKDKRGVSYPGEDYQPEKILNQSKVEVLKGLCRPKFPGSAWNKIIKRELIIREKLFFKGIYSEDIEMSNRLFNAAITTSYLDGCTYYRQGRKDSITGTVSEKIKSLYLLEK  
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## SEQ ID 2409

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TATCGCGGAAGACGTTACCGTGGGGCACAAGTGATGCTGCACGGCTGCGGAATCGTAACCGCGTCTTGGTGGTATGGGACGACCGCTTTTGAAGATGCGGTTATTGAAGATGACG  
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ATTCGCGCGCATATATGTGAAGCTGTGCAACAGTACGGGATG

## SEQ ID 2410

MNAIRTFQNRTEIHECTMIDEACVVI GEVSIAEDVSVWPCAVLRGDVNSITVGARSNIQDGSVLHVSHKTAAPBESPLVIGEDVTVGHKVMLHGCRIGNRVLVGNGSTVLDVAIVEDV  
HIGAGSLVFPFRKLEGGYLYIGSPVRQVRLLTDEKAFLEYSAHYVLEKSKQYGH

## SEQ ID 2411

GTGATTTACATCCCGTACTGTTTCGACAGCTTACATAATGTGCGCGGGAATATTCAAAAAGGCTTTTCTCATCGGTCAGCAGACGAACCTGCCTCACAGGCGAACCGATATAAGA  
TAGCCGCCCTCCAAACGTTTTCGCGCGGGAACGAGGCTGCCGCGCGATCATCACGTCATCTTCAATAACGGCATCGTCCAAACCGGTCGCCATACCGAACGAAGCGGTTTACCGA  
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CAGGTTTCGTGGAATTCGCGCGCTCGGTTTGGAAAGTCTGATTGCGTTCATTTTCTCTCTCGGTAAGGTATATATGTTAAAGGATTTATTAATATATCCGCC

## SEQ ID 2412

VISHPVLFRQLHIMCGGIPQKGFPLIGQTNLPHRRTDIXIALQTFARRNEARADHHVFNNGIVQNGAHTDQDAVTDAAVQHHPVPHGNVPAIDNQRPPFGGGFVGNVQDAVLY  
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## SEQ ID 2413

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TGCAAGCATCCACGAGTCTGCTGCTGAAATACGCGCAAGTGGCGACAAAGTGAATACGTCACCGGTGCGAATCGCGCGCTTCTGCAAGTGGCGATGCTGCGCGCAAGGCTT  
C

## SEQ ID 2414

MTDLNLFANLQQRNPQEPFHQAVEEVFMSLDPLAKNPYQOSSLIERIVEPERVVMFVTVQDDKQVQVNRGYRVQMSSAIGPYKGLRPHPTVDLGLVKFLAFEPVFKNALFTLPH  
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YAAEKALQLGAKVLTGVSDDGFFVLPDGMTEAQLAALI ELKEVRRERVATYAGEGLQYFNQKFWGAARIALPCATQNELDEBAKFTLLANQCYVVBAGANMPSFLGAVBQFIKAGIL  
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## SEQ ID 2415

ATGCCGTCTGAGGGCTTGAGCATTTACAGCGGCATTTTACCGTAAACGCTAGGAGGGCTTCAGCCTGCCAATTAATAATCGAAAAGAGAAACAGTAACCGCAGGCTGGCTTCAGTC  
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## SEQ ID 2416

HPSEGLSISDGIIFDGKRRREGFLPINNRKRNRNRVGFSLIDKQK

## SEQ ID 2417

GTGCGCGCGCGCGCACGTTTGCCATCATCTCCACCCGATGCGGGTAAAAACCGCTGACCGAAAAACCTGCTGCTTTTTCGGCGCGGATTCAAAGCGCAGGCAGGTGAAAGGTAAGA  
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## SEQ ID 2418

VRRRTFAIISHPDAGKTLTEKLLLFSGAIQSGATVKGKTKGPFATSDMMIEKQRGISVASSVMQPDYKDEFTVNLDTFGHQDFSEDYTVRLTAVIDSALMVIDAAGVQAZTIKLLHVC  
RLRDTPIVTFMNYKREVRDLSLELLEVEDILQIRCAPVTWPIGKKNFGVYHILWDEIYLFZAGGERLPHEFDILKINNPLEQRFLEIQQLRDEIELVQAASNEFLNDEFIAGELP  
PVFFGSAINNFQIQEILNSLIDWAPAPKPRDATMRHVGPDEPKFSGFIKIQANMPDPRDRIFAIRVCSGKFERGKMKHLIRINREIASSVVTFFSHDRERELAEAYAGDIIGIPNHNT





QIGDSEFSEGEOLAFPTGIPFFAPELFRSVRXINPLKIRLOKGLQOLGEBGAVQVFKPMSGADLILGAVGVLPQFEVVT SRLANEYGVGEAVFDSASTWSARWVSCDDKTKLAEFEKANAGNLA  
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**SEQ ID 2419**

ATGATGGCAAAACGTGGCGCGCGCGCAGCTGGTCGAGGATTTCTTGGGACATGTTTCTTTGCAAAAAGGTTTCAGGCCGCTTTTCAGACGGCCCGACAGTGTTTGAGACGGCGAAATTTGACAAAAAATGCGCTGATAATTCATATGTTGAGAGCGGTCAGTCGCTGTCGCCGTAAATCTCTTTTTCGCTTTTCAGGACGGCATCGCGGTTTCCACGCACCGCGGTTCATTTTGTGTAAGCAGCTTTCGCGCCCGGTGTGGCAGCGGATGCCCGGTTTGGCGGATGAGCATCAATGGTATCGCCGTGCGAGTCGAGGCGCAGTTCGCGGACTTTTTCGCTGTGTCGCGACTCTTCGCCCTTCATCCATTTGTTTTTGGCGGAAACGGCTGTAATAGTGGGCAAGCCGGTTTCGACGGTTTTTTTCAGGGCTTCGGCGTTCATCCACGCCACCAT

**SEQ ID 2420**

HMAMVRRRTT\*SRISWDNVFAKFRPLFRPPQCLRRRNCTKKCLLIQCNRRSVRAAVNLFPVFDGIGGFPRPTAVPPFFVKAAPAGVAGDAAVLGDEHHNGIADVABEQADFRLVSRIL  
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**SEQ ID 2421**

TTGGTTTTCGCGCATCGCCCAAGATCGCGAAACCAACGTGTTTTAATGTGGCGTGGATGAACGCCGAAGCCCTGCAAAAAACCGTGCAGAAACCGGCTTTGCCACTATTACAGCGGTTCGC  
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CCACACCGGGCGCGAAGCTGTTTTACAAAAAATGGAACGGCGGTGCTGGGAAACCGCGATGCGGCTCGAAAGACGMAAAGAGATTATCGGCAGCAGCAC

**SEQ ID 2422**

LVCALAQDAETKRVLVAMNAREALQKTVETGFANYYSR SRQKQWKGESGHTQKVRELRLDCDGDITVMLLAQNGGLACHTGRESFYKKWNGGAWETADAVLKDEKITYGSTH

**SEQ ID 2423**

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GGAGGCGATGACCGGGATGTGCACGGCTTCGGCAACCGGCGGGGTACGCGGCAGGTGTAACACCTGTTTGTGTCCTCCGTCCCTGTCCATACCCGTTGAGCAGGATTTCGCCCGCGCGCGGTTT  
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TACCGCGCCCGGACGCGTCAGCGGATGAAGACTTGTCCGGCAACCTCTTCGATGATGTCCAGGATGTGTCCGGTTGTTCGGATGAGCGCGGTGATGTCCAGGAAGGTCAATTTCGTCGCG  
CCTTCGCGCGTTCG

**SEQ ID 2424**

MAQTKPSSNLTASSRFLSIFPRRHSRGQRRTPMSPASRIVRLASMAISPKWKMPAASTASALPSWMPISIRCTLTPTTPPEAMTGSTASATARVSGRIKPCFVPSLSIPVSRISPA  
CISTAHSTASKFVGLRPPVWKISQRVFSGLTALASTAATMACEPKNPAASLIKSGRVTAAVLMLTLAPALSRRRMSATVTRPPPTVSGHKTCPATSSMKCRNVSRLSDAVMSRKVNSSA  
PSPL

**SEQ ID 2425**

ATGGCACTGGCAAAACGCATCATCCCCTGTCTCGACGTAAAGACGGGCGCGTGTCAAAGCGGTGAACCTTCATCGGTTTGGCGGACGCGGGCGACCCCGTGAAGCGGCCAAACGCTACA  
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TCGAAATGCAAAAACGCGCGCGGGCGAAATCTCTCAACCGGTATGGACAGGGACGGGACGAAACAGGGTTCAACCTGCCGCTGACCCGCGCGGTTCGCGAAGCCGTCGACATCCCGT  
CATGCGCTCCGCGGGTCCGCAATGTCCGCGCACTGATTGTAAGCGTAAACCGAAGGCGAAGCCGATGCCGTACTTGC CGCGCGGCAITTTTCATTTCGGGAAATCGGCATCCGCGAAGCC  
AAACGCACTATGTCGCGAAGCCCGGCATCGCGCTC

**SEQ ID 2426**

MAIAKRIIPCLDKVDKGVVKGYNFGLRDAGDPVEAAKRYNGEGADELTFLOITASSNDRDTILHIIIEVAGQVFIPLFVGGGVRTVADIRRLNAGADKVSINTAAVTRPDLINAAAGFF  
GSQAIVAADAKAVNPENTRWEIPTHGGRNPTGLDAVENAVENQKRGAGEILLTGMDRDGKQGFNLPLTRAVAEAVDIPVIASSGGVGNVRLIEGITEGKADAVLAAGIFHPGEIATREA  
KRTMRAGIEVL

SEQ ID 2427

[illegible]

SEQ ID 2428

LLKSGPYCKKEEAMQTAIDYGMGNLHSLVLSVTRAGQLAGKNTKIFLSGDPDRVSRADKVIFFPGQAMPDCMAALTGRGLDEAVKDALKNKPFPGICVGAQLLFDSHEBEGNTDGLGNFG  
GKVRPPARDLRDPOGCRLLKVPHPMGNTVROTONHPLFGPQIPONTFRFYFVHSYVFAFENPETILGESDYPSPFACVTKGKNVFPATQPTTEKSHDAGLMLKNFLNW

SEQ ID 2429

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TC

**SEQ ID 2430**

EYHRTPTARQILHEVFGYPEFRGRQEDVINTLAGGSGSLVLMPTGGGKSLCYQTPALMREGVAVVVSPLIALMNDQVASLHVAGIEAAVNSGTSADFAEAIADKLAGRILKLYVAPERLV  
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 QALQITEAAKVLKGFTEVLMKPRFLRDKPATLKNLWLRTEPERLWQALRVRWKKQAEAGTIPAYMIPGDKLFLRDLVEKPMQNLNGHLDIYGLGEAKTERFPGHILKVCQNAADFSDHA  
 VIRPQTEFERQQRLKLEAWRYEQARAENCALHTVLSDESLEADMLAATPETTLEAVHGLGSVRAAKYGRDILAVCRPFSGIDETPAKHKRCIMRALIQWNETAKHQSEPYRILSKAAL  
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**SEQ ID 2431**

GTGGATGCTTTTGCAATGATGCCGAACAGTCGGCTGTCCACTTCTTTCGGCGCCCAACAGACAGCGCGATGCGGTTTGGCTCAITTTCCAAAGCCCGAAGTTGCCACGCCCGCGCGGTGGAGGCT  
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**SEQ ID 2432**

VDAIHDAEQSAVHFFARFQADGVLHAFQARSCHAAGVGGFARSVEDAGDFKLLDRAQSRHRHARFAGNDVAAVCQQQGGFFVQFVLGRAGQGDGQGNAPRFLVFKVLQTLFLPGVGNAPFA  
ADFFQFDQGGELRFGHTDVGEEDEAVGVGDGHFRFTQLDGFPSGVLRHVAGTGNQNAFAFKTIVAGLQHLRGEIDAAVAGRLGADEAATPFQTFAGQDSEPIADFFVLSEBVADFASAYZ  
DVAGRNIGVRADVAVEFGHKGLAEAHYFGIGFAFGVEVGTAFAAAHRRGGQGVFEHLFKSEEPQHAQIDGRVEAQAAFRVADGGTHLHAVAADLQLSFVVLPGYAEHDAFGDDAPQQA  
LLGVFRIFCOKRIKAHEDFPNRLMERLLIGVALFVVGKQGVVSHSDTPFC

**SEQ ID 2433**

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GACGGCTAAATCGCAACATCCGTCGCCATTTCCGCTACGCGCTCCGCGGCATGACCGCTTGGACGACGACATCCGCGCTGTGTGCGCGCGAAAAACATGGCGTAGCAGCGCGATTAC  
GGC CGCGCGGATTTACGAGGACGACATCTGATTTTCCCAACGCGCTACGCGCATTGGCAGATTCCTCTCGAC

**SEQ ID 2434**

LNPMPSEDRFPFSDGIFISPAHLFVKIAAILQKRGGSHANRHYLRYGQPAFRIETRPDGGAACRKKYQNLFKRRPRPRVPRRQSHFSRAGRDRALRYGGTDARRLRGRSGRRLLKKQTVFRN  
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VEKLFKLVSRTPRTRRKTMLLIIPAILKEGRCVRLKQGLMEEATVFSDSPADTALHWFQEGARRLHLVDLNGAFAGVQPNLPAIKDILAAVAKDIPVQLGGGMRDLKTIGQYLDLGLNDV  
IGTAAVKNPDLFAQACAPSGRIIVGLDAKDGMAAIDGNATVTTHGVHIDLAKRFPEDGVNSIITYTDIGRDGMSGVNIDATVKLAQSVRIPVIASGGLTGLDDIRALCAAEKHGVAGAIT  
GRAIYESGIDPBAQOACKADSLD

**SEQ ID 2435**

TTGTTTGTCTATATTCAA CTTGCGCGCCCCAAGCCAAACACGGCACGCACGGCACGAGGACGGCTTTCTGCCCATATGCCGCCCTTTCACACCATATATGCCGCACACCGCAGCATATCGA  
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SEQ ID 2436

LFAIFNLRAPSQTHRHAGSRFCPYAAPSNIHCRTPOHTKGYITMAKVLVVPVSAGLNTISAAQAFKAKALDAQVQAVDARTETLLAQGSKDDWFDALVGKVAALDAANLWIEGIAFPDADK  
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SLVSSVFFMLLPNVLVFGDCAVNPNPTAQQLADIAIQSADSAKAFGIDPKVAMISYSTVNSGSPDWDTVIEATKLAREKRPDLAIDGPLQYDAATVPGVGKSKAPGSPVAGQATVLFVP  
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## SEQ ID 2437

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## SEQ ID 2438

MTAALHGHLSKSFQNTFVPLNDISLSDPGEILFIIGAGCGKFTLLRLAGFEQPDSEISLSGKTFISKMTNLPVRERRLGYLVQEGVLPPLVYRNIAIYGLNGKGRTAQERQRIEA  
MLRLTGISLGRYFHELGGQQRVALARALAPDELILLDEPFSALDQLRLQIREDMLAALRANGKSAVVFSDHREALQYADRIAIVMKGRLLQTPASPHELYRQPADLDAALFTEGB  
IVFPAALNADGTDCRLGLPLVQSGAPAGTRGTLIRPEQFSLPHSAPAAIHAVLKTTPKARETEKSLRAGQTVLTLNLPAPLSDGISAVLHLDGALPFPGLNTL

## SEQ ID 2439

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CCTTTTTTTCGCGCATCTCCACAGCTCAAACCGCATCGGACGCGGTGTACTGATCGCGCTGCATATGCTGCTGAATTTGGCGCGGTATCCATTGTAACCTACCCGATTTTAC  
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CTCAAGCTGATGAAGAGTTGACCGCAACCTGCTGCTGACCGCGGATGATTCACACGCTCTCCACGCTCTCCACCGCGCTTGGGAATACACATCGGAGCGCAATACCGCGCGCGCAACCTTAC  
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## SEQ ID 2440

MSPKKIPINLTGLILLIALFLTLPLVYVAMRSQVGINRAVELLFRPRMDLLSNTLTMAGVTLSIVLGIACALLQRYRFPKTFPQTATILPLCIPAFVSCFTWISLTPRVEGFWGT  
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AKIYHSGKVARFPVTKLPLGQIGALVLSLLILGIIIPFGLIHMVGTSGTFFALVSVDFAFIRLSVLSALGAILTLCLALPLVWASVRYRNFLTVMLDRLPFLHVAFLGLVIALS  
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ALMLVLPFGIPVFLKKYAFK

## SEQ ID 2441

ATGAAAACATCTATCCGATACGCACTGCTTGCAGCGAGCGTACCGCGCGCAACCCCGCGCTGCGCAGACATTACCGTGTACAACGGCAACACAAAGAGCGGCAAGCGGTTGCGAGATG  
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## SEQ ID 2442

MKTSTIRYALLAALTAATPALADITVYNGQHEAAQVADAFTRATGIRKVLNSAKGDQLAGQIKEGSRSPADVFYSEQIPALATLSAANILLEPLASTINETRKGVPVAAKDVVALS  
GRSRVVYDTRKLEKDLKSVLNATPKWKNRIYVPTSGAFLEQIVAIKLGEEAALKWLKGLKEYGKPYAKNSVALQAVENGIDAALINNYHFAFARKGVQNVHTRLNFRHRD  
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## SEQ ID 2443

GTGATTCCTTCTTTTATAAATGCAATAATATTTTAAATTTGTTATTATCCGATCCGCTTATGTTGTTCTGACTTGTATTTTTCGTCGATCGCGCGCG

## SEQ ID 2444

VYSFPFINANNYFLMLLLSDPVIIVCSLDLYFFRASRP

## SEQ ID 2445

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## SEQ ID 2446

LSECHRTSPFKTPEQCGRNSIAIPADTVCRDLANIVHPCSAARRPCCRDLVLIHYISHISFRFLPSDHRWRISFPNAAARWISIALCTAPIFRTEQVFSAGKPOLQTNCSHPLPM  
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## SEQ ID 2447

ATGACCGATACGGATACCAAGCGGACCGCTTCGAGCAGATGATGCGGAGCGGTTGGACAACTTTTGAACAGCATGACGGCAACTCGAAAGCATGAGCGGAGCGGAGCAGGAGCTGG  
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CAGCGCAATGCTGATCATCGGCGCGCAGACGATGCGGAAAGAAATCCGCCACTTCAATCGGAAGGTAAAAACCTAAAAAGAAATGTGGGATATA

**SEQ ID 2448**

MTDTDTQADRFQMMROAVDKLFEQHDGKLESMDGREQELVLWRAEADIGNGGILOFVCNWGFPAAEKTC SVLKKI GAVHSAMLTHRAADALGKEIRHLSQEGKNLKEMWDI

**SEQ ID 2449**

ATGACACGACAAACCTGGTCCGGACGTTTCAACGAAACCGGTTTCCGAACCTCGTCAAAACAATACACCGCCTCCATCGGTTTTCGACAAAGCCCTTTCGCGAATGGGACATCCAAAGGCTCGCTCG  
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**SEQ ID 2450**

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**SEQ ID 2451**

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**SEQ ID 2452**

SEQ ID 2432

KKPIKKA VFPVAGMGRFLPATKANPKENLPITVDKPLIQYAVEAEVAGCTEMVFPVTGRNKRSLIEDHFDKAYELSTKLEMRHKDKLLEHVNTILPPNITCLYTRQAEALGLGHAVLCARAA  
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**SEQ ID 2453**

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**SEQ ID 2454**

SECID 2434  
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**SEQ ID 2455**

TCGGAGAGTATGAATACCGTTCACGACGGCTCGGCATATTCGGATGTATCGGTATAGTGAACATAATTTAAACACAGTACGGCGTTGCCCTGCCCTTGGCGTACTATTGTACTGTCTCCGGCT  
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**SEQ ID 2456**

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**SEQ ID 2457**

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SEQ ID 2458

MELVLFIRHGOSEWNAKNLFTGWRDVKLSBQGLARAAAGKILKENGVEFDIAPTSVLTRAIKTCNTVLEESDQLFVPQIKTWRLNRHERHYGRIGLQKKQTAEKYGDQVRINRRSYDTLP  
 LLDKDAPSAHKDRRYAHLPAADVDPDGENLKVTILERVLPFWEDQIAPAILSGKRVLVAAGNSLRALAKHIGISDEDINGLEIPTGQPLVYKLLDNLKVTKEPYL



## SEQ ID 2459

ATGTCGAAAAACCGGAAAAATCGTTTGGCAAGCGCAATGCCGCAAGCTCAAAGAATTCCGCAACTTAFTCAAACCTTACGCATCACCCGATTGCCCAATCCGCAITCGGCATAC  
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## SEQ ID 2460

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VCVLVVRHKDDPRPIIABGINHGMHDTPLQNGFGYDPPYLPHEGKTAELDSEVKNRSHRAQALADLIRKLAL

## SEQ ID 2461

ATGAACCGCGGAAAAATCTATCTGTTGCTGTTGCTTGTTCACACTGGCATTATGCTGCCGCTCTCTTGGGTGCTTATCTGCTGACCGCGCGCAGCAAAATCTCGCGCTGCGCTCT  
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## SEQ ID 2462

MNRKIYLLSVLFTLAFMLPVLGAYLLTAGSKTFVAVSFLFAFGALFQIGALALYLHKLRLAAPPSSSQGNRYV

## SEQ ID 2463

TTGTGCTATCTTTCAAACCTTCAAACCTTCCCAATAAAGGAAACCAATGCGAGACTTCAAACCAATCTGACCCCGGCGAGCTGGAGCGCGGCATCATCAACGTCGTAACGAAATCC  
CCGCGCGCAGCAACCAAAATCGAGTGGAAACCGCAACTCGCGCATTCACACTGACCGCATGACACCGGCATCTTCCGCAACCGCACTACGCGCTTATCCGCAAACTTTGGA  
CGAAGACCGCGATGAATTTGGAGTGTGCTGCTTACCGAACAACTTGGCAACCGCGTATCTTGGAAAGCGCGCTTATCGCGCGTGAATTAATCTGTCGACGACGGCGAAGTGGACGAC  
AAAATCGTCTGCTACCTGCCGACGACCGCAATACCGCAACGCTACAAACTTTGTCGATTTCGCGCAACAGCTCATCAACCAATCGAGTTTCACTTCAACCACTACAAAGACCTGA  
AAAAAGCGGTACGACCAAGTCAATCTCGGGCGGTGCGGAAGAAGCGAAAAAGTCAATCAAGAATCCATCGAAAGTGGAAACCAACAGGCA

## SEQ ID 2464

LCYTFKLQTFPNKGNQMDNFQILTPGDVGGIINVNEIPAGSNHKLIEVNRKLAAFLDRIEPAIFAKPTNYGTFIPQTLDEGDGLDVLVTEQPLATGVPLERVIGVHKFVDDGEVD  
KIVCVPADRRNNGNAYKTLSDLPQOLIKQIEFPHNYKDLKAGITTKVESHGGAEEAKVIKRSIERMKNQA

## SEQ ID 2465

ATGCCGATGGCAAAACCGCTCAAAATACCCGTTTCCGCACTGGTCTCTTTATAGCGGGGACGCGCGCATCTGCTCATCGAACCGCAGCATCCGAAAGGATTTTGGCAGTCGTAAACCG  
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CTACCACTACGCGCGCAGCGCTACCCCAAGCGGTGTTGAAACCGCGCAACAGCTTCCGCGCGCAATCCGCGCGCATACGCGCTGCTGCAACCGGAGGAACAGCTCTCTCTAC  
GGCTGCTCGCTTGGAAAGAAGCGCGGAAAAAGTGTTCCTCCCTCCACAGCGCGCGGATTTTGGAACTGGGCGAGTTTTCGGGCAACCGG

## SEQ ID 2466

MPMAKPLKYPVSALVVLVYSGDGLILLIERTHPKFQSVTGSLEPGETVAQTARREWEETGILLEDDQLDRHDSVVEIYHWHRRHYPKGVFENREHVFAETPRDTPVVLQPEEHVS  
GWFLGEEAAEKVSPSNNRAITLIRFLGR

## SEQ ID 2467

ATGCGTCCGATCCGCTCGAAAGGAAACCGCGCGCTGTTCACGTTTGGCCAAAACCTGCCAGTTCAAAATCGCGCGCTGTGGACGGGAAACACTTTTCCGCGCTCTTCTC  
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GCCAGTGTGGTAGATTTCGTAACCGTCTGCTGCTGCGCGCTTGGAGCTGCGCTCTCCAGCAGGATGCCGCTTCTTCCAAACTTCGCGCTTTCGCGTTTGGGCGAGGTTTCGCC  
CGTTTCGAGGCTGCGGTTACCGACTGCGAAATCTTTCGATGCGTGCCTGATGAGCAGGATGCCGCGCTCCCGCTATAAAGGACGACAGTGGCGAAACGGGTATTTAGAGCGGT  
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GTTTCCCGGTAAATTTCTTTGTGTCAAAAAGA

## SEQ ID 2468

MRPSPSERETGRVLPFAQKPAQFNRAFPVGRKHFRFRFPQAEPAVGDVFLGLQDDGRIARDFGPDVFAVKHAFGVAVPVVVDFVNRVAVPVLPLVQLQDAGFFPNFAPCRIGDGA  
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## SEQ ID 2469

TTGAGCGGTTTTCGCTATCGCATCTTTCGCGCGGCTGCGGTAATGAAGGGCGGATTTATAGCAACCGCGCAGCTTATGGCGTTTATCTTTTCGCTATCTTTTTCGACGAGTGGGA  
CGCGCGCGGTTCGCGGTAATTTCTTTTGTGCAAAAAGATAAGGGCGGTTGATTTTATGCTTGCCTCAAAAGTGACGGCGGAAACTA

## SEQ ID 2470

LSGFAIGIFRRAAVMKGRI IANAARYGVYPPYPPFCTDGTRECLPVNPLCQDKKGGCDFNAQSDGRKL

## SEQ ID 2471

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## SEQ ID 2472

VNRLVAHLHGQVEGSENFPTTKNSERFQKRLFCRPYDIDVEYAATDIQMPSENRSDGISLS

## SEQ ID 2473

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CGGCTCAAACAAACCTTGAAGGCGGCACTGTTTACCGCTGCTATCTCGATTCATCGCGGAGAACCTACTCGATGATGCGCGGAAATCCCGGCGGACGCGCGGACGCGCTACCG  
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TTGCTAGAAATTCATCATGATAAGGTCATTTTATCACAATGAATTTGATGAAGAAGATGGTTATCCAGTATTAAGCTGTTGCTGCATACCTTTAAACTGCTTTAATGCTTGGAAAT  
GCTTTTTCGCAATTCGCTAAAGATATTCATTCGGTGGTGGAGACTGTGATTGAGGAA

## SEQ ID 2486

MMKRIKPCDKFPSPGDTFRMCIILDDYDNRVDYTVGIYDITSLMSDIYRSTIDEHPKILIELIENNPNEIYDDGGQQPCLEFHHDKVIFYHNEFDEEDGYVLSCLHTFKTALIAHN  
APLQPKSIHVSVEVIEE

## SEQ ID 2487

ATGACTAATTTAAATAGATTTCTACTCTGAAGTATTATAAAAGATTCCTGCCCTAATGATTTGTAGAAAATGGTGAGACTATTAAAGGAAAAAGGAGTGGTATTAGGTATAAGCG  
AAGAAGATGGTATAATCTATGGCTATATCTTTTACTTTTGTATATAAAATATTGTATATATAGATAAGAAATATATTATACCGACTGGAAAAAATCTCTCGCGATGATTTTAT

## SEQ ID 2488

MTNLKLDIFYSEVLIKSDPCNDLLENGETIKKKGVVLGISREDGLIYGYTILLFDIKYCIYIDKKYIIPGKKFSRDDFY

## SEQ ID 2489

TTGAAGGATTCACAGGGCAATGAGGCTGGCAACCAAGGATTGGCGGAAGCCATTAAACGAGGAGAAGTACGTAGTTCTGCTTTTACAACAAAGCACTAAAGGCAATCGAAAAAGGCA  
AAGACAAATCCCTAGCTACACTTGGCATCATCATCAAGATACAGGGAGAATGCAGCTTGTGCTGAATGGGAACATTCTAAACCGGTACATAGAGGGGACGGCAATGGGGAAGGTAA  
A

## SEQ ID 2490

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## SEQ ID 2491

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## SEQ ID 2492

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FVELPFL

## SEQ ID 2493

ATGTTGACGGCAAGGAACATCTGAAATACCAAAATACACTTGGCATCATCATCAAGATACAGGAAGGATGCAATTGATTCGTGAAGACTCGCATCATGATACCGACCATATCGGTTGGA  
GAGCATGAGTAAGGAAAG

## SEQ ID 2494

MFDGKGTSEIPNYTWHHQDTGRMQLIREDSHHDTHIGWRAHSGKG

## SEQ ID 2495

ATGTGAAAAATCATAAAGAGGATAGTGATGATTTAGGATTTGCAATTAATGCTTATCTCTCAATCTATTGATTTAAATGAATTCAGTTATGGATTGAACAAAGTAATACCGGATATGC  
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CTTGACAGCATTCGCTTCTTAAGGGGATAGATGCTATGATCCGCTATTTCAAAAGAAAAAGCATTAAAGACCTTAAAAAACATCTGAAATTTATCATAAATTTAAACGGTCTCTT  
CCTTTGTAGAGCTTCCGCTCTT

## SEQ ID 2496

MMKLIKEDSDDLGFAIKCLFSQSIDLNEFKLWIEQVIRDMPIEDIPFYIYDLADFGGIGDIDNIVGVSSYSLSKSKKNALTGIAFLRGIDVYDPPISKEKALKALKKHEPIYHKFRFP  
PFVELPLL

## SEQ ID 2497

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GCCCGCGGCAATACCGCGGTTTGGAGTGATGCAGAAATGGATCTGCTTACCGCAATGCTTGGCGAGCTGGAAATCTTACCGCTTCACTCTTCAACCGCGCTACTGGAAG  
AAA

## SEQ ID 2498

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IVFTIPGGINFASHFAALNSRLKTYWKDECRTHLLLSGSLASALYLMHTGHYAGFESLRYTAFNFVSTGLANGLSNTDPAQWPLILISLWMPFLANILASSGSTGGGIRFIRALVLF  
KPSLREMMVLHHPKAVRTVKISGAIPDRLLATVMSFIFYPTTVVLFSPFLMASGHEFTTAFVIACTINAGPGLSEVGPAGNYAGLDVMDKWCITAMHLLGRLEIPTVFLFTPAYNK  
K

## SEQ ID 2499

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**SEQ ID 2500**

LETASDSDTSSLRKKTHHVLPLRQHQQFHHGVSVHRFQRNAQTAFPPKYRPGTRTAGVVPVPRRPPNAQRVHTRPKRFRLLVVQHQHLARIGNWTKVAFGSHIAQVHVIGKHHAAAFNAV  
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MPGRVADBCQALVGMFGKMAVNLPAFVLRITHVKPPSTKSRHSAANASAWLKNQACAAPSTTSLPPFKRCRYSPIRSGVIASLPPMTSSGTSTLSNKRASALSAAKSKCIA

**SEQ ID 2501**

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GGCTTTACCTGCGCGCTGGTGTTCAAAGCCCGCATCGGCAACCACTGACCAACCATCATCTTCGGACACATGGTGTCTCTCGGGCTTACACGAATCGCGCAACCGTCACTCTGCTGGACACC  
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**SEQ ID 2502**

MAHYATGDIQCFCDELTALLGKIGFHNHGTUPLWLTGDIVNRGPKSLETLPQCFIRHENSVOIVLGNHDLVYLLAVGCGEGALKRSDTIEPLIKHPDGGKMLDLWLRAPQLIREGGGRVMHAGI  
LPQWRIAKAESLAGEABAEIRGKGVKVPFSKMYGNKPAWDEGLEGYARLRFIVNAFTMRALTFKNELDFDYKSTVKMPYPYLRPFKAPDRQNLDTIIFGHWSISGYTNADNVISLDT  
GALWGGQLTAVNLETRITQVQAAGGIDMKSPAK

**SEQ ID 2503**

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**SEQ ID 2504**

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**SEQ ID 2505**

SEQ ID 2595  
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TCGTTGTGAAAATCGCCGTTGCCGACCAAGTCATCGTGGCGGGATCGAGCGGAATCTGACCGCTCATGTAAACGGTGCCGCCGGCGCGCACGGCTTGCTGTATGCGCGGATGGCGGCGGG  
GGCTTTGTCGGTATGGATGACGGTTTGGACATTCGGATTCTCTCAAAAAA

**SEQ ID 2506**

VELCVQNEDEGFRFDLHAFGQQRGNADGGAGGERLGDKFRHHFVEDGKIAQVGVQGVVEFDVVQRTACRFGDGLQVLEHLARFGVEIAVADHSHRGGGIERNLTAHVNGAAGAGHLAVCADGGG  
GFGVMDGDPGHGFGLKK

**SEQ ID 2507**

ATGTCCTCCAAAACGCTCATCCATACCGACAAGAGCCCCCGCCGCATACGGCGCATACAGCCAGGCCGTGCGCGCGCGGGCACCCTTTACATGAGCGGTACAGATTCCCGTCGATCCCGCCACGA  
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GACCGACTTTGGGCAATTTTGGCGTCTTCAACGAAGTGTGCGGCAATTTATCACCGAGCCGTTCGCCCGCCCGCGCCGCGTTCGGCGTTGCCCTCGTCCCAAAGGCGTGCAGGTTCGAAGCG  
GAAGCGGTCTCTGTTTGAACGCA

SEQ ID 2508

MSKRTVIHTDKAPAAIGAYSQAVRAGGTVYMSGQIPLDPATHTVVGNDFHTEARQVFQNLQAVAEAAAGGSLDDIVKLNAYLTDLGNFAVFNEVMAEFTITEPPFPAARAAVGVASLPKGVQVREA  
EAVLVINA

**SEQ ID 2509**

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TGAAGCTGTGCGTGCCGCCCAAGTGGCGCGAAGCGCGGTTGAGCGTCAAGCGCGCGCCGAAATACGGTTTGACGGCGGATTGGGTGTGAAATCGTAAATGACGGAACGCCCGGATGCTGTA  
AAGTTTGAANAATCGGTGATGGGCTTGTTTATAGTTTTGTAGCGCGTGAATCGACGCCGAAGCGGAGGTCTGTGATGCGGTAGCCTGCGGAGATGCGCGGCGTGAAGCCTTTGCGAGAA  
CT

**SEQ ID 2510**

LCSPFRYMKRKQKTAEGSAVCGITRISEFDHAGGGQAGTIVDFADVVVAVAGIQIDIGCNGIAYARQYAEAGGGFAEAVAAAVVGGSAVEAQARAEIRFDGRLGVEVVNDGRADAV  
KFEIGGGGLFIVFVNRVIDGEAEVVVDVAVACGDARAEAFGR

**SEQ ID 2511**

ATGAAAAGAGCGACTTGGCGCACTGATTGCCCTCGCACTCCCGGCCGCGCACTGGCGAAGGCGCATCCGGCTTTTACGTCCAAGCCGATGCGGCACAGCCCAAAGCGCTCAAGCTCTTTAG  
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SEQ ID 2512

SECRET 2312

KKKALAAALIALALPAALAEAGASCFYVQADAAHAKASSLSGAKGFSPRI SAGYRINDLRFVADYTRYKNKYQAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDFS  
SKTSAGLGLVLAGVSYAVTFNVDLDAGYRYNYVVGKYNVKNVRSGLSAGVRVKF

SEQ ID 2513

TTGCGGTTTTTTTCCAAAACCGTTTGCAAGTTTCACCCATCCGCCCGTGATGCCCGCGTTTAAGGGCAACGCGCGGGTTAACGGCTTTGCCGTGCGCAAAGCAGCCGGATGCCCGCCGCGTAT

SEQ ID 2514

LRFFPNRLQVSPIRRVMPPFKGNARVNGFAVGKAAGCRRVS

## SEQ ID 2515

ATGCTCAAGATACGGCGGCGCATCCGGCTGCTTTCGCCAGCGCAAGCCGTTAACCCGCGCTTGCCTTAAACGGCGGCATCAGCGCGGATGGGTGAACTTGCAACGGTTTGGAA  
AAAACCGCAAGCGGGCGGGCGGCATTGTCAGATTGTTGCAGCGCAGCGGTACGGTTTTCGTGTGCGCGTTACCT

## SEQ ID 2516

MQDTRRHPAALPTAKPI/ALPLNGITRRMGETCKRFKGNKGGAAAFVRL/LQAYGFLCAALF

## SEQ ID 2517

ATGCAACGTGCTTTAATTGGTTTGACCACTATTCGCCAGGATTAGAAAAATTTTCGGAGATGTTCAATTATGGAACTTGGGTTCAAACTACACGGCAATCGCGCGCAGCGCTGATC  
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GCCGACGGGTATGGCGGTTTCCTCCCTGTCGCCGCGCAGCGGAT

## SEQ ID 2518

MQRCFNWFDHYCRLEKYFRCSIMETWVQNYTAIGGSLYL/TAAALLPIVTF/PAAL/VLKLKGYQAGLIALAVAVFGFPMPTGMAVSSLSPPQD

## SEQ ID 2519

TCTCTTCGAAAAAACCACACGCTTCTCCCTTCGGCGCAGCACCAGTTTTCACGCGGTGTCGTACACGCTTTCACGCTAATGCCAAACCGCTTCCGCTTCAATATCGCCCCG  
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## SEQ ID 2520

SLRKKTHVLEPLRQHOFPHGVSVHRPQNAQTAFPPKYRPGTTRGVVPRHRPPNAQRVHIRPKRFLFVVQHLRRIGNWIKAVFGEHLAQVWHIKHHAAPNAVFPQTGFQFRQG  
LPAEAGEKQFVRLQARFVQHGKDLFRQQGSEVRPQHIGTRFQRHGRGLAVLHAPARQ/LEPETALARGCGSRQKIRITGIVFPKYRQRIALRQQAADVIRIRTKQIMPGRVADBCQA  
LVGMFGKMAVNLPAFLIRLHVKPPSTKSRH

## SEQ ID 2521

TTGCAACGGTTTGGAAAAAACCAGCAAGCGCGGGCGCGCATTTGTCAGATTGTTGCAGCGCGAGCGGTACGGTTTTCGTGTGCGCGGTTACCTTAGGCGTCGGACATTTCCGCGGGC  
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## SEQ ID 2522

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## SEQ ID 2523

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GGCTGCTGGAACCGACCGGACCGTATTCGCGCGCACCGAAAAAGGACGCTGTTTTCGCAAGATTGTTGTCAGTGTTTTTTA

## SEQ ID 2524

NHTISFPNRTRLTALPPLSLYTHIPWCIKKPCYDFNSHSLKNGLEPAAYIDALLTD/LQLEPNIWGRPVETIFFGGTSPSLQAESIDRLLSGVRSLRLQPEAKITLEANPGTVEIEKF  
QGPKDAGITRLSIGVQSFNDMLSLGRVHNGREALTALATALKLFDKVNIDLMYALPNQVQ/TALDDVQTAIATDATHISAYHLTMEPTFPFHTPKGLPDQREALDIEDAVHGLEGA  
GFHYETSAFAPKPMQCRHNLANFYQFDYLGIGAGAGHKISYFDRIERTVRRHRPNYDALM/QSQPGEAVERKTVAEDLPEFPMNMLRLTDGVPAAHLQERTGVPAAKINQVJETARQK  
GLLEDTPTVFRPTEKGRFLNDLLQCFI

## SEQ ID 2525

ATGAACCCGACCGCACACGCATACAGCAACTCACCGACCTCTCAACCGCTACGCTACGAATACACCTCGACGCGCCAGCATACCGGATGCGGAATACGACCGCTGTTTCGCGG  
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## SEQ ID 2526

MNPFAQRHIELTOLLNRYAYEYTYLDAFSPDAEYDRLFRELEALERNHPELKLPSPTQVRGGEPLAGFAEVRHEVPMLSLTNAPSQDENGVPDHAEMYPDQVRVRLDGGNPEYVIE  
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LAEBHIQELAYFQALGFLPNGNPGCFKNIGEVLAIFYEHMQKRPELPEYIDGTVVKNLSLAQOHELGFISRAPMVAHAFKPAEALTIIVRAIDVQIGRTGAVTPVARLQPVFVGVTPT  
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ASRKAMIDIGLERQIEQLVAQDLVRHFADLYRIDIPTLQKMKETADKGSEENNGDAETVSGDLSKYNTQNGKKOPTKWAQNLILAGIESGKTPELARFLFALGIRHVGERAKTLAQAFG  
TLERVRRAPEPVLACLPDITVVARSLAHFPAQAEQQAMIDELLAGVAPQAQAVSLPAQYAGPQRMITRLPGFKISENKAQALMELAGQSTBGLQNDKALPADWQAMRSKAQNTALLEN  
LRTFFAQMPSEDEAAQSDGINKAVAGTFFVLGTLPFTFKRDQAQALIEAAGKVSQSVSKTQVYVAGETAGSKLEKANALGVSVLSEAEHLTLIC

## SEQ ID 2527

GTGCGGTTCGGGTTCATGGATTCGTACAGGTTACAGCGCATGGACAAATGCCGTCTGAACGGTAAACGTTGGAAATGGTCGGATTTTACC

## SEQ ID 2528

VRSGSWIRTSDDMKRLNGKTCWKWSDPT

## SEQ ID 2529

TGTCAAAACCCCTTCGACAAAGTCGCGGCACAGCGCGCAACGCTTCGCGATGGCTCAAAAACGCGCGGTGTCGCCCTTTTCATCACAACAGCCTGCTTCCTTCAATGCGCATGC  
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## SEQ ID 2530

CQTFPDKVAQRGRFRMAQKRRVRLFHNNQSPASQPMQILAHQRCNRVFAAEHQYRNILYVQMPRI RPRRVQSFL\*GLRRAAARQIGQSDADDGIRRVQKLEL\*KLFDMPGI  
IRSEADHFAQCRKPGKPGIVFGSRQPCETRRQAERTFDPVGMARRQIQRDQAE\*PAENWRRIRIDLGNVAGSCLNIEGLRBGRVPSVSGQIDGGRHPRCQARHQIVERVAVRPPPTVYQVN  
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## SEQ ID 2531

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## SEQ ID 2532

VIAIYIYVFLAAVAVVAYNMYQENYRKKVRDQFGHSDKDALNLSKTSHVDRGKPSGGPVMMPKPQPAVKKPAKPD SAMRLQSBQDAVYIAKQKAKASPFKTEIETALEZIGIIGNS  
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SAFRRQADAPQSMGGQTLHTDLAAPIEVSALDAPCARVDQTLAHLVSPSTISGVELRSVITGVGVLEDDGAFHYTDTSGSTMFISICSLNNEPFTNALLDNQSTYKGFSLMLDIPHSPA  
GKTFDDLLFMDLAVRLSGQLNLNLVNDKNEEVSTQWLKDVRTTVLARQSEMLKVGIEPGKTAIRLFS

## SEQ ID 2533

ATGGCAATCACTTTAAATTTCCGGATGCAGGATGCGCAAAAGTCGCGGTACTGCGGTAAATCGGGCTTCCGCTTCCGCGCAGTCTGACGGAACGCGCGTTATAACGTT

## SEQ ID 2534

MAITLNFQMADAQAGTAVKSGLRFRQSDGTAGYV

## SEQ ID 2535

ATGCCGTGAAAAACACAGATTTACAGCGGCATTTCCGAAAAATTTCCGCTTATTTTCGACACACTGCTGTCAGACCTGCAATTTTCGTTATAATTCAAACGTTA

## SEQ ID 2536

MPSENHRFQTAFRKISAYFDLLSDPAIFVLIQTL

## SEQ ID 2537

TTGCCCGCCGAGCAGGAAGAATCATGGACAATCAGCCGGAGCACACTGGCAAAACGCGTGGCTTCAAGCATACGCCATAACCCGTCGCCCAATTCAGCCCGAGGGAACCGGAGAA  
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## SEQ ID 2538

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## SEQ ID 2539

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## SEQ ID 2540

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**SEQ ID 2541**

TTGGGTTTATCTGTCGCCCAATTTTAAAGAGTATTCCGAATGCTGGGAATCCTACCATGTTGAAAAAATGTTGAAATGGAGTCGCCGTTTPTTTTGACCGTATCGGCAGCCGTTTTCGCCG  
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**SEQ ID 2542**

LGYTVARILRRIPNAGNPTMLKKMLKWTAVFVITVSAAVFAALLFVPKDNGRAYRIKIAKNQGISSVGRKLAEDRIVFSRHVLTAAYVLGVHNLHJTGTYRLPSEVSANDILQKRRGGRPD  
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**SEQ ID 2543**

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**SEQ ID 2544**

LRFHACSSCKGMPSENTNPSDGHVYFFKTYLRTAALCSVKSWLNLKPVPSILTDKYRYPAGTIVGGGIECRLAGQRNRGWRQAPARIGVVRVAAQVGFDFALVCRTHAVNHGRVGLQA  
HTDFQAVDEEDGSDMVAVGLMPRFLFDQARENHQFIRVFIQRPVLPACPCLVQAALHRLVGLGLVQLQIAARIDFVAVGGKLPFRILAAEGIGRNFHQFFIAPAGVWSDVGRCVDDFPHHR  
KTRTFDNLHGNGIRPAAAHFLQDIPSRHFRQSVRPRMQPVVHTQNVGRRRQNMPEHDAVFGKFPADRRTWLPFGNLDVCPAVVFRDKKQREGNGCRYGQKNGSPFQHFQHGRIPISTR  
NFS

**SEQ ID 2545**

CCGCAACCGTCAAAACATATAGTGGAT

**SEQ ID 2546**

LTAHYKIGKSTRIGLDFENVPNKRCRTMPDIHVYGTPRSLTATVKEHVD

**SEQ ID 2547**

APTGGTGATTTCACACCCCGCGAACTTGAAGAAATCAAGACCGGATTCCCAATCTGATCAACATCATCCGGCTCGCCATCTGTTTTCCCGCTGATGATTATGCACATCCTCGGGCTGGAAA  
 CGGCGAGCGGTGCGAACCTGCACGCCCTCATGGACGGCGTGGGGGTTTTACTTTGTGGCTTGCATTGCTGTCTGGCTGATTTCCTTTTTCACACCTCAACCCGCAATGGCAATGGCA  
 GGCCTTGAGAAATACCGAGATTTCAGCGCGGTGGCCGACATCAGATGATCGCGGTGCTGACCTACTCTGTTGGCGCGCATGATTGGGGTTCGGCATCTGATCCTTCTGCTGGGCGAGT  
 TCCCTGCCTACTCAGTTTACGGCGCTTATCCCTGCTCTATGCGCAGCTATGCATCCATCCTGCTGATATTCACCGGCCCTTGCAGACAGCAATATCAATATGTATCCGCTGATCTTGTGATGCAA  
 AAACCGCTCACCAATACTCTGCTGCTGATCCCGGCTCTATTTCGTGCGTATGATGTCCTGCTGCGCTCAGATACATCGACGCTGCGCGGCAAACTTGCCCATGAAAAACACGTCGCTA  
 CGCGCGTATCAGGGGCTTGAACCAAATCGTCTCAACCGCGTTTCAGGAAGCGGTGCTGCTCATCAACGTCGAGCATCAGACCATACTGTTTCAATAAAAAAGGCAAAAGATCTGCTCCCATG  
 CTTGAAATCGGACAGCATACCTCCCTGTTTGGACCTCTGTCGCATCTTATGGGATAAAACATCTCAGCAGCTCTCGAACACCATATCGACAGCGCCGACCTGACCGCCCGCATCGCGCGCG  
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 CCACAGAACTCCGCAACCCGATGTCCCGGCTCCGCCACGCCCGCGCGGCACTTTATTTTGGAGAGTGGCGGACCTGCTGCCCTTTCCATGTGAGCTGAAACTCTTGGCGCGCAATCAAGAA  
 AAGAGCGTGGCCGATTCGCGCACCGACAGCGACCGCGCTGATGTCCCGATGTCGTGCGGCCAACCAAAAAACCTCGAAGCCCTTGTGGAAGCGCGCATTCGCGCAAGACCTGTATT  
 ACCGTCTCAATGTGCTGACGCTCAATATGCCGTCCCTGCGTGAATGCGCGAAATTTGAAGCTGCCACCCCTACCTCTGTACAAACACAGGCCACAACACCGGCCCTACACACTCTC  
 CCGCGCGCGCAACAGATGCTCTGTAATTACAGTTATCCGGGCAATTTCCGCGAATCGAAAAATCCTCGAAGCGCGCGTCCGCTGCTGCGTGGATATACAGTGGAAATTCGACGACCTG  
 CAAATCCAGATGTGCACCAACAAACCCGTCGGACGCGAAACCGCGTCCCGTTGCGGATACCTTTCGCGTGAATAAGCGCCGACCGTCCCGCTTCTCCGTTTCGACCCCGATACCA  
 TCGAGATACAGGATCTATTCGACAAAAATCGAACCGGACATCATCGGACAGTCTCAAACAAACCGAAGCCACCGCACGCAAGCGCGCAACGCTTGGCATCAGCTTCGCTCTATGCG  
 CTACCGTATGAAAGCCCTCAACATGAC

**SEQ ID 2548**

MVI SNPRELEKLDRI PNL INIIRVAI VFLMTMHILGLETGRANLHASWTAMAFYLHLAIA CMLIFFSTLNPQWQHQALRIPSPS AVADITHIGVLT YLFGGIDSGF GILILFFVGS  
 SCILSYGRPLYLASYASITILIPNALADSNINMYPLILDAKT VNTNTFFV VAGSYFVAMTASL SVRYIRDRAGKLAHEHNVA YRRIRGLAQIVIANVQOEAVVWINVBERQTILFNKAKD LILP  
 LEIGQTSILFDPVAILWKTSSRTYEHHDITPEL TARIRAVPMNKKQNLILYIRPOSEIQAELS VKLAALGQLTANLAHEIRNPMSATIRHADGGTFLPDEVA DILPLSMQVKILRATQE  
 KAVRRIGHATEPQVDVVRICLATHKNEALAEVDSAGFLPDDQLYRLMVSLAMPSLREMRENKLLPFTYLLYKHSHNNRNPYLTILSPAAQCMLLNYSPFGNPRELENILERAVALCVGTFYQIDDL  
 QIOQVHHKPRVTEFVAVADTFLSEALAPASGRLLPDDPTMQIQDVLKIERDIIQGV LKQTEGNRTQA AKRLGISPSRMYRMYERLNTD

SEQ ID 2549

ATGAAACCGCAATTCATCACCTTTGACGGCATAGACGGTGC CGGAAAAATCCACCAACCTTGCCGTCATCAAGGCATGGTTTGAACGGAGGGGGCTGCCCGTCTGTTTCA CGCGGAGCGCGG  
CGCGAACCGCGGTCGGTGAGGCCCTTGCGCGAAATCTTGCTCAACCCGTAAACCAAGCCGGTTTGCCTGCGGAAACACTGATGAGTTTCGCCGCGCGTATGCAGCACATCGAGGAAGTCAT  
CCTGCCCGCGCTTTGACAGGGCATCATGATGCTGCCGACCGTTTACCGATGCGACCTTGCCCTATCAGGGCGGCGGGCGGGGGATGCCGTCTGAAGACATTGAAATTTTGGAACTTGG  
GTGCAGGGCGGTTTGCGCCCCGATTTGACCTGCTGTTGGATGTGCCGCTGGAAGTATCGATGGCGCGTATCGGACAGGCGCGCGAGAAAGACCGGTTTCGAGCAGGAGCAGCGCGAATTTCT  
TTATGCTGTGTCGCGCGCTTATCTCGACCGAGCCGCGCTGTGCCGACGGTATCGCCGTATCGACAGTAAACCGCAGCTTGGATGAAGTCAGAAACAGCATAGAAAAAGTGTGGACCG  
ACATTTCCGCTGT

SEQ ID 2550

MKPQF1TLDGIDGACKSTNLAVIKAWFERGLPVLFTREPGGTFVGEALREILLNPETKAGLRAETLMMFAARMQHIIEVILPALSDGHHVVSDFRPTDTATFAYQGGGRGMPSEDIKILEHN  
 VOGGLEPDLTLLDDVPLEVMARIGQAREKDRFEQDADFMRVRGVYLDRAAACPERYAVIDSNRSLDEVNRNIEKVLDGHFGC

## SEQ ID 2551

ATGGAAGAACTCATTTGAAAGAGCGCCCTCAAGTTCCACGAATTAACCCGTTCCGGGCAAAATTTCCGTTACCCCGACCAATCTCTGGCGACCGACAAAGATTGGCGTTGGCGTACTCTC  
CGGGCGTAGCCGCGCCCTGTATGGAATCCATGCGCGATCCGCAAAATGCTTACAAATACACCGCAAGGCAACTTGGTCGCGCTCATTTCCACGGTACGGCGTTTGGGCTGGCGA  
CATCGCGCGCTGGCGGGCAACCCGTGATGGAAGGCAAGGCGTATTGTTCAAAAATTCGCGGTCATCAACCTCGAAGACATCAAGCACCCGAGTGTTTTACATCGAACGCGAATTACGCAAACTGCGCAAAATCCCGTATTTCATGATG  
ATCATCGCGCTTTGGAGCCGATTTTCGGCGGCATCAACCTCGAAGACATCAAGCACCCGAGTGTTTTACATCGAACGCGAATTACGCAAACTGCGCAAAATCCCGTATTTCATGATG  
ACCAGCACGGCACGGCCATCATTTACCGCGCGCGCTATTGAACGCGCTGCGTTATACCGCGCTTAAATCGAAGAACGACTTTGGTGTGCTCCGCGCGCAGGTGCCGCGCGATTGCGCTG  
CCTGAACCACTGCTGGATTGGGCTTGAACGCTGAACCGTAACCGTTTGGGACTCCAAAGCGGTGATTACCAAAACCGCGAAGACAAAGACCGCATGGACGAATCCAAAAATTTCTAC  
GCCGTTGAAGCAACGGCGCGCGCTACTTGGCGATGCGGTAAAGGCAAGACATCTTCTTGGGCTCTCCGCGCGCAACCTGCTGACGCTGAAATGTTGAACACGATGAACGAAAAAC  
CCATCGTGTTCGCGCATGGCAACCCGAATCCGGAATCTCGCGCGCTGGCGAAGAACCCGTCGCGACGTGTTATCGGTACCGCGCGCTGCGACTTCCCGAACCAAGTGAACACGCT  
ATTGTGCTTCCGTTTACTCTCCGCGCGCGCTTGGATGTCGCGCAACCCACCATCAACGAAGAAATGAAACGCGCTGCGTGTATGCTTTGGCAGATTGGCGATGGAAGAAATGAACGAA  
GAAGTGGTTCGCGCTTACGCTAAGAAATTCGAATTCGCGCGCGAATACCTGATCTTCTACTCCGTTGCGATTCCCGCTGCTGCTGCGCTGCGTACCGCTGCGCGCAAGCAGCGATGGA  
CGCGCTGGCAACCCGTCGATTCGAGATTGGAAGCTTACGCTGCCAAGTTGGCGAATGGAAGCTG

## SEQ ID 2552

MENSLKAAALFHELPVPGKISVTPPKSLATDKDLALAYSPGVAAPCEIHADPQNAKYTGKGNLVAIVISNGTAVLGLDIGALAGKPVMEGRGVLPKFFAGVDVFDIEIDEKDPQKLV  
IAALEPTFGGINLIEDIKAFECFYIERELRKRKLPVPHDDQHTAIITAAVLANALRYTGRIIEATLVCSGAGAAAIACLNQLDLGLKRENVTVCDKSGVITYQTRDKRMDSESKPY  
AVELNGRVLADAVKGDIFLGLSGANLLTPEMLNTHNEKPIVFAMANPNFKLPLAKETRPVNVIGTGRSDFPNVNVLCPFPPIFRGALDVGATTINEEMKRAVCYALADLANEVE  
EVVAAYGKRFEGAEYLIPTPDSRLLPVATAAAMESGVATRPADLEAYAAKLEENK

## SEQ ID 2553

TGCGGATATACCGAAACTTCAAAACAAACCGCCCGGTCATGACGACAGGCGAGTGGTGTGACGATGATTGTTTTCATGATTCTTTGGTCAATATCGTTATGTTTGTGTTGG  
CGTTCGCGCAGAGGCAACCCCAACCGTGCCAAATCTGTAAAGCACTGTTCTTATTTACCTTGTGTGCTTCGCTTATCGGTT

## SEQ ID 2554

LAIYPLQNKPPFVMTGQVLMIVFMIPLVNIIVMPVWAFGRGNPNRANPCKALFLFTLLVRLSV

## SEQ ID 2555

TTGCGATATTTCATACAAATCTTCGAAGCAGAATCAGCCGGCAGTAAATATGCGTACCCGATGCGAGCCCACTATAAGCAATATGAAAAATCAACCCGATAAGCGAACCAACAGGTAA  
ATAAGAACAGTCTTTACAGAAATGGCAGGTTGGGTTGCCCTCTGCCAACGCCCAACAAAAACATAACGATATTGACCAAGGAATCATGAAAAATCATGCTCAACCCCACTG  
CCCTGCTGTCATGACCGGGGGCGGTTGTTT

## SEQ ID 2556

LAYSQIFAEBSAGTLINRTRCPTFKYQYENQTDKRTNKVNKNSALQKLARLGLPLPNAQTKNITILTKGINKTIIIVNTHCPVMTGGGLF

## SEQ ID 2557

TTGGCAGCATCAGGCATGAATTTTCTCTTGTGTGGCGGCGCATCGCAGACGCCCACTATCAGGCGTTCGCTATTATGCCACGGTTCGTCGCGGCTTTCAGACGGCATCTGCGCGGCT  
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GATGTGGGCTGCTGCTATACGAACCCCGCTCAGCAATATGATACGCGCGCTGAAGCACTTGGCTGATTGCGCATGCGCGACGCGCTGGCAGACTGACGATGCAAGATCCGCGCGAC  
CGGCTTTCAGACGAATGTTTCAATTTCTCTTACCCTGTCGCTAAGCAGGAGCGGCTGCTGCAACCGCGGTTCAACCAAGCGAGAGCATCTGCGGGTTGTTGGCGCAACGCTACGGCT  
GGCAGATGCTGCGCGACACCGCTATTCGCGACACCGCGCGCGCAAGCAGCTCAAGCGCGCGCAACCGCGCGCAACCAACCGCTTGAATTCGCGACACCGATACCGGA  
AACTGTAATATTGTTTAAATGACGATGCTTTPACCACCGCGCGCAGCTGACGAAATGGCAAGACGCTGAAAAATCGCGCGCAACCGAATCTGCTGCTGACGCTGCGCAGCGACG  
CCAATGAAAAAA

## SEQ ID 2558

LAAGMFLSCWRRRIADAPTIRRCVLCHSSGVSDGICAGCNFTDLASPRTDAAANSCPLFRHVQGGAVCGGQKPPAFDRMWASLHYEPPVSNMIRALKHLADLMAQPLADLTQNPFD  
RLSDECFNFPVPLSRERLLQRFNGQSESVIGLLAQRYGWQILPRHTVFRHRPQSTLKGERRRINKNAFEIRTPPIPEWCNILLIDVFTTGATLDELAKTLKSGANRIICWTLART  
PKK

## SEQ ID 2559

TTGTTAATCCACTATATGTTTGACGGTTGCGGTGAGGCTGCGCGCGCTGCCGTAACGTGAATGTGCGGCATCGTGCAGCGAGCTTTGTTAAAGAGCTTTCAAAGTCCAAACCGATGCGG  
GTGGATTGCGGATTTGTAATGCGCGGTCAAGTCCAGTGTAGCGTATGGGCGTTGGGTCATCCGCTGCGCGGACAGGGAAGAAACCGCATACCGCTGCGCATCCGAAGCGGAATA  
CGGCAACGGCAAGCGCAATCAGCCCGCGCTGATAGCCTTTCAGCTTCAGGACGCTGACGCGCGCAAGAAAAAGACGATGGG

## SEQ ID 2560

LLIHYMFDGCGQARRAVNVNVGHRAAFVKDVFVKVQTDAGGFADFVMRGQVQCSVWGVGSIRLRQGRNRHTRRHPAEFYNGKRNQPLRIAPQLQDQGRKEKDDG

## SEQ ID 2561

ATGCTCGGCGAGACCAACCGTTTGGTCAAGCGGATGCCATGCTGTGTGACAGTATCGAAGAAACGCTGCGCGCTGGCGATACCGGCAACCGCTGCGACGCGCTTCCC

## SEQ ID 2562

MVGQSNRLVKADAHVCQSIEETLRPGDTGNRCALP

## SEQ ID 2563

ATGCCAAATTTTTTAAATTTTACATCCGTTATCGAACGGCATTTGGCAAAACCTTATCCGTTTGTCTTTTCTGCTCAAGCGCTTTCCGGGCTGTTGCCAAAAATGCGGCAAAATGGC  
GGGCGGATTTTTATCGGGAAAAACGGCAAGGAAAGCTGTCCGTGCTGTGGTGTGGTGGCAACATCCACCGCGGCGGAGCGGCAAAACGCGGATTCGCGCGCGCTGTTGCGG  
CTTTCAGGAAAAAGGTGTCAGGTCGCGCATCTACCGCGAGGCTACGCGCGCAGAGCAAGCGGTTTATGATTTGAATGCCGCGAGCGCTGCGGAAGATGCGGCGACGAGCTTTGCTG  
CTGTTCCGTAAAAAGGTGCGCGCAGCGCAGTGGCGAGCGCGTGTGGAGGAGGCAAGGCGGTTGCTGCGAGCGCATCCGAGCTTGAATTTGATTGTCGCGGACGAGCTTTGCGCAT  
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TGGGTTGTTGTCGCGCGCAGGCGCGCGGATGTTTATGCGGCTGTAACATTTTGTGCGGCGCGGATTTGAGGCGGCTGCGGTTTACTGTTGAACCGTCCCTGTGAAAACTGGATATT  
TCGACATTTGTCAGGGAAGCGCTGCGAGCGGTTGCCGATTCGCCAGCGCGCGGCTTCTTCGATACCTGACACACATGGGCATCCGCTTGACCAACCGTTGCTGTCGCCGACCATG  
CCGATATTTTCAATCGGATTTGCCGCTGCCGATGTTGCTGTAATGAAAGATGCGGTCAAAATTTTCAGACGCGATTGACACCGATAATGTTTGGGTGCTGCGCGTTTGTGCGAT  
AATCGAACCTGATTGCGCGAGTTTGTCTGAGCGGTTGGAGGTTTACCGAAGCGCTC

## SEQ ID 2564

MPNFKFTHTVIERHWQKPYVLSFLKFLSGLPKIAAKWRADFLSGKRQSEKLSVPPVVVGNIIHAGGTGKTPIAAALVSLQEKGVKVIISRGYGRKSKAVYVINAASRAEDAGDEPL  
LPRKTGAPTAVGSSRVEAGRALAAHPELEIVADDGLQHYALQRDVEIAVFPADTGTDLDLLPNGNLREPLSRLESVDVAVVGGRAADGMPSEHLFGSRIRAGAVYRLNRPSEKLDI  
STLSGKRVAAVAGIARPPFDLTLMGIRLDQTVALLPDHADIENRDLPPADVVLVTEKDAVKFSDGICTDNVWVLPVCAIIEPLDLAEFVLERLEGVKAV

## SEQ ID 2565

GTGGATATGAAGCTGAAACCTTGTATTGCCCTTCCGCGCACTGGCAITGTGTGCCAACGCAATTTGCCGCCCGCGCGGACGCGCTGTTGGCAGCTTGGCTGGATACCGAGAATTTCC  
ACCGGATATAGAAAAAATATGATTGAAGCTTTAATGCCGATTTAAACCGTATCGCGCAAGACCCCTTCCGCAATGCCGGAAGCGAAAAAGATCAGCGCGCAGAGCTTTAATCC  
TTATCGTGAGATGTTTGAAGATTGATTACGCCCGAAGTGAACAGGCTGTCCGCAATACCTTATTGAAGAAATGCCGTGAAATATACACGCAAGAGAAATTGACGCGCATGATTGCC



TTTTACGGTTCGGCTGTCGGTCAGTCCGTCGTTGCCAAAAATCCGCGCTTAATCAAGAAATCGATGAGTGAATAGCGGTATCTTGGACTGCATTGTCAGGGAAAAATCGCGGCACATCATC  
TGCCCGAGTTTACGGAAGAGTTAGCGCGCATCATCTGCGCGGTATAGTGGAT

## SEQ ID 2566

VDMLKLTLLPFAALALCANAPAPGDASLARWLDTONFDRDIEKNMIEGPNAGFKPYADKALAEHPEAKKDQAAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREITYTQERIDGMLA  
FYGSPVQGSVVAKNPRLIKKSMSEIAVSWTALSGKILARHHLPEFTFELRIICGGIIVD

## SEQ ID 2567

TGCTCGCGCTGCGCTACTATTGTGACGGTCTGCGGCTTCGCGGCTTGTCTGATTAAATTTAAATCCACTATACCGCCGAGATGATGCGCGG

## SEQ ID 2568

LPRLAVLFVRSAAFPCLDLNLHYTAADDAP

## SEQ ID 2569

ATGGAAAAAANTCTTAGACATCTCGTTCGCCCGTTACCAAAAGGCAGGCTGGAATATCATCAGGACAAACAGGAATTGTGGAGCGCTCAGGCGAAGCTTGCTATCCGATTAAAGACG  
GCATTCCTTATATGCTGGAACCAAGACGAGCGTTGAGCGAAGGAAGCACTCAAGCA

## SEQ ID 2570

MEKKFLDILVCPVTKGRLEYHQDQELWSRQAKLAYPIKDGIPYHLENARALSKKEELKA

## SEQ ID 2571

ATGACCGAATTCGTCGATTGATTCGCGCGCGCTGGATTGCTGCGGCTGCCCGGAAAAGCCTTGGCGGACATTCACGGCAACCGATGCTGCGCGCTGCGGAACAGGCGGCAAAAA  
GCAAAAGCCGCGCGCTCGTCGTCGCCACCGATCATCCGACATTCAGACGCGCTGTGAGGCGCAGCGTATCGAAGTCGTCATGACTTCAAAACCGGCACGAAAGCGGCACGACGCGCTTGC  
CGAAGCCGCGCGCGCTGAAGCTGCCGCGCATTTGATTGTTGTGAACGTACAGGCGCAGCAGCGCTGATTGCCCGCAACTCATCGACCGCAGCGCGAAGTACTCGTCGAAAAACAAC  
GTCCAAATGGCGACCGCGGCCAGAAATGACGATTTCGACGAATTTGATGAATCCCAATCCGCTCAAAGTCGTCCTCGACAAAAACGGCAACGCCATCTACTTCAGCCGCTGCCCGGATTTC  
CCTATCCGCGCGATGCGATGCGTGGCGAAACCGGAAATGCGCTGTGAAACCGCGCTCTACGCCATATCGGCAITTTACGCTACCGCGCTGCGCTTCCTGCAACGCTATGCCGAAATGAG  
CGTCTCGCGCTGGAACCATCGAATCGCTGGAACAACCTGCGGCTCTGTGCGCAGGCTACCCCATCGCGCTGAAACCGGCAAGAGCCCGCGCGCTGTGATGATGCGGAGAGAT  
TTGACAGCGGTTGCGCTGATTTCAGACCGTA

## SEQ ID 2572

MTEFVLLIPARLDSRLPGKALADHKGPMVVRVAEQAAKSKAARVVVATDHPDICTACQAHGIEVMTSNRHESGTTRLAEAAAALKLPPLIVNVQDZELIAPELIDRTAEVLVERN  
VQMATAGHLDHDFDELMNPNAVVLKNGNAIYF SRAPIPYPRDAMRAGKREMPSETAVLRHIGIYAYRVGFLQRYAEMSVPLETTESLEQLRVLNHGYPIAVETAKEAPAAGVDTOED  
LDRVRAVFQTV

## SEQ ID 2573

ATGCAGCAACATATTGAAAGTGGCAACACTTGACCGGTGAAGAACAGAAATCCTTGCCGAAGTATGGGGTCTCGTGCAAAACGATGATCAGGAGGTTCACTATGAAATGCTCAAATTGA  
ACGCACCTGATGAAGTCAGCGGTGAATTTGGTTGAGAAATGGCAGAAACACTCAGCACCTGCGGCCCAATCGTTCCCTCGACCTTAGAATGAACGGCGCAGGCTGTGACCGCGGTATC  
CATCTTTCCGTCATGATTGAAGACAATCCGACATACCGCAGCTTTGGCGG

## SEQ ID 2574

MQQHIKQWHL SREEQKILAEVWGLVQNDQEVHYEMLKLNAPDEVSGEFPFRMAETLSTLFPNRSLLDRMNGGRLSTAVSILSVMIEDNPDIPQLHA

## SEQ ID 2575

GTGTCGCTGACCAATAATTGAGGGCGTAATTTTTCACGCCAAAGCTGCGGTATGTGCGGATTTCTTCAATCATGACGGAAGGATGATACGGCGGTGACAGCGCTGCCCGCGTTTC  
ATTCTAAGGTTCGAGGGAACGATTGGGCGCGCAGGCTGCTGAGTGTTCGTCATCTGTAACCAAAATTCACCGCTGACTTTCATCAGGTGCGTTCAATTTGAGCATTTTCATAGTGAACCTCT  
GATCATCGTTTTCACGAGAGCCCATACTTCGCGAAGGATTTTCTGTCTTCACGGCTCAAGTGTGCCACTTTTCAATATGTTGCTGCATATCTTTTCCCTT

## SEQ ID 2576

VSVYQIIIEGNGFLRPLKRYVGIIVFNDKDG YGGRQPAAVHSKVEGTIGRQGAECFCHSEPKFTADFI RCVQFEHFIVNLLIIVLHETPFY GKDFLFPTAQVLEPLFNMILLHIFSL

## SEQ ID 2577

TTGATATTATGCTTACCATCGTTTATATACAGCCGGAATCCCCCGAACACGGGCAACATCATCGGCTGTGCGCAATACCGCGCGGATTTGCACCTTTGTCAAACCGCTCGGCTTCC  
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GACCAACCAAGGCACGCGCGCGCGGATGAAACCGGCTTCAAAAGGCGACGTTTACTGTGTTGGGCGGGAACCGCGGCTGCTCGCGACATCTCGACAGGCTGCCCGCGCGCA  
AAATTCGCGCTGCGGATGCGCGCGCGCAGCGGAGTATGAACCTTTCACACCGCTCTCGTGATTCTCTTTGAAGCGTGGCGGCAACAGGTTACGAGGCGCGCTT

## SEQ ID 2578

LIFMLTIVLYQPEIPPNTGNIIRLCANTGADLHLVKPLGFLDSAKMKRAGLDYHEFASLTVHENFDCLKSLAGRRIPALTTKGTARPDSTAFQKGDVLLFGPETRGLPADILDSLPAAQ  
KIRLPMPGRSRMNLSTVSVILFEAWRQHYAGGV

## SEQ ID 2579

ATGACCGACATCTCATGACGATACCGCCACCGAAGCGCTCGCACCTGATACGGGCAATCCCCCTGCTGCCGCTTCCCAACCGCGGCAACAGGCAAGTACCTCCTGCTGAACAG  
ATACCGTCAGCTCAGGCTTGTGCGGGAAGCAACGCTCATGTCGATTTTACCTCCGCGCGCGCACAAATACCGCGCGCAAAAAGCGGAGGAGAACTCATCGCCAAAGCGGTCAACCA  
CACCGCGCACCCACCGCTATGGGATGCAACCGCAGGATTTGGGCGCGACAGCTTCGTCCTCGCTCGCTCGGACTGACCGTTACCGCTTTCGAGCAACATCCCGCGCTGCGCTGCTGCTT  
TCAGACGGCATCCGCGCGCGCTCTCTCAATCCCGAAACGCAAGACACCGCGCGCGCATCAACCTCCATTTTCGCAATGCGCGGCAACAAATGCTTCCCTTTTAAACACAAGGCAAC  
CCGACATCGTTTATCTGCAACCGATGATCCCGAACCGCGCAAGAGTGCCCGCTCAAAAAGAAATGGCTTATTTCCACCGCTTGTGCGCGAAGCGCAAGATGAGGTGCTCTCTCTTCA  
TACCGCACGCCAAACGCGCAAAAACGCGCTGCTCAACCGCGCGCTCGCGCAACCTTCCGCGCAAGCCCCCGCTACCAATACACCGGCAAAAGCACCGCTTTCGAGCTTTAC  
CTGCCCTACGAGCGGCAAGGGA

## SEQ ID 2580

MTDILIDTATFAVRTLIRAFPLVPVSPPEQGSYLLAEHDTVSLRLVGEKSNVIVDTSGAAQYRRRTKGGELIAKAVNHTAHTVMDATAGLGRDSFVLASLGLTVAFAEQHPAVACIL  
SDGIRRALINPETQDTAARINLHFGNAAEQMPALVKTGKPDIVYLDPMYPERKSAVVKEMAYFHLVGEAQDEVLLHTARQTAKKRVVVRPRLGEHLAQAPAYQYTGKSTRFDVY  
LPYGADRG

## SEQ ID 2581

TTGGTACACGACACAAAGCCGTCGCCGAGGTTTGGTACACAGCCGACAAAGCGGAGAGCAACGAGGAGGAATACCTGACCAAGCCCTGTGCAAAACCTGCTGTAACATTGG  
ATGCCGCACTTGACGTTTCTCTGAAGACGCGTGGTTTCAGGAAATCAACAGGATGCACAAAGCAATTTTGCT

## SEQ ID 2582

LVHGKARADGLVQPPDKAAEANEVEYITKALSONLLSTLDAALARFPEDANFQEIQRQDAQKHPA

## SEQ ID 2583

ATGCACAAAGCATTTTCTTGGAGCTGCGGCTCAGGAATATTTCCATTGAGGAAGAAAGAGTGCCTAATTGGGTATAATCAGGTAATCTTATTTTATTTTCAAGAT

## SEQ ID 2584

MEKSLLEDVAVRNISIQEKKCLIGYNQGRSYFISED

**SEQ ID 2585**

TTGAACGAGGCAAAAATAAACGGCAAACATCTCGGATTAACAAAATTTCAGAATCAAGACAGGGCAATACCATACCGGGTTTGGCCAAACCGCTATAAAATTGCA

**SEQ ID 2586**

LNEAKINGHLGLTKFRIKTGQYHTGFAPTRYKIA

**SEQ ID 2587**

TTGCCCTCGTGTCAAACGGCGGCTCTGATCTCGCGGGTTTCGTGTTTCCGCTATTCCGCTATCCGTCACCGCAAAATGTTATACTGGGAAAAAATCACCAGATTGATTTTACGGCGTATTTCGCCGATAGGATGGAAGAGACAAATGAGCAGAAATCCGGCAGGGCTTTTCCGCTTTTGGATGGCGGAAAGGCATTGATTCCTATATTCGCGGTGGGGCACCACCGATATTTCGGCAACATTTTGGCATTTGATGCACGGCATGTTTGC AAGCGGTGCGGATATTTTGGAGTTGGGGGTCCGCTTTTCGGAATCCGATGGCGGACGGGCGGTTATTACAGCTGCGGCGGAGCGGGCTTTGGCAAACGGGATTTCCGCTGCGCGAGTCTTTGGATGTCGTCAGAAAAATCCGTGAAACCGACACGCAAAACGCCGGTGTGTTTGGATGGGATTTGAAATCCCATACATAGAATGGGTTATCCGGAGTTTGTCTCAGGAAGCCGCAAAGGCGGGGTGGACGGCTGTGTAGCGTGGATTTCCGCCATCGCAACATCGMTCTTTATATTCGCGAGCTCAAGGATACAGAGTCGACTGTATTTTCTGATTCGCCGACGACGACGGAAGCATGATATAAAACCATTTCCGCGGTGCGGATTTGTCTATATCTTTCGCTCAAGGCGCTAACGGGCGCGGCAAGTTTGGATACGGATGAGGTTTTCGCGTAAAAATAGAGTACCTTAAGCAGGTATATTCGATATCTCCCATCGGTGTGCGGTTTCGGCATCAGCAATCGGAAAGCGCGCGCAAAATCGGCCGGGTTCCGCCGCGCATCATGTCGGCAGCCGGATTTGTGAAGAGATTGAAAAACAATGCGGGCAACGAGGCTGCCGCGCTCGGTGCTTTGGTCAAAGAGTTAAAGGATGCCGTGCGC

**SEQ ID 2588**

LPSNGSGSLRFGCLFYSPIRTANVLKGIHRLYFTAYLPIGWKQMSRIHQAFALDGGKALIPYIAGVDPDTRITTLALMHGHWASGADILELGVFPSPDMADGVPYIQAARALANGIS  
 LRDLVDVVRKFRETDTQTPVVLMGYLNPIHKGMYREFAQEAAKAGVDGVLTVDSPETIDSLYRELKNEVDCIFLIAPTITTEDRIKTIARELAGGFPVYVSLKGVGTGAASLDTPDEVSRKIE  
 YLRQYIDIPIGVGFGISNAESARKIGRVAIAIVGSRIVKEIENNAGNEAAVGAIVKELKDAVR

**SEQ ID 2589**

TTGTCCATGAGCTGGT TAGATAAAATCTGCCACCCAAAATCAAGAATCGTGGGAAAGACGGTGCTTCCAATGTTCCCGAGGGTTTGTGGCCAAATGCCCGTCTTGTTCGGCAACCGGTT  
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TAATGTCAAACCGACCGATCTCTTTGAAGTTTAAAGACAGCAAAAATATTCGCGACCGTTTGAGTGGCGCACGCAAGCTGACCGGGGAAGATGACCGCTGGTGGTGATGAAGGGGATGATG  
AACGGTCTGCCGCTGTCGTTGCCCGGTTTGAATTCCGCTTTATTCGGCGGTTCCGATGGTTCGGTTGTGGGCGAGCGTTTCGTACAGGGTGTCGCCGTCGGCTTCCCGATATTTCGCGT  
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GGTGTCGACCGATCCGACTATGGCGGCTTATCTCGCAGCTTTCGCAATTTTAGCGGATGTCGATGTCGCGAAACCGGAACCGCGCTGATCGGTTTTCGCCGCTCCGCGCTGATTGAGCAGAAG  
GTGCGTGAAGACGCTCCGCGAAAGAGCTGCCATCGCGCGGAGTTTCTGCTGGAAAAAGCGCGATCGACCAAGATTGTGTCAGCCGCGGATATGAAGCGGCGCATCAGTGATTGTAATACGCTGT  
TGTGCCGTACGGACAAAGTTTCCGCCACC

SEQ ID 2590

LSMSLDKIILPPKIKNRKDGASNVPEGLMRRKPCSCSATVYSTELQNNQVCPKCNHNHPLSARQLNLLLDEEGREEVAGNVKPTDPLKFKDSKKYPDRLSAARKLTGEDDALVVMKGM  
NGLFVVAAFEPRFYIGGSMGSGVGERFVQGVRRVADNCPFVCAASGGARMQEGVNSLMQMTXTSAAHLHLLTEKRLPFLSVLTDPTMGVVSASFAGLDVVLAEPNALIGFAGPRVIEQT  
VRETLPEGFORAEFLLEKGAIDQIVDRDMKRRISDLITLLCRQDKVSAI

**SEQ ID 2591**

TTGGAGAAACCTTATGCGCCGCGCCATCTCTTGATTTCTGACCCTGACTGTGCGCAGCTCCCTTGTCCGCCGGCTTCAGCCAAAAAGACACGCGGATCAACACCCGGCTACCCGCGAAACGCGCG  
AAGAAGCCGCGCCGCCGGAATTTAAAGAACATACCGCGGAAGCTGCCGCCCTCTGCCCGATGCGCACTCGGACGGCTGGTTTGACATTTATGTGGATGAAATTTACGGCAACACGCCGAAAT  
CTGCTCGACAGCTGCAAAATTTATGCCGCGCCCGACGGCAGCATCCGCTACATTTCTCAATATCCGCTCCGACAAAGGCTACGACAACTTGACTCGCGAAGGCCATATTTCTGCGCCGCTCC  
TCCATCGGGTTTCGGCAACGGCAAACTTTCTCTCTACAAAGTATTTCCGATACGGCGATACGGTCAACAGCCGCTGGATACAGCCCGCGAAGTCGGAACTGGAAACCTATAGCGCGCACATCTG  
GGCGCAACGACGCAATTCGCGCGCGTCTGTATCAGGCAATTTCTGCGAGGGCGGCGTACCCTCCGACACGCAAGGTTTGGTACAAACGCTGAAAGAACGTGCGCGGACGCTATGCCCGCTGAT  
GAAGCCGACGACATG

**SEQ ID 2592**

LEKIMRRRAILLILITLVGTSLAAGFSQKDTINTRYRETPEAAAREPFKEHTAEZLPPLDAHSDGWFIDYVDENYGKQPKILLDSLQIMPAPDGSIRYILNIRSDKGYNLTAEGTFCARS  
SIFGNGEKLSSYKVFPGYGLDTNSKTIOPRNAEWKPIGGTLGRNDALRAVLVYQAFCEGGVPADTQGLVORLKERAGRYAPSMKPHDK

**SEQ ID 2593**

GTGCGGGCTCATCGACGGGGCATAGCGTCGGGCACGTTCTTTTCAGGCGTGTGATCAAAACCTTGC GTGTGCGGGGGTACGCCGCCCTCGCAGAAATGCCGTATACAGGACGGCGGCCAATGCG  
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ACCCGATCGGAGAGCGGGCGCAGAAATATGCTTCGGCAGTCAGGTTGTCGTAGCCTTTTGTCCGAGCGGATATTGAGAATGTAGCGGATGCTGCCGTCGGCGCGGCCATATTCGACGGCT  
GTCGAGCAGGAATTTTCGGCTGTTTGCCGTTAATTTTCATCCACATAAATGTCAAACGACCGCTCCGAGTGCGCATCCGGCAGAGCGGCAGTTTCGGCGGTATGTTCTTTAAATTCGCGCGCG  
GCGGCTTCTTCGCGGCTTCGGGTTCAGCGGGTGTGATCGGCGGTCTCTTTTGGCTGAAGCGCGGCCGAAGGACGTCGCCAGCAGTCAGGTCAGAATCAGAAGGATGGCGCGGCATAA  
GGTTCTCCAAATGAAAGCGCTTTATTTTATGTGTTTGGCGGGAAGGGCTGCAAGCAATCGGGGTATAATCTGACC

**SEQ ID 2594**

VLRRHRRGIASGTFQALYQTLRVGGYAAALAECLIQDGAQCVVAPKCAAYRFPFGVSGLYPAAVDRILAVSEYFVGKGFAVAEPPDGGAGAEYAFGSQVVAIVPGADIENVAADAVRGHNLQA  
 VEODPRLFAVIFIHINVKPAVRVRIQORRQFGMFFKFAAGGGFFGRFAVAGVDRRVFLAEAGGKGRADSGQGNQDKGAHKFLQIENGFLILFPGGKCKQSGSYNLIT

**SEQ ID 2595**

ATGAACAGCGAAACTTTAGACGTAAACGGGATTGAAATGTCCTCCCTGCCGATTTTTCGGGGCAAAAAAGGCTTTTGGCGCAAAATGCGGCAGGGCGAGGTATTGACCGTCTCTGGCGCACCGACGGCG  
CGCGCGCGGGGCACTTTGAGGCTTTTTCGCCCAAAACCGGTCATGTCTGTGGAATCTTCCGAACAGGACGGCGGTGTTCACACTGGTCGTCAAGCACAAA

**SEQ ID 2596**

MSSETLDVDTGLKCPLEPIIRAKKALAO MROGEVLT VLTATDGGAPGDFEAFCRQTGHVLLDSSEQDGVFTLVVVKHK

SEQ ID 2597

TTGAACGCGTGGCGCAACACGGTTACGCAAGGCGCGCTTTGAACGCGAGGTTTCATGCCGCTCGTAAACCGTTTCGGACACATTCCGAACCGCTGCCCGCAGCGTGCGCGGGTTTCGGAACGCGTCCGTAGGCA

SEQ ID 2598

LRGGNTVTOAAFERRFMPSNRSDTFRATAAACGGSEVRRA

SEQ ID 2599

TTGATGTTATTGCTGTGCGCATTTTGTGCTTGTCTGCGTGTAATGCGCCAAAACCGGCAATCTCGGTGTACGGCATCAGGATTTTGCACGCGTAGCCGTGATTTGTGTTTCGGAGTGCCCTGCGTCC  
TGACTCAAGGTAGTTTTCGACCGGTTTCCAAGTTTTCGCGCTGTGCGGACATTTTGTCCCTGTGCGAAAGGAAGACCTGTCCCGCTGCCGCCCGCTGTGTGCAGAACCCGATGTACAGCGTTC  
GTGGAGCGCTTGAAGCGGATGGCGGCATTTATTATTGTAGGCTGACGCGCGACAGTGTGAGTGTGAAAGCCGAGCGGGCAGACAGTGCCCGCGCTTTTGGAACATTTCTCAGGGCTTGTCCGA  
CAGCGCCGCAAAAATGCCAATATA

SEQ ID 2600

LMLLLSAFLAACNAQNRQSGVRHQDFARVAVDLFRSACVLTSQSFEPVSKFAVGVHPVPVGKEDLSRLPPAVARPDVQALWFLERDGGITYYLSLTRDSCSVKAERADSAALEHFSGLVR  
 OPPKNVLA

## SEQ ID 2601

TTGACTATATATGCGCATTTTTCGCGCGCTGTCGACAAAGCCCTGAGAAATGTTCCAAAAGCGCGGCACTGTCTGCGCGCTCGGCTTTCACACTGCAACTGTGCGCGCTGAGGCTCAAATA  
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TTGGAACCGGTTGGAACCTACCTTGAAGTACGACGCGGCACTCCGAAACAAATCGAGGCTACGGGTGCAAAATCTGTATGCGGTACACCGGATTGCGGTTTGGGCAATTACACGACG  
CAAGCACAATTCGACAGCAATAACATCAATCAGGACATCCGCAATTCAGACGCAATTTATTTGTGCT

## SEQ ID 2602

LTIYWHFSAVQALRNVPKARHCLPARLSHCWCRASGSNNKCRHRVQASTTPVHRVLQORADGTGLPFRQGNVRQRTWKIPVKNYLESRRHSETRRLRVQNPDAVHRIAGFGHYTQ  
QAQMPATTSIRTSAPQTAFICA

## SEQ ID 2603

TTGTACGCGACGCGCTTTGCCATGCGCCCAACAGATGCGGATGGCGCGCAAAAAGACCGCGCTTACAAAAGGACAGACCGCGCCAAAGTAACGCATTATTGACACGCGCGCGG  
GATTTTCGCGATGCCAACGCGTTTGTCCGATGAAACAGGATTGACGCGCGCTGTTCGCGCTTATGCCGCGAGCTTGAAGGGCAAAATGCGGAAGCGCGGATAAGTGGGAAAAGATA  
CGGCGCTTATCTTTGGTGTCCGACAAATCGGCAACCGCGGATTGCTCCGATGTTTGTCAAAATACGGTGGCGGGGTCTTTTGAAGCGCGGTTTCAGCAATGCTACTGCGCCCA  
TTGGCTCAAAAATCGGTGATTATTTCAGATAATGCGCGATTTCGCGCTATGGGTGCTTACGGGAACGCGGGAATAATGGGACATAAGGTATTGCTCCCGCACTTGTTCGCGCGAGC  
CCAACCGGATTGAGAAAGTGGGCGAATATTAAGCGGTATTCGGAACCGTTTGTCTGATTACGCGCGGATTGACGATGCACACTGTCTTATTGATTTAAT

## SEQ ID 2604

LYGSRRLPCAQTADGAQKTAAYKQDPKAVTHYLTRPAGFSDCQRVCPDETGFDRRLFRPYARSLKGQMAKARISGKRYRRLSLVSAQVGNRPIAPHVCQNTVAGVFFEARPOCCLLPA  
LAQKSVIISDNARFRMGALRGTAELGKHVLPAPCSPEPNPIEKVWANKRYLRTPVLSYARFDDALLSYDFN

## SEQ ID 2605

ATGCCATCTCTGCGGACTTAAGAAAACAAAGCTTTAAACCATAGCGGATTAACAAAATCAGGACAGGCGCGCGCGCGAGAGCGGTACAAATGGTACGGAACCGATCCGCGCGCGCTCC  
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TCAAGAAAACAGCTTTTACCTGCGGATTGCGCTTAAAAAACAACAGGCAGCC

## SEQ ID 2606

MAYSADLRNKALNHSGLTKIRTRRAADGTNGTPIRPAHLHRESFPLSRGATPYRFLIRYITDNAKTPAKPQRLTCQETRTCTGALKNKQAA

## SEQ ID 2607

GTGACGCGACCGTTTGAACACAGGCAAAATCAGTATGCTTGGCGGGAATCGGCGAGCCCTGAAGAAACCGTATGACCGCAAAAACCGCGGATTCCCGGATTACCGGTACAGGCACTAT  
TGAACCTAACGCAACCGTTCCCATACGGAACCCCTAATTTCTCC

## SEQ ID 2608

VQAPPETRIQISYANRESGSPRETVLTAQTADSPDLFVQAVLNLTHRSNGKPLILP

## SEQ ID 2609

TTGTCAATCCACGGAAGTGGGAATCCGATTGCTTCACTTTAGTTGTTTCAAGTTTCAGGCAACTTCCAAACCGTCAATCCCGGAAAGTGGGAATCCGGA

## SEQ ID 2610

LSFPRKWSDFSFSFCFQVSGNFQTVIPAKVGIRK

## SEQ ID 2611

ATGAATACATACATTGAAAACTACCTTGACCTCTGTTCGACAGCCCTTGCATTGTCTGCTGACCATGATTCTCAATACGAGCAGCCCAAGTCGAAGTGGCGAAACCTTCCAAAACG  
ACACATCGGTTTCTTCCATCCGCGCGGTGATTGGGTGGGATGACTATTTGCGGACCGCGCTTGCAAAAGCTGATCGACATCGCACTCGAGCGCAATACCACTTTGCTACAGCGGT  
ATTGAACACGGAATCTACCGCAAAACATACATGATCGAGCGCAACCACTCTGCGCCACGCTTGGCGGCAATCGGAACGGCTCGCGCCAAAGCAGCTTGAAGCGCGCAATGTCAGCAGC  
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GCAACCTTGATTACCGCTCGATACCGAAGACTTGGCGCGGTTTTCGCTTGGCAAGCAGTTTGTGTGAAAACCTGCTGCGGTTTGTAGTTCCGAAGTATTGCTCGACCGTCCCG  
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ATTGTTGCTTATGAATCCGCGCTTCAATCCGCTTCAAGACGTGGCAACGCAATGCGCGCGCGGAGCAGCTGGATAAGCTTATGAGCTTTAAGCAACAAAGCGCGCTTAAAG  
AAGCGTTGCGCTTGGTGGGACTGCGTTACAACACGCGGTATCCGCGCGCTGATTGTCTGATGCGGAACGCATCAGCTATTCGCGGGAAGGTGCGGCTTGTGCGCAACCTGACCGG  
CGCGGAACCTTCCGATTGTACAAGCGCTTGGCGCGGATTGAAACGCGATACCAAAACCGCA

## SEQ ID 2612

MNTLTLTSLTVAAPALSACTMIPQYEQPKVEAETPQNDTSVSSIRAVDLGNDYFADPRLQKILIDIALERNITSLRTAVLNSEIYRKQYMIERNLLPTLAANANGSRQGLSGGNVSS  
SYNVLGAASYELDLFGRVRSSEALQGYFASVANRDAHLJLIATVAKAYPNERYAEKAMSLAQRLKTRREETYKLSERYKAGVISAVALRQOEALIESAKADYAHARSREQARNAL  
ATLINRPIPEDLPAGLPDLKQFFVEKLPAGLSSEVLLDRDIRAAEHALKQANANIGARAAPFPSSIRLTGVSVTGSVELGGLFRSGTGWAFAPSIITLPIPTWGTNKANLDVAKLRQQAQ  
IVAYESAVQSAPOVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHVSGALDLDLDAERI SYSAEGAALSAQLTRAENLADLYKALGGGLKRLDTQTK

## SEQ ID 2613

TTGTTCTTTTAGATTTTTGGTTTCCAGACGCGATGCGGACTTTATGCGCTGGAAGTACGGGAGAATAGGGGTTTCCCGTTATGGGAACGGTGGCTTAGGTTCAATCTGCTGTAC  
GGGTAATCCGGGAATCGCGGTTTGTGCGGTCAATACGTTTCTTACGGCTGCGCGATTCCCGCCAGGCATAGC

## SEQ ID 2614

LFLFRFLVSRHADFPSEVRGELGVSRVNGALGSLIPVRVNPGRFRVRSIRFLQCCPIPARHS

## SEQ ID 2615

ATGCAACCTTGACCATCATCGACCCGACGATATGCACCTGCACTGCGCGACGCGGACGCGCTCAAAGCGTTGCCCTTATACCGCGCGGAGATGGGCGCGCGGCTCATCATGCCCA  
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CACGCGGAACTCGTGGCGGAAGCCAAAGCGCGGATCGTGGCTTCAAACCTTACCCCGCAGGCGCGACCAACATTCGATTCGCGGTAACCGGCTGTTCAAGCTCATCCCGTG  
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CGCAAGTGGCGAATCTCAAAGTGGTTCGAACACATCAACCGCGGAAGCGCGCGCTGTTTGAAGCGGCGACAGCTTGGCGCGCGGTTACCGCGCAACACCTCTGCTCAA  
CGCAACGACTCTTGGTGGCGCGGTGCGCGCCATCATTTCTGCTGCGCGCTCAAGCGGAAACCAACCGTCAGGATTTGGTGGCGCGGTTACCGCGGAGAGGCGCAAAATTC  
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GCGCGTGGCAACCTCGAAGCTTCGCTCGCAAAACGCGGCAAGGTTCTACGCGATTCCGGAACCGCGGACAGGATACCTTGTCAAACAAAGCAACCGTTCCCGCAAGCGTCC  
TTACGCGGACGCGGAACTTGTCCGATGCGCGCGGCGGCAATCGGCTGGACGGTGCAGTAT

## SEQ ID 2616

NQTLTIIRPDDMLHLRDGALKAVAPYTRQMGRVIMPNLKPVVSVADALAYKARIMAALPEGSAPFELMTLYLTDQATPELVREKAAGIVAFKLYPAGATTNSDSGVTDLFKLI PV  
LEZHAQKQILFVHGEVVDPEIDIFDREAIFGRVMKPVLAQVPMKVVFEHITTAEARLVLREAGDNVAATVTPQHLLNRRNDLLVGGVRPHHFCPLVLRRETHRQALVAATVTEKAKHF  
PLGTSAPHAKSARENACGCAGMFSAITAELYAEVPEKAGALDKLEAFASKNGARFYGIPENADTTILVKQSQTVPASVPYGDGLVPMRAGGEIGMTVQY

## SEQ ID 2617

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TCGCGTGAACATACCGCGCAGCCGAGCGCTTTTCGCGGATTTCGCGTGCGCCGCCGAGTCCGTCGCCAGGAAGAATTGTGCGCGCTTCGCGCGTAACGCGCGCAACGTTG  
CTGACGGTGGGTTTCGCGCTTTCGAGACCGCGCAGGACAGAAATGATGGGGCGCACGCCCGACCAAGAGGTCGTTGCCGTTGACGAGGAGTGTTCGCGGTAACGTTGCGCGCAACGTTG  
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ATTGGTGTTCGCCCTGCGGGTAGAGTTTGAAGGCGACGATCCGCGCGCTTTCGCTTCGCGCAGGATTTCGCGCTGCGCTTGGTTCGCTCAGGTAAGCGCTCAGCGGCTCAACCGG  
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GGGCAACGCTTTCGAGCGCTTCGCCGTCGCGCAGGTCAGGTCATATCGTGGTCCGATGATGTCAGGTTTCGATGTTTCCTTTTATAGATTTTGGTTTCAGACGCGATGCCG  
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## SEQ ID 2618

LTVQSLHRRPADFAARHRDKFAVAVRDACNGLALFDKGNRVGVFRNAVEPCAVFRGEFVQRAFFKHFVKLVDSGHRAEHTGAAAGVFFGFGVRRGVGAEEFVRLLAGNGDQC  
LTVGFALEDQAEEMGAHAADQEVVAVEQEVLRNGGGNVVAGFQNEAGFGGGDVFEHDFEIRHLRQNGFHHAPDKGFAVENVDGFGVYFVAVNEQDALCHFPQHGBLELQVGYAGIG  
IGGRACGVFEEDDAGGFGFAHEFGRGLVQVQRHQRKRAAFQRRHNRVFKRVGYADDWRFVGHDDGAPHLAGGIRNGFERVAVAVQVQVHIVSGDDGQGLHGCSPDLDFWPDGMP  
TLCLKSGEN

## SEQ ID 2619

ATGAAACAGCCCGCGCGCTTCGCCGAGCTTCGCGTACAGCGCTTTACCAATCCCTTATCAACCGCACCGCGCGCGCGAAATTGCTAAACATCCGCGAAATGTCGACTTTGCCA  
AAGCGGACGAAGAATGTTCAACAACCTTCTTCGCGCACAAACCAATGACGCGACTTACATCAAAAATCCGCGCGCTTCGACAGGAGCAAAAGACCTCAACCCCATCGAAG  
CGCGCTTTCGTCAGCGCTTCGCGACGAGCTTCGCTATGCCGCGCGCTTACCGCGCTATCAACGAAGCATCGAAGTTACCAAACTTCGCGCGCAGGACGCGCGCAAAATTC  
GTCAACGCGATCTTCGCAAACTCGCGCGCGCAATCCGCGCAGAGCGCAACGCGCT

## SEQ ID 2620

MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFPGTQNAADYIQKIRPLDRDEKOLNPIERAVLLTACHELSAMPETYPVPIINBAIEVTKTTCGTDGKHF  
VNGILDLAAQIRDEPKRR

## SEQ ID 2621

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CGCGCGCGCGCTTTTCATGATTTTCCTTGAACGGTTCGCGCGCAGGCTATCGCTCTGAACCGGAAGGGCGCATCGGTGTACGCGCTTGTGTTATCTTCGCTTCAAACTGCTC  
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ATCGGATGTTG

## SEQ ID 2622

LNGQAKRLKGQTAFFVYPIRIFRVSTAFGLVMADLGGFEVDAVDFVVRAAEGFNGDFVNDGVRFGHSGKLVAGGQNGAFDGVFVFPVVEQRADFLDVRCIGLCAEEFV  
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IGML

## SEQ ID 2623

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## SEQ ID 2624

MPSETERAHRCTPCLLFFVFKLFPEQKVDVGFYDGGIRGFFSNFPNCLRVVFGGQDGVGNRNVVBCDAADPCAGFVGNQLEMVGPATDDADGNQVFPGRGKVHQRDGFKRAG  
YGGDGVFVQYQFLGAAADFEHLAADFVGEACLYDADAEVFAVEVGGDVHVSFGIRGFGMPSBGFSLAAASRQRFGHCRLLQAPTCLRLRVGKAVRFQWFW

## SEQ ID 2625

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## SEQ ID 2626

LPTGSRKTEFPRRHSETPNTKGHPMNTIAPNLDGKHLRIGIVQARFTNEIGSQMLKVCCTRLQELGVADENTIVATVPGALETPIALMNFASSEKFDALIAIGVIRGETYHPELVANESG  
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## SEQ ID 2627

ATGAACGCAATTGCAACAAGCACTTTCCTCGGCACTTCGACGCTGCAATCGCCACCAACACCGCTCGCAAAACAAACCGCGCGCTTCCTTTACCGGAAAGCCCGCTTTTGAACAG  
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TTCCCAACCGAAGGCGAGCGCTGGGAGCTTCGCAAGACGCGACATTCCAACCGTTGCGGACTGCGAGCGCAAGC

## SEQ ID 2628

MNAFAQALSSALDRCIATNTVAKQNRVPGLYREAPVFNDSGWRFFSGDETDEYTDPDFNSTVSLADITKTNPETALLSQPEGSANWELAEQGTQTVADWQPDQ

## SEQ ID 2629

TTGGAAAGCAGTTCGCGCGTTTCAGGTTGCTTTGCTGATGTCGCGAGGCTGACGATGCTGAAGTTGTCGCGGTCGTCGCTGTTTCGTCGCTTCGCGCGTGAAGAAACCGGAG  
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## SEQ ID 2630

LKGQCGGFRVFGDVEADDAEVVGVGVFVAAEETPAAVFVNGGFAVKADGPVLFGDGVGDDAAVECRGKCLCKVHCNTLGGGKLADFTTIPALSADGGGLVVQCAPFAALRC  
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## SEQ ID 2631

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CCGCTTGGCTCGCAGGAACGCGCGCGCAAGCGGACGAGCGAGCGACCGGATGTTGCGGCGGTAAGTACCTCCGCT

## SEQ ID 2632

LFLRKTLFLITAAFGTHSLQTASADAVVKPEKLHASANRSYKVAEFTQTGNASWYGGFRPHGRKTSGGDRYDMNAFTAARKTLPIPSHVRTNTKNGKSVIRVRNDRGPPHGNRIIDVSKA  
AAQKLGFPVSGTAHVKI EQIVPGQSAFVAENKDIIFLDLSPGTGHEAQAYLNQAAQNPFASSSSPNLSVEKRRYEVVKGFPFASQERAAEAQAQGMVRAVLPSG

## SEQ ID 2633

TTGCCGTTCTTATGCAAAACGAGAAACCGGTTTTTGGCTTTTCGACTGTTTTGGATAAGTCATCACACCTTAAAGTTTGTCAATCCCAAGGAGTGGGAATCCGATTCTGTTCACTTTAGTTG  
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## SEQ ID 2634

LPFLCKRETGFCVSTVLDKSSHLKVCHSHSGNPIRSVLVVPKQATSKPSFPRKWESGNERQQEFIVND

## SEQ ID 2635

ATGCGTTTCATCATCCAAAAATACAGAAACACCTTAAGGCTGCAACCGCGCACATTGTACCACCAACCGCGCGCTCTGCGGACACCGCGGAATCGTGGTAAATCCGCAAGTTTCC  
CCCCCCCCAAGTATTCGCGCA

## SEQ ID 2636

MRFFTFKIQKHLKAANGAHCTTKPPPSADNAGIVVKSASFPPPNVFPQ

## SEQ ID 2637

TTGCGGAAGACGGTAATGAAAGACGATGTTTGAACCGCGAGGCACATCTGCGATACAGAAAAAGTTAGGCTACCGGTTCCCGGATATGTCGCTTTTGGCGGCGGCTTTGACCCACAGGA  
GCCATCATGCGAAGCACACGAACGGTTTCGAGTTTGTGCGCGATTCGATTTTGAATATACGGTGGCGCGATGCTGTTTACCGGTTTCCGAAGTTGACCGAGGGCGAGTTGTGCGCGTT  
GAGGCGAGTCTGTCAATGAGGCGCTGCTGCGGAAATGCGCGCGAAATGAATGTGCGCGACGGTCTGTATTTGGGGCGGCGGAGTTGAAGAGCAGCGGCTTACGACGCGCTTCGATA  
CTGCGGACGCGATGGAGGCGATGTTTCCCGCGTCAGCTTCGATGCCGATTTCAACACCGCGGAAAGAGTGGTGGCGCATTTTGTTCGAGAAGCGCTCCGCGCGCGCGATTTCCAAATC  
AGGCAAAAGACGCGCAAACTGCTTTTCAGGAGGCGTTTCAGGCGCGCGCTTTCGCTTTCGCGAAATACCGCATCGAAGAGCAAAATCGGCCATGCCGACGACAGTATGTTGTCAATTCCTG  
CGATTTGGCGCAACTGGGTTTCGTGTGCGGTGCCAAAGGGACGAGCGCAAGCGCGCGGAACAGGAGCGCGCAAGAGGCTTTGAAATGCTGGAAGAGAAGCTCCCGCTGAAGAAGAAAA  
AAGAAA

## SEQ ID 2638

LRRFTVMKDDVLRKQHTAIQKKLGYAFRDMSLRLRALTHRSHEAKHNERFEFVGDSILNYTVARMLDAPFKLTGELSLRLASLVNEGVLAEAAEMNVGDGLYLGAELKSSGFRPSI  
LADAMEAMFAAVSFDAFNTAEKVVRHLFAERVRRADFPNQAKDGKTALEALQARRFALPKYRIEBQIGHADDSMFVISCDELGLGFPVCRAGKTSRKAABQEAKEALKWLEKPLPKK  
KX

## SEQ ID 2639

GTGGATATGAAGCGAATATGGATATTTGAACCTTCTTGCAGGGGAACGCGCGCGCGCGGATACCGTTGCGGCTTCGTGGCGATTGTGCGTCTGGAAGCTGGGCAATCAACGCTGA  
TGAACCATCTCATCGGTGAGAAATCAGTATTACAGCAAAAGCGCAGCAGCGCGCAACCGGTAACGGGATTTATACCGAGATACCGCGCAGTTCTGTTTGTGCGATACCGCGGG  
CTTTCAAACCGACCCCGCAACCGCTCAACGACAGGCTGAATCAAAATGTTACCGAGGCGCTCGCGCGTGGATGTGTTGTTTCTGCTGCGAGGCGATGCGCTTACCGATGCGCGAG  
CGCGCTGTTTGAACCACTGCCAAGCACACGCGGTCATTTAGTGATCAACAAATCGACAAGGACAAGCGCAAGAGACCGTTACCGCTGGAGGCGTTTGTTCGCCAAGTCCGCGCGG  
AATTTGAATTTGCGCGCGCGGAGGCGGTTCAGTGCAGAACAGGTTTCGCGATTGCCAACCTGTTGGAGCTGCTCAAGCGGATCTGCGCGAAAGCGTACCGATGTATCCGGAAGACATGTT  
TACGGACAATTCGCGCGCGGTTTTCGCGATGGAATCGTGGTGAATACTCTTCGCGTATTTGGCGGAGGAGCTGCTTATGCGATGAACGTCGAAGTGGAGCAGTTTGAAGAGGAGAGC  
GTTTGAACCGCATCTACATCGCGTTTTCGTCGACAAAGAAAGCAAAAGCGGATTTGATCGGTAAGGCGGGGAGCGTTTGAAAAAAATTTCCACCGAAGCGCGGCTGGATATGGA  
AACTGTTTGAATACAAAGTATTTTGAAGTCTGGGTCAAAGTCAAATCGGTTGGCGACAGCATTCGCTTCTGCGGAGCTGGGTTG

## SEQ ID 2640

VDMKANMDETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTNRNVTGIYTDTAQFVFPDTPGFPQDHRNALNDRLNQHVTALGGDVVVVFVEANRLFDAD  
RVVLKQLPKHTFVILVINKIDKAKDRYALEAFVAQVRAEFPAABAVSAHGLRLIANLLELLKPLPESVPMYPEDMVTDKSARPLAMEIVREKLFVRLGELFVAMNVEBQFEBGD  
GLNRITYLAVLVDKESQKAILIGKGERLKKISTEARLDMKLFDNKVLKVVVKVSGWADDIRFLRELGL

## SEQ ID 2641

TTGCCCCCGCCCGCACCAAGAGGCGGACGCTGATTTCAGAGCGCAAAAGCGGGGGATACAGGCAAAACCGCTTACGGCAGTAAAAACCGCAATTTATGAAGTCGCTCGGCGCGG  
GGTTACGCAAGACGGTTGGGAAGGGCTGCTAATCCGAACCGCAAGGGCGGGAACCGCGCCCGCAGCGGATATTCGGAAGCGGGTGAATACCGCATAGACCGTTTGGACGCGTT  
CCGCGACATACGATATTAACGCAAGACACAGAGCCATTTTCTTAGTAGAGGCGGAGATACACTCAAGCCGTGCAAAATTCGCGGCTACCGGATATATTTGAACCGCGACGCTC  
AACCGCTGGTAAAAAGCGTATTGAACAAATCAGCTTTAAGTCTGAAGAAGAGGCGCAGGTGCGGAGGCGCAGCGCGCGCAAAACCTGTCGCGCCAGGCTACACGGCGCGG  
CGAGGATATTCGCGGATCCGATGGAATTACCGACGCGCTCTTGGCTTCCCAAGCTGGGCTACCGCTTTCGCGCGGAGGATATGTCGCGCGGCTGTTTGGAGGATACCAACAGCGTTACGA  
CATCCCGGATATGACGCAAAACAGTATTACGTTACGAGCAGGCGGAAAGTTAGAGACAAGAGCGGGGTGACGACGCGGAGGATTTCGCGGACGCTTGTATTTGTGCGCAATA

## SEQ ID 2642

LPRPGTKEADLISDGKSRGIQAKTAYGSKNRQFMKSLGAGFSKDGWEGLLIRTERQGRETRPHGDIADGVEYIDRLDAFRQYTDIKRKTTEPFLVGEENTLKPVAKIAGYIYLNRL  
NRWVKERIEQNPLSAEEREAQVREARHENLSAQATTGGGRILPDPHYRSGSWLAKLGYRFGGRHYVGVFEDTKQRYDIRDMFENSITVTRRSLSTRAGCTPATISATACILCRI

## SEQ ID 2643

GTGTACGACGCGGACGATTTCGCGACGCGCTTGTATTTTGTGCCGAATATAGAAGAGTGAAGGGCGATAAAAAATTTGGTCAAGGCGATAGTTTGAATATTTCCCGACCAAAATTTATG  
ACGAACATCACCGCCCGCGGATGGGTTTGTGTACCGTTATGAAATGAGAAATCTCGGCAACTGCGCGGATAAGGCGGTGTTGCTGTTTGAACAAACGGCGGTGCAACCGACAA  
CAACACGCTGAAGCTGAATTCGCGCGGTATCTCTGCGGTGCAAAATCTGCGCGCGCTCGCGGACAAACCGTATTTCTACGACAGCAGCGGCTTCCACTACCGGCAACAGCACAAAT  
GTTTGAATGCTGTTTGAAGTCTGCTGAAACCAATGGAAGAACACCATCTGACTTTGGGCTTCGGTTACGATGCTTCCAAAGCAGTATCCGCGCCAGAACAGCTTTCCCAATATG  
CGGCAAGGATTTCGAATCCACGGGATTCGATGAAAAGAAATCAAGATAAGTACCGTTTGGGTAAAGCCGAGTCTGCAAGGGTTCGCTGCGGCTATATCGAAACCTCGCTTCCGCGCA  
ATGCGTGCAAGAAAAATCAACGCGACGATATTCACATTTCTTTGAACGACCGGTTTTCATTCGCAATATTT



**SEQ ID 2644**

YDGDGDFRDGGLYFVPMLEBWKDKNMLVKGIGLKYSRTKFI DEBHRRRRNGLLRYRYENEKYSDNWADKAVLSFDRQGVATDNNTILKNCVAVYPAVDKSCRASADKPYSYDSSDRFHYRQHN  
VLNASPEKSLKNKNTKHRITLPGPYDASKAVSRBPQLSHNAARISSESTGDFEKNQDKYRLGKPEVVBGSGVGYIETLRCKRCVPRKINGSNIPHFPERPFPRQIIF

**SEQ ID 2645**

TTGACAGCAGCTTTTTC AATCGGCAAAATATTTT PGTATTCAGCTTTGGGCGG CAGGTACGACCGGAAAAA ACTTACCACGTCGGAAGAACTCGTCCG CAGCGGGCGGTATGCCGACCGTTCGT  
GGAACAGCGGCATCGTGTTC AAACCGAAACCGGCATTTTTC CGTGCTTACCGCGCCTCCAGCGGCTTCAGAAACGCCTTCCTTCC AAGAACTTTTCGGGATAGACATTTATCAGCATATATCC  
GAAAGGCTGGCAGCGCTCCGCGCCTGAAATCGGAAAAGGCAGGCCAACCGGGAAATCGGTTTCAGTGGAAAGGGCGATTTCGGCTTTTGTGAAATCAGCAGTTTTCGCAACCGTTATACCGAT  
ATGATTCGCGTTCGGCATCAAAAAACCAATATTCGCGGATTCAGCAGGACGATTCAGACAGATTTGATATACGCGATTATTA CAATGCCCAAAATATGTGCGCTTCAAGGCATCAACATCTTGG  
GGAAATTCGACTGGAACGGCGTATACGGCAAACTGCCCGAAGGCCGTGTACACCATATTTGGCGTACAAACCGTATCAAAACGAAATCGGTATCCAACCGGGCGGACFTGTCCCTCCGACGCTA  
TGCTTTGGATGCGGTACAGCCGTCGCGTTATGTTTGGGGTTCGGATACGACAGCCAGCGGGGAAATGGGGCGCAAAACATTTATGCTGATCTTCCAAAGGGA AAAACCTCAGCAGCTT  
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ACAATATCGGCAACTACCGCTACGTTACTTGGGAATCCTTGCGCCGAGACTTCGCGAAAGCAGCGCAAAACCGGCACGGCGCGCAGCAGCAACTATGGAAGGTATGCCGACCGGGCAGGAACCTT  
CAGCCTCGCGCTCGAAATGAAGTTT

**SEQ ID 2646**

LNDRFSG1GKYFDFSLGGYDRKNFTTSEELVRSGRYADRWNNGIVFKPNRHFVSUYRASSGPFPTSPQELPGIDIDYHDPKGMQRPAKLSKAAANREIGLQWKGDPGFLBISFFNRYTD  
MIAVADQKTKLPDSAGRLTEIDIRDYNAQNMSLQGINILGKIDMNGVYGLKPEGLYTTLAYNRKPKSVSNRPDLSLRSYALDAVQPSRYVLGFGYDQPEGKGWGANIMLYSKGNPDEL  
AYLAGDQKRYSAGRVTSWKTADVSAYLNILKRLTLRAAYINIGNYRYVTWESLQTAESTANRHGGSNYGRYAAPGRNFSLALEMKF

SEQ ID 2647

ATGCGCTAAATTCCTTTATCGACCGCCCAATTTTCGGGTGGGTATTTCGATTTTCATTATTGCGGCAGGATTTTCGGCATTAAGAACGCTGCCGGTTTCGCAATATCCGTCGGTTGCCGCC  
CGACCAATTACTTTTCACGCCAATTTATCCGGGTGCGTCCGCACAAGTGATGGAAGGCAGCGTACTTTCGCGTATCGAAGCGAATATGAACGCGCTGGAAGGTTTGAGCATATATGTCACACTTC  
CGCGGATTCGAGCGGCAGCGGCAGCGTGAGCCTGACCTTTACGCCCGATACCGACGAAGATCTGGCGCAGGTGGAAGTGCAGACAAGCTTTCCGAAGTATTGAGCACGCTGCCCGCAAC  
GTCCAGCAATACGGCGTAACCGTATCAAGGAAGCGCGCTCCAAATTTCCGTATGATGCTTTTCGTCGATATGTCGATCAACAGAGAGTGAACGATACCGCGCGCGCAACGTCGTTTC  
CCGAATTGCGAGTATTCGAAGCGGTGGGCGAGTTCGCGCTGTTTCGGCGGCACAAGCCGCGATGCGGAATTTGGGTCGATCTCAAGAAATCGCAAAACTACAAATTTGCTGCTTGCCTGATGTCGG  
CAGCGCGTTCGTCGCGCAGAAATATCCAAATTTCCGACGGTTTCCATCGGTCGCTTCCCGCTGTGCGCGGCAGACAGGGTTACGGCTACCGTAACGGCGCAAGGGCAGTTGGGTACGCGCAGAA  
GAATTCGGCAACGTCATCCCTCCCGCCAATACCGACGGTTCTAATATTTACCTGAAGGATGTGGCGAAAGTCGGAATGGGTATGGAAGACTATTCCTTCCTCAACCCGCTGAACCGGGTAA  
ATACACCGGATATGCGCGTAAATGTTGTCCAAACAGCGCAATGCGATGCGCAGCGCAAGAGCGGTAAAGAAGCGCTTGGCGGTGCTGGAAAAATACTTTCCGACGGGTATGAGTTGGAANA  
CCCTTACGATATCTCCAAATTCGTTGAAATTTCCGATTGAAAAGTGATTCACACTTTAATCGAAGCGATGTGCTGGTGTGTTGTCGTAATGTACCTCTTCTTCGCAAAACATCCGGTTATAG  
CTGATTCGCAAGATCTGCTGTACGATTTCCCTGTGGCGGGTTTCGCTCTCATCTTATATGGGATGTGCTGATACGATATGAGCATATGTTTGGCATATGATTTGGCATTCGCGCATCGGTG  
TCGATGACCGAATGTGGTGGTTTGAAACCGTGCAGCGCAATATGCGCGGTGAGGGCTTCGCGCCCAAGAAGCGACCAAAAAGCGATGGGTCAGATTTTCGGCGCGGGTCATCGGTATTAC  
CGCGGTCTGATTTCCGTGTTTCGTGCTCTGGCGATGTTTCAGCGGGCGCGCGCAATATTTACAAACAGTTTGCCTTGACGATGGCGTCATCAATCGCATTTCCCGCTTCTCTGGCGTC  
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ACAAGGCTTCGTTATGCTCAGCGTGAACCTGCTTCGCGGTGCGACCAACCGGATCGGCGAGCTAGCAGCAAGTATCCCAACTGCCGAAGACGATTTCCCGAAATTCGCAACCATCAT  
CCCGTTTCCCGCTTCAGCTTTTCGGGACAGGTCAGAAATGTCGCAATGGGTTTTCGCAATATGAAGAATTTGAAACGAAGCTACCGCTCCGCGACGATGCCGTTGGCGTTGCGGCGAAGC  
TGAAGGGTATGATGATGGGACGCTTAAAGACGGTTTCGGCATCTCCGTCGTCGCGCTCCGATTCGGAAGTTGGGCAACGTTTCGGGCTGAGCATCAACCTGCAAGACCGCAACATAC  
CGGCCATACCGCATTTGCTGGCGAAGCGCAACGAGCTGATTCAGAAAATGCGTCCGACGCGGTTGTGTTGACCCGACAGACGCTCCGTGCGCGCGGTTTGAAGACTCGCGCAGGTTGAAAATC  
GACATTAACCGTCCGCGACGCGGCGCGCAAGGACTTTGGTTTCCGACATCCGCAACCGCATTCGCAAGCGCGCTGAGTTGCTTATGTACCGGACTTCCCGCAACGAGGCGGTCGCAAC  
CGTGATGGTGCGAGGCGCAGGAGTGCCTGATCGACCTGCGGATATGTTGAACCTGACCGTACCGGCGCAACAAATCCGCGCTGCGGTCACCGCTTCCACATTTGCTATTTGGGA  
AAAAGGTCAGAACAGGCTGACTGCTTCCACGCGTATTCCTTCGATGAAGCTGTCCGCTTCGCGTGCACACCGCGCTTTTCACACCGGCGAGGCTATGCGCGCGGTTCAAAAATGTTGATGACGAA  
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GTTTGCCAACGACATCTACTTTCCAAGTCGGTTTCGTTGCTGATGGGTTTGTAGTGGCGA AAAACGCGATTCGATTATCGAATTTGCCAAAGACCTTCAAGCGCAAGGGAAGAGCGCGCT  
GAAGCGCGCTTTGGAGGCGAGCGCGCTGCGTTTCGCTCCGATTACGATGACCTCGTTTGCCTTTATTTTGGGCGTGGTTCCCTCTGATATTGCGCTGGTGGAGTCTGCCACGACGCGCG  
CCGCTGCACAGCATCTCAAAAGCGGATATAACCGGTTTCGACGATAAACCAATAT

**SEQ ID 2648**

MAKPIFDIPRIANVISIFILAAAGIFGIKSLFVSQYPSVAAPTITLHAITYPGASAQVMEGSLSVIERNNMGVEGLDMYSTADSSSGSGSVSLTFTPTDNDENLAQVEVQNKLSVLSTLTPAT  
VQOYGVTVSKARSINFLMTVMLSSDQSTEDNDYAQRNVVPELQRIEYGVQVRLFGAQRAMRIWDPKKLQNYNLSFADVGSALSAQNIQISAGSISGLPAVRGQTVTATVTTAQOGLSTAE  
EFGNVILRANTDGSNTLYLKDVAKVGLMEDYSSSTRFLNGVNTTGMAVMLNSNGNAMATAKAVKERLAVLEKYTPQGMWMTKPYTDFSKPVEISIEKVLIHTLIEAMVLFVVMVLYFLQNTTPT  
LIPTTVVPISSLGGFAFISYMGHSINVLTMFAMILVIGIVVDDAIVVENVERIMAGEGLPKKEATKKAMQISGAVIGITAVLISVFVPLAMFSGAAGNIYKQPALTMASSIAFSAFLAL  
TLTPALCATMLKTIKPGHHEKKGFGFWNKKFDSWTHGYBGRVAKVLRKTFRMMVVYIGLAVGLVFLFMRLPSTLQDQGVFVSVQKLPGAGATKERITDATLAQVTLAKSIPETNII  
TVSGFSFGSGSQNMAMGFAILKDNWERTASGSDAVAVAGKLTQMMVGLKDKDGGPIVSVPPPILGLGSGSLSTINLQDRNNTGHTALAKRNNLQJXRASGLPFDSTRVAGGLGSSDQPKI  
DINRAAAAQGISPADIRITALASALSSYSDDPFNQRLGRVWQADEARMQPADILNLTIVPNKSGVAVPLSTLATVSMWKEQTSVRNGYPSMKLSASPATGVSTGQAMAAYQKMVDE  
LGGGYSFVGGGQSREARKGQSQTLLYGLAVAYVTLAALYESWSNIPLAVILVPLGLIGAAAGVTGRNLFEGLLGSVSPFANDIYTPQGVFTVMGLSAKNAILIIEFAKDLQAQGSXAV  
EAALEAARLRPRPIIMTSPAFTILGVVPLYIAAGASSAQRAGITTFVWGLVGLLVSFLVFLVYVVRKPKETAHEHEMAVRHASKAGITGSDIXQY

**SEQ ID 2649**

TTGGGTACGGCAGTCTTCAAAGTCGTCGAAAAATCAGAAGTCTAGATTCCTCGGTTTTCACGGGAATGACGGAAATTCAGACGGCATCTCTCCGCCCGGTCATTCCTCCGCGCAGGCGGA  
ATCTAGTCCGCTCGGTTTCACTCATTTACGATAAAATCTCTGTTGCTTTTCATTTCCGGATTOCCACTTTTCGGGGAA

**SEQ ID 2650**

SEQ ID 2055  
 LQSGNLOKSSEKSEVLDSRFHGNDGLSDGILPPRHSRAGGNLVRSVSVIYDKFLLPFI SGFPLSRE

SEQ ID 2651

SEQID 237  
ATGGGCGCAAGCCTGATCCAGCCATGCCCGGTGTCGAAGAAGGCCCTCGGGTGTAAAGGACTTTTGTCCAGGGAAGAAAAGGCCGTTGCCAATATCGGGCGGCCGATGACGGTACCTGAAG  
AA

SEQ ID 2652

MGASLTQPCRVSEEGLRVVKDFCOGRKGRCOYRRPMTVPER

SEQ ID 2653

SEQ ID 2553  
ATGCCGTCGGAAGCTTGATCTGCACCCCAAAGTCGGACTAAACCGCCAACTGATTAAGGTGCAGGTTTTTTTTGATTCAATATAAAACAAGATTTCCGCGGTCAATCCCGCGCAGGCGGGA  
ATCCGGCAATCAATGC



## SEQ ID 2654

MPSGSLICTPKVGLNRQLIKVQVFLIQYKQDFRRHSRAGNPDICQ

## SEQ ID 2655

GTGGGAATCCGGTTTTTTCAGTTTCAGTCAATTTCCGATAAATTCCTTAGCATTAATGTCGGATTCGCCCTGCGCGGAATGACGGCGAAATCTTGTATTATTAATCAAAAAAAC  
CTGCACCT

## SEQ ID 2656

VGIRFFEFQSFPPINCLSEICPDSRLRGNDGGLVYIESKKPAP

## SEQ ID 2657

ATGAGGAAAAATCCGACCAAAAATCTGCGGCATCACCACACCGGAAGACGCACTGTATGCGGCCACGCGCGCAGACGCAATGGGACTGGTTTTTACCCCCAAAGCCCCCGCTATCG  
ACATCATTAAGACCAAAAAATCGCGCGCACTGCGCCCTTTTTCAGCGTTTGTGCGCTTTTCGTCACGAAAGCGCGCAAAACATCCGCGCATCTTGCAGAGTGGCGATACACAT  
CATCCAATTCCACGCGACGAAGACGATGCAATTCGCGCGCATTCGACCGCCCTATATTAAAGCCATTCGTGTTCAGACGGCATCAGACATCCGAAACCGCGCCACGCGCTTCCCAAC  
GCTCAGGCACTGCTGTTCGATGCTATCACTTCGGAATACGGCGGCACCGGACCGCTTCGATGGAAGCTGTGGCGGAATATTTCGGCAAGCGGTGGTGTTCGCGCGCGGTGA  
CCCCGAAAACGTGCGCGACCGCTCCGATCACCAGGCGGAAGCGGTGACGATTCGCGCGCGTGGAAAGCGTCTAAAGGCAAAAAGACCCGCCAAGTCCGCGCTTTATCGCAAC  
CGCCAAACCGCTATCCCGT

## SEQ ID 2658

MRKIRTKICGITTTPEDALYAAHAGADALGLVFPQSPRAIDIIKAQKIAAALPFFVSVALFVNESQNRRLIAEVP/IIHQPHGEDDAFCRQDFRPIKAIKRVQASDIRNAATRFPH  
AQALLFPDAYHPSYGGTGHFRDWTLLAAYSKPWLACGLFPENVGEAVRTGAEAVDVSGGVEASKGKDPKVAAPATATANRLSR

## SEQ ID 2659

GTGCGCTTGTGCGTTTCAGACGGCATTCGCCATCAGTCGATTTTGATGTATTCGACAGAAAGGATTTCAATTTCTCAGCGCTTCGCGGTGTTCAAAACCACTTCGTCGCTTCGCGC  
GCTTTAATCAGGCAACGCGCAACGCGGCAATCCAAGAAATTTGTTTTGCGCGGTATCGATTTTCATCGACGCGGACGATTTTGACGTTTTCGCGCGGTTCGCGCGCAACGACGCGA  
CGGTGCGCGCAAAAATCTTGTGTCGCTTCGCGCAATTCGGGATCGACGACGCGGAGCTCCAAACGTTTGTTCAGGAAACGGATGCGCGGTGATTTTCGCGCATACGCGCTTT  
GCGGTAAAGATAGTCCGCTTTTCGCTGCGGTGCGCTTCGCGCGCGGATGACGATTTTGACGATTTTCGCGCGCTTCTTTATGACAGTTTCATAAGCTCGTCTTTCAATGCTGTC  
CATCGCGCGGTGATGATGATTTTGTGTTTGTGCTACTCATATTGTGTCGGA

## SEQ ID 2660

VRLCRFRHSRSDVDFVDRKDFNLTAFRRVQNHVAFARFNQATQRNRNFRVLRGIDFTDADDFDGLLAPVAAQQTGDAEKYLVGRFAQPGIDDDGSLQTFGQETDAAVDPAHTAF  
AVKIVAVFAAFAVACRPVDDLDFGAFPIDQLIKLVFQCLPSGGRNVVFGFTHIVCG

## SEQ ID 2661

ATGAGTACCGAAACCAAACTACATACGCGCGCGGATGGCAGGCATTTAAAGACGAGCTTTTCACTGGTCAATAAAGAACGCGCGCAAAATCGTCCAAATCGTCACTGGGCGGCGAG  
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ATTCGCGGAAGGACGACCAAGATTTTTCGCGCGCGGCTGCTGTTGCGCGGCGGCGGCGGAGCAAAACCGTCAAAATCGTCCGCGTCCGATGAATCGATACCGCGCAAAACAAA  
ATTTCTTGGATTTCGCGGTTCGCGGTTCGCTGATTAAGCGCGGAGCGGAGCAAGTGGTTTGAACACGCGCGGAGCGCGTGAGGAAATGAATATCTTCTGTCGAATACATCAAAA  
TCGAC

## SEQ ID 2662

MSTETKNYITPAGQALKEDELYQLVNERPEIVQIVNMAAGNDRSENGDYLYGKRRMREIDRRIRFLTKRLEAAVVVDPELREATDQVFFGATVGLLRGDRBQFVKIVGVDEIDTAQNK  
ISWISPLARCLIKAREGEFVLATPEGREETELSVYIKID

## SEQ ID 2663

ATGTGCGCGCATTTAGGTTTGTGTCAGTCATGAACCGGTGAACAGCTTCTGTACGACGCTTTGACAGATGTTGACGACAGGGGGCAGGATCGCGCGGCTTGAACCGCGGAAGCGGTA  
CCTTCATATGACAAAAGCAAGGATGTTGAGCGAAGTGTTCGCGACGCGCAATATGCGGATTTGACCGGCAACGCGCGCATCGCCACGTCGTCATCCACGCGGCAACGCGG  
CAGCAGCGCGGAGCGGCGGCTTTCAGTCAGCTCGCTTTCGCGCATGTTTGGCGCACAACGCGCAACCTACCAACACTGCGGAAGTGTATGAACAAACCTGCGC  
CACATCAACACCGGCTCCGATTCGGAAGTTTGTCTCAACGATTTGCGCGACGAATTCGCGCGGCAAGTCTCTAAACACGCGGACCGCGCATCGCGCTCAATGCGGACAAATTTTCAACGCG  
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CGACAGCGAAGGACGAAATCTATGCGCTGCGCTCGGAATCGCTGCTTCAATGCGCTTGCCTACGATTTGGAACGCGATATCCGCGCGGCGGAGCGGTATTTGTCGCGTTTAAACGGC  
ACAATCATCGCGCAATGCGCGGACGCGGCTGCGCAACTGCGCGCTGCTTTTGAATATGTTTATTTGCGCGCGCGGACTGTGATTTGACGCTGATCGGTTTACCAATCGCGCTTGG  
ATATGGCGGTCTCTTGGCGGAAAAATCAACGCGGAGCTGCGCGTGGAGCGCATCGACGCTGATGCCATTCGCGATACGACGCGCGCGGAGCGGCTTTCGCGCTTCAACCTCAA  
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GCAAGCAAAAGCGTGTGCTGTTGAGGACTTCCATCGTTCGCGGAGCAGCAGCGCGGAAATCGTGAATGTTACGCGCGCGGCGCGGCAAGTCTATATCGCTTCGCGCGCGCGG  
AAGTGGCTATCCCAATGTGTCAGGCAATCGATATGCCACGCGCGAAGAGTGTATGCAACGCGCGGCGGCGGAAATCGCGCGGAAATCGCGCGGAGCGGCTGCTGTTTCAAGA  
CTTGGCGGATTTGGAAGCGCTGCTCAAGCACTCAACCGGAAATCGAATCTTCGATTCGCTCTGTTTCAACGCGCATTTATCGGACGCGGACATCGATGATGCTACCTCGACCGCGCTG  
TCTCGCGGAAATTCGCGCTGCGCGGTCTGAATATCCACCGGAGGATGGAACACGACATCAGCATCAGCGATGCGCGCGACGAAGA

## SEQ ID 2664

MCGVLGLVSHFPVNLQYDGLMLQHRQDAAGLATAEGGTFHMKGKGMVSEVFRTRMRDLTGNAGLAHVRYPTAGNAGSSAEQPFYVSSPFGIVLAHNGNL/TNTAELYENVCKHLR  
HINTGSDSEVLN/VFAHELRRVSKNADPHRLNADNIFNAVAEVHRLVRGAYGVVAMLAGYGLAFRDPYGRPLALGSDTSEGRKSYAVASESVAFNALAYDLERDIRPGEAVFVPG  
TILARQCSDRAKLSPCLFEYVYFARPDVSDVGVSVYQSRLLMGVSLAEKIKRELVDGIDVVMPIPTSRPSAMELAVHLNKPYPREGLIKRYIERTIMPQSTREKSVRQKLSPMETEF  
AGKSVLVDSDIVRGTTSREIVEMVRAAGARKVYIASAAPEVRYPNVYGIDMPTREELIANGRSAEIAAEIGADGIVFDLGDLEAVVKALNPKIESFDSSCFNGYRTGDIDDAYLRL  
SAEKSGCAGLKIHPSRMEHSISISDAGDEE

## SEQ ID 2665

GTGCGTTTCAGACGATACCTGATTTATGCGCTCCGAAACGCTTTTCTTTCTTTCGACACACCCGACAGACAAAGCGCACCTGCTGACTTTACACAAATATTGTCACAAATTCGGG  
AAAAAGCGCGCTTTGCTTTTATAATTCGTTTCACT

## SEQ ID 2666

VAPQYAYLIYAVRNAPFLDTPROTCTCLTLHKYQQFGQAACVCFIIPHP

## SEQ ID 2667

ATGGGTGGTTTCTCTTTTTTGGCAAACTCTTTGCCGACCTTCGCGGACCTGCGCTTTGCTCGTTCCAAACCGCGCTGTTGCAATGGCTCTGTGATTCATTTCCCTGTTCTGTCATT  
GCTGTCTGATCCAGAAATGCTCCGTTCGCTGCTGACCGCGCGAGTTTCGCGGTGCGCTGCGGCTTTCGCAACCGCATTTTGGCGGTGATTCGCTGATTTGAAGCGGTTTGTATG  
TTACCTGCTGATCATGCTTGTCTCAAAAACCGACTGCGCGATACCGAAGATGCGACAGCTCTATACCTACCGTTTTCGATGCTTTCGGAAGCGGTGTTAAACCATACGGACAA  
CGACCCGGAATCCCTGACGACGACTAATCCGATACGTGGCTTTCAGACGACATACCTGATTTATGCGCTCGAAACGCTTTTCTTCT

## SEQ ID 2668

MGGFLFCQTLCLRTLRRLCLVPTPVCIGSVIHPVRHCLSDPENAPPAADRRSPGGRSGLCQPHGRCIRCIERRPDCYPADHACPKNRPARYRRHATVLYRTVFRIAFRSVKPYGQ  
RTRIPRRRLIRIRGVSIDSIPDLCRFKRLFFP

**SEQ ID 2669**

EQ ID 2669  
ATGAACATCAAAACACCTTCTCTGACCGCCGCCGCAACCGCACTGTTGGGCATTTCGCCGCCGCACTCGCCACCAAGACGGACACGGCGATGACGACCAAGGACAGCCGCCACACCAAC  
ACGGCAAAACAAGACAAATCATCAGCCGCCCAAGCCGAAAAAGCGGCTTGGGCGCGTGTCGGCGGCAAAATCACCAGCATCGATCTCGAACACGACGACGGCCGTCGCGACTATGATGT  
CGAAATCGTCAAAACCGACAGGAATACAAAGTCGTTGTCGATGCCCGTACCGGCCGCGTGATTTCCTCCGCCGCGACGAC

**SEQ ID 2670**

SEQ ID 2670  
 MNIKHLLLTAAATALLGISAPALAHHDGHGDDDHGHAHQHGKQDKLISRAQAEKAAWAVRGKITDIDLSHDDGRPHYDVZIVKNGQSYKVVVDARTGRVSSRRDD

SEQ ID 2671

**SEQ ID 2671**

**SEQ ID 2672**

MLLSIKVVSRRSRKSGNPDHWVAAIFKSRLKNQKF

**SEQ ID 2673**

SEQ ID 2673  
ATGAAATAGCCTCCCCATTGCGGACCTCCTCGCCTCCGCGGTCAATCGCGCCCTGCATCGTCAATTTCCACGATGCGCGCGGTGATTGCGGAAGCAGGTTCGATGGTGGCATGGGTGGTTTCCT  
TCATTTTGGCCAAACTTTTGGCGCACCCCTTCGCGGACCTCGCCCTTGGCTCGTTTCCAACCCCGCCTGTTTGCATTGGCTCTGTGTCATTCATTTCCCTGTTCGTTCATTGCCGTGCTGATCCA  
GAAAATGCTCCGTTCTGCTGCACGCGCGCAGTTTCGCGCGGTCTGGTCTGGGCTTTGCCAACCGCATTTTGGCGCGGTGATTTCGGTGCATTGAAAGGCGTTTGATTTGTTACCCCTGCTGATC  
ATGCTTGCCTTCAAAAACCGACCTGCCGATACCGAAGAATGGCAACAGTCCTATACCGTACCGTTTTTCTGATCGCTTTCCGAAGCGGTGTTAACCATACGGACAACGCACCCGAATCCC  
TCGACGACGAC

**SEQ ID 2674**

SEQ ID 2674  
 NNSLPFIADLLASAVLIAACTIVSTMRCGVIAEAGSHVAVVVSFFFAKLFAAPFADLAFASQPRLFALALSLFISLFPVIACTIQKMLRSLLTGAVSAVGLGFANRIIGGVFGALKGVLLIVTLLI  
 MIAKSTDLPTDEWQOYSTYVFFPVSLSAVALNHTDNPESLDDDD

**SEQ ID 2675**

[illegible]

SEQ ID 2676

SEQ ID 2676  
MSENKQNEVLTCGEQLKRRNRRLVTASSLVAASCILLAAALSSDPADSNPAPQAGETGATESQTANTAQTALPKSAAENGETAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRL  
EDSNIKGLEESEKQLQAATAKTEPKQAKQRAAEKVSATADSTDTFVAVEKPKRTAEPPKQAEKRTAEAKPKAKETKTAEKVADKPKTAETKTKPDTAKSDSAVKEAKKADKAEGKTKAEKOR  
SDGKKHETAQKTKDAKTKTAEEKESGKAGKAAIQAGYAEKERALSQRKNKAAGIDSTITETLMTDNGKVVYKVSNNYNKARDAERDLNKLKVHGIAGQVTNE

SEQ ID 2677

SEQ ID 2677

ATGAAACACTACAGACTCGGCTCTCGCAATTGGAACACGCCACAGCGCGGTTTGATCGACATGGGTTTGGAGCGCGTAAGCGGAAGTAAAAAGCGCATGAACCTGACACCGCAATGCC  
CCGTCGTCGTCGTCGCGGGACAAACCGGAAGGTTGCGTCTGGCCTACTGTACACAGATTTACAAACAGGCAAGGCTTCAAACCGGCACGCTGACCAGCCCGCATTTATTGCTATTACAA  
CGAAGCTCTGCGCATCAACCGCGAACCCGTTTCGGACGATACGATTATTGCCCTTTTCGAGCGCATCGAAGCCGCGCGCGGCGAAATATCGCTGACTTATTTTGAATTCATGCTTGGG  
GACTCGGACATTTTCATACCGGAACAAGTGGATGTAATGATATTGGAAGTCGGCTTTGGGCGGACGTTTGGACGCGGTCAACGCGTTTTCGACGGGATTCGCGGTTGTTACTAGTGTGGATT  
TGGACCATCAGGCATTTTGGGCGATACGTCGGAACAGGTGCGGCTTTGAAAGGCAGGCGTGTTCCGACGCGGCAAAACCGGCATCTGCGGTCAAACCCCGCGCCCGCATCATTCGCTCG  
ACACGCCGAAGCCATAGGCGCGAAATCTGCTGATGGTACAGCGGATTTTCGAGTTTCACGCGATGAAACATCCAATGGAACTACCGCTTCGCGCGGACGATTCAGACGCGGCGGACCG  
AACCGCATGCGCTTGCCTTCCCGCATTCGCGCGCGCATACGAGTTCTAACCGCGCTCGCGGTTGACCGATTGGAATGGAATGATGTCGACACACACCCCAACGCGCGCGCGCTTGCGCGCAACTAAT  
AACCGGGGCTGCTGCTGTTGAAATCCCGACGCTTCCAAGTCTTCCCGCGCGCGCGTACGCGTATGGAATGTCGACACACACCCCAACGCGCGCGCGCTTGCGCGCAACTAAT  
CAACCTTGCTACGCGCAAAAGCGCAACGCGCTGTTTCAGTATGCTGCCGACAAGACATAGACGGCGTGTGCGAAACCGTTAAAGACCGTTTACGAGTGGTATATCGCGCTTTGGAC  
GTGCGCGCGGTATGACGCGCGGATGCACTGAAAGCCAAATTTGGAACAACACCAACATCGAAACATACAGACATTCGCGCGGTCGCGACGCTACCGCGCGGCAACGCTCAAAGCGGGG  
AAGACGACAGAATGTCGTATTTCGGCTCATTCACCGTCGCGGACGTAATGTCGGTACTG

SEQ ID 2678

SEQ ID 2678  
 MKTQDWLSHLSHTAHSGGLIDMGLERVSFVKRMNLTPOQCPVVVAGTNGKGSVCAYLTQIYKQAGFKTGTLTSPHLLHYNERIAINAEVPSDDTTIASFERIEAARGEISLTYPFENALA  
 AYDIFIREQVDVIMILEVGLGRLDAVNAPDGCNAVTVSDLDHQAPLGDTEVQVGFKEAGVFRSGKPAICQNPAPASLVAHAEAIGAKLLMVQDFEFHAMENIQWNYRFRPQHS DGP  
 RRNALPFPALRGAYQLSNAACALTVLECLDDRLPVDIGAIKRGLLLVENPGRPOVLGPRPLTVLDVGHNPHAARALRRNLINLAYAQKRTAVFSMLSDKDDIGVSETVKDQFDEWYIAPLD  
 VPRGMTADALKAKLSHHHLENTQTTFAVRDAYRAAASKAGEDDRIVVFGSFHTVADVMSVL

SEQ ID 2679

SEQ ID 2679  
ATGCGCGGCTTTTCAGACGGCATFTGAGGCCGTCCCGCATCTGAACATCTGACCGTATCACTCCACTCGGCTTCCATTGCGCTGCGCTGACTTGGTTTTACGGCGGATGATGTGGTTGG  
GTTTGGCGGCTTTGGCGGCAAGTTACGCATACTCGCTCAGGATAACGAATCTGAACACCGCCATGCCATACCGCCATTACCATAGACCGCGACGGACGGCGGCGGAANTCGTATCGGCCAA  
AGACAAAACAGCGGCAACATCTGCGGCAGCAGTATGGTATCAGCCCTTATGCTTTATCTTACAATGGGACACAGGCGGCAAAACCGTCCGCCAATGCATCATGCCGCACATGACGGACAAA  
GAATCCTTACCGCGGCTGAAAGTCTGGTGCTTTGGCGGCAGCCGAAAAAACCGCGGAACCGATACATCAGAC

SEQ ID 2680

SEQ ID 2680  
 MRAFTALRPSRIILNLTIVSLHSASTAVCLTWFGMMWFGLAALAASYAYSRLRITNLKRRHAIITAITIDRGRATVSGKDKTAATLAGSSMTVPYALFLNDTGGKTVQCPIMDITK  
 ESYRLIKVWVLRPPKKTAEITDSD

SEQ ID 2681

SEQ ID 2681  
TTGAGAAGCACACCATGTATTTTGTGACCGCACCGCCGCCGTCTCAAGCCGACCGCGCGCTTTTGGAAATGCGTCAAAGCACCGACGAAATAATGCCGACCTGACCATAGAACAGC  
TTCGCGCCGACGTGTCCTCTTCCCTGTTCCGCACTGCGACGAACCGGAACCGCTGTTTCTTACTTCGACGAACCGCTATCCGCGAGATTTTGGAGCGGAGCTGGCAGGTGGGCATCGA  
CAAGGACAAATGCCCGCAAGATATGGGGCTGAAGGCGTTTGGGAATTTTTCGACATTGAAATCCACGATATGGTTTGGATATGGAAGAAGCGGATTTGAACATCACGCCCGTGTTCGAC  
AATATGATG

SEQ ID 2682

SEQ ID 2682  
LRKHTMYFVDRITAAVLKPTARFLEWLKSTDENMPDLTIEQLRADCSVFLVLPQFDEPAVVSYFDERYRQIFEARLAGNDIDKDKWQDMGLKAFWEFFDIEIHDVLMOEADLNITPVFD  
NM

## SEQ ID 2683

ATGGCGTTACATCATATGTGCGAACACGGCGGTGATGTTCAATTCGGCTTCTTCATATCCAAAACCATATCGTGGATTTCATGTGCGAAAAATTCOCAAAACGCCCTTCAGCCCCATATCT  
TGCGGCCATTGTTCCTTGTGCGATGTCCCAACCTGCCAGCTCCGCCCTCAAAAATCTGCGGTAGCGTTCGTGCGAGTAGGAAACGACGGCTTCGGGTTCGTGCAACTGCGGAACGAGGAAGA  
CGGAACAGTCGGCGCGAAGCTGTTCATGTCAGGTCCGGCATATTTTCGTGCGTCTTTTGAGCCATTCCAAAAGCGCGGTTCGGCTTGAGGACGGCGCGGTTCGGGTCAACAAAATA  
CATGGTGTCTTCTCAATCATCTTTCGGGTTCGGGTATGCCCTCTGAACGTTCGGTTCAGACGCCATAGCATCAATGGGTTCAGTCTGTCAGGAACCTGCTTGGCGCTTCGTGT  
TTCGGGTTCGTGAAAAACGCTTCGGCGTTCGTCTCAAGGATTTCGCCCTTATCGACGAAAAATCACCGGTTCGGCACTTCGCGGGCAAAACCCCATTTTCGTGGGTTCACGACATCATCG  
TCATGCCCTTTCGCCCAAGTCTTTCATCATCTTCAACACTTCGCCGACCAATTCGGGGTCGAGTGCAGGAAGTGGCTTCGTCAAACAGCATCACGGCGGCTCCATGCCAGCCCCGGCGC  
AATGCCACCGCTTCTGCTGCTGGCGCGCGAAAGTGGGAAGGGAAGCGCTTTTTCGTGTCGCAAGTCCGACGGTTCAAAAGCTCCATTGCCCTTTTCCTCGCTGTTTCGGCATTTTGC  
CCCTTAACCTTCATCGGTGCGAGGGTATGTTGTCCACACGGTCAGGTGCGGGTAGAGGTGAAACTTTGAAACACAAAGCCGACTTCTTCGGGATTTTGTTCAAATCGGTTTTCGGGT  
CGGCAACGTTGACGCGCTCCACCCAAATCTCGCGCTTTCGATGCTTTCAAGCTGTTGACGGTTCGGATGAGTGTGATTTCGCCGTGCCGAAAGGCCGACAGACGACCTTCGCC  
TTTTTTCATTTCGAAGTTTACGCGGTGATGACGTGACGCTTTGAAATGTTGTGTACGTTTTCGAATTTGATCATAGTGTCCATCTTTTCGGCGAGTC

## SEQ ID 2684

MAHHIIVEHGRDQIRFFHIQNHIVDFNVEKFPKRLQPHILRPFVLVDVPTCQLRLKNLFPVAFVEVNDGFRFVELRNEEDGTGAKLYGQVGHIFVGAFFEPQKARGLEDGGGAVNKI  
HGVLSQSSCGVGLCRINVRPSDGLASMGHDLLELGAFFVVRVGEKRRFRFVKDLFFIDENHAGVNFAGKPHFVGYAHRHAAPRQVPHHPQFADHFGVECGSRLVKQHARHLHBQPAR  
NRHALLAAGLKGREGVFVVCQSDAPQLHCLFLRLFLPLNLHRCGSDVQHGQVRVEVETLEHKADFFADFPVQIGFVGNVDAVEHPNLAAFDAPKLVDGDECGFAAARRPADDDHFA  
FFDFQVYAVDDVQVFMFVYVFEFDSVHSFRAV

## SEQ ID 2685

ATGGACACTATGATCAAAATTCAAAACGTACACAAACATTTCAAAGACCTGCACGTCATCAACGGCGTAAACTTGGAAATCAAAAAGCGGAAAGTGTCTGCTGCGGCCCTTCGGGCA  
CGGCAAAATCCACACTCATCCGACCGTCAACAGCTTGAAAGCATGAAAGCGCGAGATTTCGGGTGACCGCGTCAACGTTGCGCGACCCCAAAACCGATTTCGACAAAATTCGCGAAGA  
AGTCCGCTTTGTGTTTCAAGTTTCAACCTTACCCGACCTGACCGTGTGGCAACATCACCCTTCGACCGATGAAGGTTAAGGGCAAAATTCGCGAAGCGGAGAAAAAGCAATG  
GAGCTTTTGGAAACCGCTCGGACTGCGACACAAAAGACGCGCTTCCCTTCCCACTTTCGCGCGCGGACGAGCAACGCGTGGCGGATTCGCGCGGCGGATTCGAGCGCGCGCTGATGC  
TGTTTGACGAGCGGACTTCCGCACTGACCCCGAAATGCTGGCGGAAAGTGTGAAAGTGTGAAAGACTTGGCGGAAAGCGCATGACGATGATGTCGTAAACCGAAATGGGTTTTCG  
CGCGAAGTTTCCGACCGCGTATTTCGTGCTGATAAGGGCAATCTTGAAGACGAAACCGCGGAAAGCGTTTTCACCAACCCGAAACGAAACGCGCCAAAGCAGTTCCTGCAACAGTGC  
ATGACCCAT

## SEQ ID 2686

MDTHIKFKNVHKFIDLHVINGVNLKIKRGEVVVVCPSGSGKSTLIRTVNQLESIESGKIWDGVNVADPKTDANKIREBVGFPVQSFNLYPHLVLNLTPLAPHKVKQNAEQAEKKAH  
ELLERVGLAHKDAFSPQLSGGQQRVAIARGLAMEPRVHLFDEPTSDLPENVGEVLKVMKDLAESGTMCMVTHEMGFAREVADRVLFVDKQILEDETPEAFPTNPKHERAKQFLQGV  
HTH

## SEQ ID 2687

ATGAAATACACAGCCGACTCTCTGACTTTTCTTTTAACTGCTGATGAACCCGAACGATGCGCTTTTCCAAAACCGCGCTTATCAATGCGCGAGGCGCAATTTGAACGGTTTCAACGCCG  
TTTTCCATTACGGTTATTCGCAAAATCCGATCATGATTATTGGTGCAGCAAGTCCGCGTCCGCGGAGCGGTACAGGGCTTCATTTCGCGGGGATTCGATAGCGAAGGAGCAAGTTACCG  
CAAAACGACTCGCTACTGAAAAAGCGAAAGCGGGGTGACGTACTACCTTCGCGATGCGGAAAGGATTCACGGCACAGCTTTCGTCACTATGTCGTGAATATGAAAAACGAC  
AAAGCTACGTCGAAATTTACCGGGGATGAATAAGCCGAATCAGGAAGAGTTAACCAATTCGTTGCCGATTGAAATAAGTTTACCTT

## SEQ ID 2688

LNCRQAALKPFTTYVYKIRNKHINRI PDFSPNRSEPTMYTAALLTFLI/FACMNPDAFPQNNRYQMPBAQLNGSNVPHYGYSONPDHLLVDQVRVPDAYRASPARDWIAKEQYRKN  
DCVLEKAESEGGVYTYTCDAREKFNTRFVITYVVMKNDKGYKVVYRGMKNFNEELTKLVADLNKFPY

## SEQ ID 2689

ATGGAAGCAACCTGCAGAAAACCGAGCGTTGATCCGCGAAATCAACCGCTGCACGCAATATTCGAGGATTATTTTGAACCGCGCAAGTTCGCGAAAATCAATTTGAGCCACACGC  
TCAAAAACGCTCCGACCGAATATTTTGTCTTATCGCTTAAATTTGCAAGCAAGTTCACGATTATTTAGCTTTTTCGCGATACGCGCGGATAGACTTTTCTACCGCGTGAACCCGC  
AGAAAGCATACATGATAAATCAACCGCTATCTGCGACGCGGACCCCAATATCCGACCAACAACATCTGAACGATATTTTCGCGCGCGCGCTGATTTCGCGCTGAAACAGTTCGCGG  
ATTTTACGAAATTTGACCGCTGGAACAGAAATACGCGCTTGAACAACTGGTATTTGCGCGATGCGCGCGGCTATATCGGCATACACATTATTTCAAAAACAGCAGCAATTTCTACTATC  
CGTGGAAATTCAGGTTTGGGATGAAAAAGATGCCAAAGCCAAATATTGAAACCATATGCGGTACAAACGGAATTTTCGTGCGT

## SEQ ID 2690

MESNLQKTERLIRINRIHAQYSQDYFETGKVRKINLSHTLKNVPTHEILSYRLNHEAVNDYLAADTRGIDFFYRVKTAESIHDKINRYLARGTQYPNNILNIDIFGARLIWPSETVAG  
ILEKLDGKWTREYGLKNWYLDAGGYIGIHIYFNSSNFYYPWELQVWDEKADKANIENHMAKRNPFV

## SEQ ID 2691

ATGAAAGAACACAAAGCCCGCAAGCGTTTCGGGACGATTTTTCGAGGACACCGGATTTATCGGCGATTTGTCAACCGCTGCGCGCGGAGCGGATGATGTCGATTGAAATCGGCC  
CGGGTTTGGCGGCAATACCGAACCTTTGCGGAAAAAGCTGAACCGCTGCACGTTGTGCGAAATCGACCGGACATCGTATGCGCTGTGAAACCGCTGCGCTTTTCGGGATAAATCGGTGAT  
TCACGAAGCGGACGCTGTCAGTTGATTTCACCGCATCTCAGGCAAAAAGAAATCGTCGCAACCTGCGGATATAACATCTCCACGCGCTTTGTGTTCAAACTGCGCGAGGTGCGGAG  
GATGTGCGCGATATGCACTTTATGTTGCAAAAAGAGTGTGCGAGCGATGTTTCGCGCGCGGAAAGCAACGACTACGCTGCTTGGGTGTGATGCTGCAATATTTTTCGATATGGAGC  
TGCTGATTGACGTGCGCGCGAATCGTTGATCCGCGCGGAAATCGATTCGCGAGTGTGCGCATGATTCGCGTGAACACCGTATCGGCAAGCGGACGATTTCGATCATTTTCGCCAA  
ACTGGTGAACCTGCGCTTCGCGCAACCGCGCAAAACCATACGCAACACTGAAAGAACTTGCAGCAGCATGATTTCGAGGAGTGGCGCATCAGTCCGCAAGACCGTCCGCAACATC  
CGCGCGGAGAAATATGTGGCGTTGAGCAATATCTGCGGACAAAGCCGCT

## SEQ ID 2692

MKEHKARKRFGQNFQDTRII GDIVNAVPRQADDVVIETGPLAAITTEPLAKKLNRLHVVEIDRDIVCLRLTFLADKLVHIEGDVLFQDFNGISGKKIVGNLPYNISTPLPLAEVAD  
DVADHFMQLQKEVVERHVAAPKSNNDYGRGLVLMQVFFDMELLIDVPPESFDPAPKIDS AVVRMTI PVKRIKADDPDFAKLVKLAFPRQRRTIRNNLKLADDDDLQAVGISPDRAEHI  
APEKYVALSNYLADRAV

## SEQ ID 2693

ATGACCGCAGCTTCGGCGGCAACACGGGATCGAAGGGATGGGTTTCGATTTCAGCAGATTTCAGACAGTTCATCTCTCCAAAGGCAAGCGGACAGCGCGGTTTCACCAAACT  
GCCAAACACGGCAAGCTTCAACAGCATATACAGCGCTCGCGTTTCGGTTTACAATCGCGACATCAACCGATACGTAAACACATTATGTTCCAAACACAGGACGACACATAAAGC  
ACCGCCCTATGTGTCTCTC

## SEQ ID 2694

MTAAGGNGTSGKGVSISSRFSDTFNPTGKAADSRFAPNRQTRQAFKQHYHALPFSVTMTPTSNGYCKHIYVPTHTRTHKAPTVSS

## SEQ ID 2695

TTGACCCGACACTTCAGGATTCGGCACACATGATCAGCAGACTGACCGGCAAACTGGTTGAAAAAAACCTTCGCAAAATCGTCATCGATGCAACCGTGTGGTTATGAAGCCGACGTAT  
CGATGCAGACCTTCTACAACCTCGCCCGCTGGGTGAAAGCGTACAACGTGTTTACCAGCTTATCATTCGGAAGACGCACATCTTTTATTTGGTTTTCGCACTGCGGAAGAACGCAAGAC  
CTTCCGCAACTGATTAAAGTTCGGCGGATCGCGCGGAAAAAGCGCTTTGGGCATTTTGTGCGGATGACGGCAGACGAGCTGGCGCGGCTGTCAGAAAGATGTCAACCGCTCTCC  
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AAGACATCGTCAGCACGCTGCTTGGCTGGGTTACAAACGACGAGGCAAAAGCGCGGTCAAAGGCGTTCCGAAGGGGACGGACGTGGGCGAAGGCGTGGCCCTTGCCCTGAAAAACCT  
GCTGAAA

## SEQ ID 2696

LHPFLQDSAHMISRLTGKLVKNPPQIVIDVNGVGYEADVSMQTFYINLPVGVESVQLFTQLIIRDAHLILFGFATABERKTPRQLIKVGGIGAKTALGILSAMTADELARAVABEDVKRLS  
SAPGIGKKTABRMVLELRGLVAHTVTDGLFAASPAADETIDVSTLILALGYNEZEAKAAVKVPGKTDVGEVRLALKNLK

## SEQ ID 2697

TTGGACATATCCAAGCTGACATTGACGCAACGCCATGGTCGGCAAAACGGAGCATTCGGCAAGTTTGACAACGATTCAAAGGTTTAGATCAGTTTTCGGACCGGTTGAAAAGCTTGG  
GATATCAGAATCTGCATATCTGCATGGAGGCAACCGGAGTTTATTGAAGAAGTTGCCGACTACTTCCGCGAGTATTAAGCGTTTACGTAGTGAACCCGCTGAAAATAAGCAAGTATGCG  
AGAAAGCAGGTTCAAGCGAACCAACAGACAAACAGGATGCAAGCTGATAGCGCAGTATTGCCGCTCGGCGAAAGAAAGCGAGCTTGTAAAGAGGCAAGGCTACGGACGAGCAATAC  
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CCATGAATGAACAGCTTGAAGTTTAAAGGAGAGATAAAGAGCAGACGAGAGGCTTAATGCAAGGAAGCGGTGAAGCGTCTTGAAACCATACCGCAATAGGCAAGTACCGCCAGC  
CGTATGTTTCATCATTAACATCTTGAATTTGAACATCAAAACAAATTTGACAGATTTCGAGGCTTTAAGCCCGCAACAAAGAAATCCGGGCAAGCGTAAAGGGGAAAAGGCAAACTG  
ACCAAGTTTGGCAACAGGAAATACGCGCGCTCTGTTTATGCGCGCATGTCGATACCGGATAAGGCACTTCCGACTTCATCAAAAGGCTGGAAGAAAGAAAGAGGCTAAAAAG  
TCATCATCGCAGCATGATGCGTAAACTCGCCCTTATGCGTATCAGTACATAAGAAAGCGGAGATTACGATCCATCGGCTTACAAATCGCGG

## SEQ ID 2698

LDISKLTFDATAMVGKTEHSAKFDNDKGLDQFSDRLKSLGYNLHICMEATGSYIEVADYFAQYYSVYVNVPLKISKYAESRFKRTKTDQDAKLIQYCRSAKESLVRKQKPTDEQY  
RLSRMTAAYAIQKSECAAMKNRHHAARDERAAKAYAIKAMNEQLEVLKEKIKETPKNCKEKGKRLLETPAIGRMTAAVLPHLITSSKFETSNKPAFAGLSPQKQESGTSVRGKGL  
TKFGRNKLRAVLFPMAVAYIRAPDFIKRLEKKPKKVLIIAALMRKLAIVIAVHVHKKGGVDYDPSRYKSA

## SEQ ID 2699

TTGCGCGCGAAGCGTCCGCTCATGATGATGGGAGCTTTCCGCCCAAGGAAGCAACCGCGCATGCGATTTCATTATCCGAATTTCCAAAACGATATGTGGCGGTTTACGGGCTGGTGT  
TTTTTAAACGATGCGCGGCAATTTCGGATGCCGTCCACCGGGAGGCTCGGCACCTCTGAAAAGCGTTTGACCGGAGAAAATCAAGGCGTTTTCGACGAAACGGGGATTCGCTCCTGTCC  
GACCGTGTGAAGGCGGCAAGGAGCAGCGCAATGCGTCCGACAAGTTTAAAGTAGTTGAACCGCTGATTTGGCGCGGTTTGGCGAAAATACAGACTGCCGCCATATTGTAGC  
ACAGGCGGCAAGGCGACGGAATCTGCTCGATATTCAGGGCGGCGCATCAAAATGCCGAAAACGGCGGAAACCGTCCGCTTCCGTTTGGCGGAGGGATTGACACTGACGCGCTGC  
CTTCGACTTCGCGGCTTATCTTTGAGTTTGGCGAAAAGGCGAGCGGCTATTCGGCGTTTTCGAAATGGCGGGCTTGTGTGAAAAGCAGTTA

## SEQ ID 2700

LPPKAAVMNGTTPPKEDKRAMQFHPNPNQDMRVYGLVFNDAAHFRMPSHGEAAHSEKAFDAEKIKAFHERGIASCTPVLAAREHGNASDKFLKVVETVDLAVALAKIPDCRHICT  
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## SEQ ID 2701

ATGAAGAACTACACCGCGCCGACGAAAAGGGCTTTTTCGGCGAACACGGCGGGCTTATGTTTCCGAAACCTGATTCCCGCTTTGAAAGAGCTGGAACAGGCTACACGAAGCGGAA  
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GCGCGAAGACTTGAACCAACCGCGCGCACAAGTCAACACCATCGTCAGGCAATGCTTCCCGCGCTATGGGCAAAAAACCGCTCATCGGCAACCGCGCGGCTCAGCAGCGC  
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CGGTACTGACAGCGCTTCGCGAGCTATCTGATGCGAGACGAAACCGGCAAGTCTTTGGGACGCACTCTGTTTCCGCGGCTTGGATTACCCCGGCGATCGGCGCGGCAACACAGCATCTGCA  
CGACATCAAGCGCGTGAATACACCGTTGCCAAGATGACGAAGCACTCGAAGCTTTGAGCTTGTCTGCGGATTCGAGGCGATCATCCCGCGCTCGAATCCAGGCGACGCGTGTCTGG  
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## SEQ ID 2702

MKNYHAPDKGFFGEHGLYVSETLIPALKELEQAYNEAKNDPEFWAEFRRLKHVYGRSPVYTHAARLSEHLGGAQIWLKREDLNHTGAHKVNNITGQALLARRMKKRVIAETGAQGHG  
VASATVAARFGMTCDVYMGADDIQRQMPNVFRKLLGANVIGVDSGSRITLKDAMNEAMREWVARVDITFYIIGTAAGPAPYPEHVRDPQCVIGNEAKAQMQEATGRQPDVAVACVGGGNA  
IGLPYPIIEENVRVLGVVEAGGLGVDTPDHAAPITSGAPIGLVHGFRLSYLMQDENGQVLGTHSVSAGLDYPIGPEHSHLDIKRVEYTVKRDDEALEAFDLICRFEIIPALESSHAVAN  
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## SEQ ID 2703

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AATGACTTGAATTTTGAACACATCCGCAACGCTGATGAAGCGCGCGCATTTGTCACCAACACACAGACACGCTCCCAATCACTAACGGGTAAATCTTTAATACCAATCCGAAC  
GCCCTTTCGTACATAGTATACAAATGACTATGACGAAGATAATATAGTTATTTATACCGGCAAGCGGACCCATCCCAAGGCAAGATCTTTATACAAAACTATCGTTATTACGC  
AACAATCAGGTTATGACGCTTTAGCGGTTTTCGCTTTGCGGAAGAAACGGAAGGACATAACGGCGCATTTAAACCTTAATTTCAATGGCAAAAGCGCGCAAAACCGTTTCTGTTAACAG  
CGCGCGCAATTTAAACGGAATAAAGCGTAACCAAGGCAATGCTTGTATCAGGTGCTCAACACACACAGACACGCTCCCAATCACTAACGGGTAAATCTTTAATACCAATCCGAAC  
CTCCAAAAACAAAGTACGTTTGAAGACGATGATGATAACCGCACATTCAGGCGCGGAGAAATTCGGTTAAACCAATCCGATCATCTCTTCGCGGAGAAATGTATCCGATCACC  
GCCAATCATCCGCAACAGCAACGCCAAAGTAAATTTGGGTTACAAACCGCGGATGAGGTTTGGCGTGGCTCGGACTATACCGGTTACGTTACCTGCAACACAGGCACTTATCCGATA  
AGGCTTTAAACAGCTTTGATGCGACACGATTAAACGCAATGTGAATTTGAATCAGATTCGGCATTTGGTCTTGGCAAGGCTGCAATATGGGGGCAATTCAGGCGCAAGGCAAGCGG  
TGTGAGCTAAACCAACATAGCAATGCGATTGACCGGCGCAGGCAAGTACCAATTCAGGATTCGATTTGGAACAGCTTGTGATGGAACAGCTTCGATTCGCAAGCTTCGATTCGCAATGAA  
TACCACGATCAAAATCAATCATTTATCGGTAAACGCGCATTTTCAITATCTGACGAGCATTTGGCGAAAAATCTTGGGATAAAGTGTGTGGAAGGATCCGATCCGCGCATTCAGC  
TCCATGTTTCAAAATAAAGCGGCAACCTAATCAGGAAGGCTGGATCTCTTTGATGATCATCCGTACAAGACGCTCCCGCTTTTGTTCCTTGGCAATCATTCAGTTCGATTAGG  
CGCATTTGCTATACATCAAAACAGAAACCGGTTTACCGGTTGTACATCTTTATGCGGGAAACCGCGCGGACGTAAGCGCGCGCGCTCTCTGCGGCAACACCGGCTTCTCAAGCA





**SEQ ID 2716**

EQ ID 2716  
LKMIRMOTKSLSIIRDNGKLSIVIPAKAGIQRQKAABIYRKEPNHKNRLPIFA

SEQ ID 2717

[illegible]

SEQ ID 2718

SEQ ID 2718  
NFLFPLSLFCYSSSEDGKPVFVVRFFPINF CGPLSLDSRFGNDGKFAVVS DNTEAFRLHSYHFQILL

SEQ ID 2719

SEQ ID 2719  
ATGATAAAGCAAGCCATAAAACCGTCATAACAAGATTGTAAATGATAAGAATGCAACGAAAGCGCTCAGTATTATCCGAGACAACGGCAAACTTTCCATCGTCATTCCCGCAAAAGCG  
GGAATCCAAAGACAATAAAGCCGAGAAATTTATCGGAAAGAACCGAACCACAAAACCGGCTTCCCATCTCGCTTGAATACAGAACAAAGAAAGCGGAAATAAAAAACATCGGGATTCTTT  
TTTTAAATTGGCAATAAAACACCAAAATGAA

SEQ ID 2720

SEQ ID 2720  
MIKOSHKTIVITRFENDKNANEKPYIYPRQOTFHRHSKSGNPKTKSRNLSETEPQKPASHLFLNNRTKAKIITSGFFFFKLAIKHNE

SEQ ID 2721

[illegible]

SEQ ID 2722

SEQ ID 2722

MTVLMLCPIVCFLYREWGDVFRREWLPWCWVVGVAVSFALSVVPHWFWLAAFAVLAVLARRFAPAGLMCLVLAGAAYGVFRTEAALLSQWRAEAVSGVPLTVEVTDMPRSDGRRVQFAAK  
AVDSGGRTYDILLSDYKRREWAVGSSRWRTARVHPVVGELNRLGLNREAWLSNGVGGVTVGADRVLLHGSSGWIATVWRSRISRNWQADADGGLSDGIGLMRALSVYSGESALRPELWQ  
AFREPLGLTHVTSIGLEHTVMVAVLFAWLAKRLLACSPRLPARPRAWVLAAAGCAGALGYALLAGFSVPTQSRVLMILAAFAWAMRRGRLSAWATWQALAAVLLFDPLAVLGVGTWLSFGLVA  
ALIWACAGCLYEGKRQYAVRGQWAAASVLSVLILGYLFASLPLVSLPVLNAVSIPIWFWLTPALILGSGVVPFAPLQQAQFLAETTLRFLVWLADVSPFEVAVAAPLPLLVLAACAILLLGL  
PRQGLRLPWAVLGLGQFVSYRPEAVPENEAAVTVWDAGQGLSVLVRTANRHLLFTDTGTVAQAQTGIVPSLNAAGVRRLLDKLVLSHSDSHDGGFAPWQKTIPIWGKIYAGQPEFYEGARHCAE  
FQRMWDGVDVFEFLRPSERKNIDNGKSCVLRVVGAGAAALLVTGDLDTKGEESLVGKYGNLVSQVLVLGHGSGTSSSGVFINAVSPEYAVASSGYANAYKHPTAEVQNRVRAHGIKLLRT  
DLSCALQFGLRGGVKAQRLRVYKPYWQKPFPE

SEQ ID 2723

SEQ ID 2723  
ATGAAAAAAATCTTTTAAACGGTTTCATTAGGTTTGGCACTGAGTGCCCTGTGCCACTCAAGGTACGGCGCATAAAGATGCCAGATTACCCAAAGATTGGAGTGTGGAGAAGCTCTATGCGG  
AAGCCCAGGACGAATTGAACAGCAGCAATTTATACGGCGGGCTGTCAGTTTATACGAATTTGTGAAATTCGCGCTCCCCACCAGCGGCCATGCCCGGCAATCCCACTGGATACCCCATPACGC  
CTATTTATAAGACGATGAAAAGACAGGGCTCTGGCGGCAATCGAACGCTTCCCGCGCTCCATCCGCGAGCATCCGAACATGGATTACGCGCTGTACTTGC CGCGCTTGGTGCTGTTTAAAC  
GAAGATCAGTCTCTCTGAACAAACTGGCTTCCCAAGCATGTGCTCGACCGCACCAGCCGAAAGCCAACCGCGAAGCGTACAGCGCTTTGCGGAATCTGTCACACGCTTCCCGAAGACGAAAT  
ACGCGCGCGGATGCAACCGCAGCATGTGCTCAACTGGTCGATGCTTTGGCGGCAATGAAATGTGGTGCGCGTTACTACATGAAGCGCGCGCATATATCGCGCCGCGCCCAACCGCGCCAA  
AAAAAATATCGCGCAGCTATCAAATACACGCTATGTGCGAAGAATCACTGGCCATATTGGAACCTTGCTTACAAGAGTTGGACAAGCCCCAGCTTGGCCCGGATACGCGCGCGTATTGGAA  
ACCAACTTCCCGAAAAGCCCGTTTTTGACGCACGCTTGGCAGCCGACGATATGCCCTGGTGGCGCTTACTGGCAT

SEQ ID 2724

SEQ ID 2724  
MKKILLVTVSLGSLASACATOGTADKDAQITQDWSVEKLYAEQDELSSNYTRAVKLYEILSRPPTSRHARQSOLDTAYAYYKDDKDKALAAIERFRRLHPQHNPMDYALYLRGVLFN  
EDQSFLNKLASQDSDRDPKANREAYQAFELVQRPFPNSKYAADATARMVKLVLDALGNGEMSVARYMKRGATYIAANRAKKIGSYQNTRYVEESLAILELAYKKLDPQLAADTRVLE  
TNFPKSPFLTHANQPDPMWRYWH

SEQ ID 2725

SEQ ID 1275

GTGGCACAGGCACTCAGTGCCAAACCTAATGAACCCGTTAAAAGAATTTTTCATGCAGAACTACTTCCTTTGATAATGAATCCGATTATAGCGACGATTACAGACTTTGCGTCAGCTTCGG  
GACTGAAAACCGTATCGGCTCGACCGTTCCGCTCGAGGCTTCGCGGGCGGGCGGTGGATCGCGTTGGCGGAAACTTC7GCCCCGACTATTTCGCGCAGCGCGCTGCATCATGGATTAAAGA  
AGGCGCGGTATTGTAAACGATAAACCTTCGCAACCCAAAGACAAATGATAGGCGCGGCAAAATTTGTGTAACCGTCCGTCGAGTGAGGAAAAATCTGGCGTTTGTTCGCGAGCGCATG  
GAPTTGGATATTGTTACGAAGACGATACCGCTCATCGTCTCAACAAACCGCGCGGACTGGTGGTGCATCCGCGCGGCGGCAACTGCAGCGGGAGCGCTGCTCAACGGCCCTGTTGGCGCAT  
GCCCCGAGCTGTCCCAAATTCGCGCGGCTACCGCTGCTACCCCTTTGGGACAAAGAAACAGCGGGCTGATGTGTGTTGCCAAACCCCTGCGCGCGCAAATTCCTCTGTGAGGACGCTTCA  
AGAACGCACCGTCAACGCACTCTACGCGCGCTCGCCAAACGGCATCGTCCCCCTTCGACGGTAAATTCGAAACCCAAATTCGACGCGATCGGACCAACCGGTAACCATGCGACGCGCTCAAA  
TTCGCGCGCAAGCTCGCGGTAAACCAACGCTCAAAAGTGTGGAAAGCTATCTTCGCCCACAGCTACATCGAATGCTTCGCTCGGAACGGGACGAGCGACCAACCTAACCTCCGCTCCATATGCGCGGAG  
CCACCATCCGCTTCGCGGACCGCGTTCACGGCAACCGCGCATTCGCTCGCGGACACCGTGAAGAAAGCGCTTAATTCATTGTTGCTTCGCTCCGCTTTGAAGCGGTTTGGATTGCTCTTTGACCAATGAA  
TTTTACCATCCGGAAGCGCGCAACCGTTTCGTTTGAGGACCGGATTCCGGAAGCATATATCATTTGTTGCTTCGCTCCGCTTTGAAGCGGTTTGGATTGCTCTTTGACCAATGAA

SEQ ID 2726

SEQ ID 2726  
VAQALSAPKNETVKRIFMQNTSFDNESDYSDSDPASAGTENRIGLTVPLELAGGRDLAVLAKLLPDIYSRSLTSWIKEGAVIVNDKPSQPKDKMIGEIQVTPVRPSEENLAFVPEFM  
DLDTIVYEDDTVIVVKNPAGLVVHPAAGNWTGTLNLGLAHCPELSQIPRAGIVHRLDKETSGLMVVAKTLPQNSLVRLQERTVVKRIYRAVANGIVFDGKIETQIGRDPHNRLKMAAVK



FGGKPAVTHVKVLERYLAHSYTECSLGTGRTHQIRVHREANHPLAGDPVYGNPRHPCGDTVKEAVKSLGARQALHAYRLSFTHPESGRTVSFEAPTDDIYHLLSVLRLEAGLDSSLSNE  
EEHQDKFGADDDDDNEDDYDEVVYVRE .

**SEQ ID 2727**

TTGAAAGGCGGGGCGAACG CAGGCAGCCGAACCGGAGCAGCCGGGCAATCGTCCCGCCGATTTC AAACAAAGGCCGTCTGAAGGGGCCGGCAGAAAACCGCCGTTTCGGTTGCCCGGTT  
CAGACGGCATTATGATGAAAGGCGTT

**SEQ ID 2728**

LKGGANAGSRTGAAGQSSPPI SNKGRLKGPGRNRRFRLPRSDGIMKGV

**SEQ ID 2729**

TTGACGCTCAAACTTCCGACTTCGATATTTTGTGTCAAAACCCCAAAGCCGTCATCATCGGCGTAATCGCACAAATTGCACATTATGCGCGGCAACCGCCTGGCTGCGCTCCAAACTGTTGA  
AOC TGCTGCGGAAATCGCGGTGCGGCGTGAATTTTGTGTGCGGTGCTGCCCGGGCGGTACGCGTTCCAAATGTGATGACCTATCATCGGCGCGCGGCAATGTGCGCTTTGTGCGGTTGCGGTACGCT  
TGTTTCCACCCGTGAFTTCCCAATGTCTGACTCCCGCCCAFTTCTCTGATGCTTGC CGGTGAAATGCTGGAAATCCAAGCGGCGCGGTATGTTGATGTCCATCGTCAAAATGGT TTTGCTCCC  
ATTGTTTGGGTTTGATGTGTCATGAAGTTTGTGGCAGTAAAAACGAAAAAGCCGACCGATGCGCTGCCGCTGGTTTCCGTTGCCCGCATCGTGCTGAFTTATCGGCGCGGTAGTGTGGGCA  
CAAAAGGCAAGATTATGGAAGCGCGCTGCTGAFTTTTGTGCGGTTGTGCTACTCCGCAACGGCATCGGTACTCTGCTGCGCTCTTTTGGCGCGAAATGGAACCGGCTGCCCTTATGATGTCACA  
AAAAACGCTGCGGCATCGAAGTCGGAATGTCABAAACTCGGGCGCTGGCCGCGCGCTGTTCGCGCGCGCACACTTTGCGCGCGCGCGGCTGTGTCGCGCTCGGGCGCATGTGTTTCAGCGTGTGGCAC  
AATATCTCCGGCTCGCTGCTGGCAACTTATTGGGCGGCGCAAAGCCGGTAAACATAAAAAAACCCCTAAACGCCCTTTCATCATAATGCCGTC

**SEQ ID 2730**

LTLKPSDFDILFKHPKAVIIGVLAQFAIMPATAWLPSKLLNLPARLAVGVILVGCCPGGTASNVMTYTLARGNVALSVAVTSVSTLISPLITPAIFLMLAGMLELTAQAGHMSIVKRVLLP  
 TVLGLIVHEKVLGSKTEKPTDALPLVSVAAIVLIIGAVVGASKGKTHESGLLIPAVVVLNRNGIGYLLGFFAAKWTGLPYDAQRTLAIEVGMQNSGLAALAAAHFAAAPVVAVPGLAFSVCH  
 NISGSLATYHAAGKAGKHKKTLNAPHENAV

**SEQ ID 2731**

ATGGATGCTTGTGTTTTTTCGTCAATCCCGCACAGGCGGGAATTCGGAGATTCCGGGATTGTTTTCAAACGTTCCGGTFCGGATTCTTCCCGGTGCGGGAATGATGCCCTTATATACTTCTCCG  
AGCTTTTATATGCTTCAACAGGGGACGGCACAATCAAGCACCGCACTGCGTGTTGCCCGAACGAGGCTGCCCTCCGATTAGATTCTATCGCTATAAACAGACGGGTTTCAACCGAAAAGGAAT  
GGGGATAAAGTCCATTCCGCACACTCTCGGCGGATGCCGCTCGAAAACCAATCTCCACTTTTCAGACGGCATTTGTT

SEQ ID 2732

MDACFFVIPAQAGIRRFGIVFKRSGRILAGAGMPLYTFSELYMLQOGTAHQAPHCVLPERGCPPIRFYRYKQTGFNRKGMGIKSISDTSRAMPSENQSPISDGIV

**SEQ ID 2733**

ATGAAACCACATCACGAAACCCCTAAATCTCGCCCCGAAAGGCAAAACTTCTGTACCCGCCGATTGGCCCGCGCCCGCCAATGTGAAACCCTGATTACCAACGCGCAACGGCGCGGTGAGCC  
AAGGTGCGTATCAGAGTTTGAACCTCGGTACGCACGTCGGCGACGACCTGAAACCGTGGCCCGCAACCCGGAATCTGTGCACACAGCAGGTGCGATTGGCCGTTGCCATATCTCAATCAAAT  
CCACAGCACAAATTTGCGTCAATGCTGCCGAAGCAATTTGGAGCGCACGCCCGGATGCCGACGCTCTCCGTGGACGACACGGGTAAAGCCGCTGTGTGCCGTGATGACTGCGAGACTGTCTGCGCGGTT  
CTATTTTGGCGACAGGGCAGGTACGGCGGTTGCCGCCGACACGCGGGCTGGAGCGGTTTGGCGGGCGGCGTATTGCAAAACACCAATTGCCGGATGAAGGTTCCCGCTGTGCAAAATATATGG  
CGTATCTCGGCCCTGCCATCAGTGGCGGATGCGTTTGAAGTCGGGACAGGACGTTTGTATGCGTTCTGCACGTCCTCATGCCCGAAGCCGCTGCTGCACTTTGAACCATGCGCGGGCGGCAAAAT  
CCTTGCCGACACTCTACGCGCTCGCCCGCTGTAATCTGAAAGCGCAAGGCGGTGGCGCGGTGTACGCGACGCAATGTACGGCTTTTGGAAACGGGATATTTCTTTTCCCTACCGCGCGGAC  
GATGACACAGCGGCGGTATGCGCACTGTTTGGCTTACGACGGCAATGCCGTC

**SEQ ID 2734**

MKTITFETLNLAPKGNFLTADWPAPANVKTLPITRNGGVSQGAYQSLNLGTHVGDDPETVRNRNKREIVQQQVGLPVAYLNLQIHSTIVVNAEALDGTDPDASVDDTGKAVCAVMTADCLPV  
 LFCDRAGTAVAAAHAGWSGLAGGVLQNTIAAMKVPVPEITMAYLGPASADAFEVGGQDVFDAFCTSMPEAAAAFPEIGGGKFLADLYALARLILKRBGVGGVYGTHCTVLERDIFFSYRD  
 GATGRMASLNLGNAV

**SEQ ID 2735**

ATGAACAAAATATTCCTTACTGCCGACGCTTGGTGTGGGCGGTGCGGTTCACACCTGAAAGGTGCAGACGCGATTTCCTCGGCGTGACCTACCGGAGCTGGCACCATCGAAGCGGAC  
AGGCATTGCAGTTTCCTTTGGAAACCGCGCTGATCAGGCTTCGGGCAAGGTGGACGATGCTGCCGGCGCGCAGATGACCTGCGTATAGACAGCGTTTCCAAAAACAAGGAAACCTATAC  
CGTTACCGCTGCGGCAGTCATCAACGAATATCTTTTGATATTGACGTTGAAGCGCAGGATTGAAACGCGGCGAGCGGTCGGCAAACCGATGACCGTGTCCGTCCGCGCGCATTTTGGAT  
TATGCGGACAACGAAATTTTGGGCAACAGGAAGAAGAAACCTCTGGGCGGAAATGCGCGCAGGATGTTGCCGAACAGATTGTCGCGCGCGTGACCTTTCTGAAGCGCGAA

SEQ ID 2738

MNKIFLITAAALVLGACGPHLKADGISPPITVRSWHIEGGQALQFPFLETALYQASGRVDDAAGAQMTRLRIDSVSQNKETTYTVTRAAVINEYLLILTVEAQVLARGEVPVGKPMTVSVRRILD  
 YADNEILGKOREEETLWAEKRODVASQIVRRITPLKAE

SEQ ID 2737

[illegible]

**SEQ ID 2738**

MRPICAATSFTVRKQKGQAADNLPGNLIPLHFPRQGGFFFLFAQNFFVGIQNAADGCHGRFADRLAAFPYLRFNRQYQKIPVDDCRTGNGIGFLVLGNNAVYTOGHLRAGSIVHPARSLIQRGF  
ORKLOCI.SAFDVPAPVPGORRRNAVCTFOVETARAHOCCGSGKEYVHRLPFSKA

SEQ ID 2739

GTGCGGCGACATATCGGAGCGCATCGATACGGACGCGCCTTTGAAACCTCTGTACGTCATCCACGGCGAGGAAGAAGCTGCTGCGTATCGAGGCGATGGAGCGCATTTGAGGCGGGCGGCGAAGA  
AGCAGGGTTATCTCAACCGGAGGCTATACCGCCGACGGCTTTTCGATTGGAACGAACTGCTGCAAAACCGCAGGCAATGCGGGTCTGTTTGCCGATTTGAAACTGTTGGAAGTGCATAT  
CCCCACGGAACACCGGCAAAACCGCGCGGAGGCATTTCAGGATTTTTCGCGCCGAGCTGCGGGAAGATACGTTAAAGCTGGTTTTCGTCGCCAACTGGAGAAACCCGGCTCCAGTCC  
AAATGGTTTTCGCGCATATGGCGGCAAAAGGGGGAATGATGGGAGGCAAAACCGGTGCGGTGCGGCGGGCTTTGCCCCAATGGATACGCGGAGCGGCTGGACAAAATCGGTTTGGGTATCGAGGCGAG  
ACGCAATGGCACTGTTTTCGCGAGCGGCTGGAAGGCAATCTGTTGGCGGCACGTCAGGAATGCAAGCTCGCGCTGCTGTATCGAAAGGGCATGCCGTCATATCGATGAGGCGCAAC  
CGCGTTGCCAATGTTGCCCGCTTCGACGCGTTCCAACTGGCAGGCGGCGTGAAGTGAAGGGCGATGTCGCCGCGGTATGCAAGGCTGTTGGACGGGTTCGGAAGGAAGGCGAAGAACCGGTG  
CTGCTCTGTGGGCGGTTGCCGAAGAGCTGCGGACGCTGATTCGGCTTGCCCTGCCCCTGAAACAGGGGCGAGAGCATCCAAATCCGTCGCCAACAGCCTCAGGCTTTGGGCGCAACAAAGA  
CAATCGCACCGCTTGCGGTCAGCGGATTTCCGCTGTCGCCCTGCTTGACGCGCTCAAAACCTGCGGCCAAATCGACCGAATCATCAAGGCGCGGAAGACGGCGACGATGGAACGGTATT  
CGACCTCATCTGTCTGTCTGCTGGCGGAA

SEQ ID 2740

VAHHIGRIDTDAPLKPLYVHIGREELRLI BAVDALRAAAKQGYLNREAYTADASTFWNEGLIQTAGNAGLPADLKLELHHPNGKPGKGGEGALQDFAARLPEDTFTVLVLLPKLEKTRIQS  
KMFALAAARGEVWEAKPVGAALPQWIRGRDLKIGLGIEADALALFAERVEGNLLAARQIEDIKALLYPKHAVNIDEAQTAVANVARFDAPQLAGAMEKGDVPRVCRLLDGLKEGKEEPV  
LLHVAVEDVRTLIRLAALKOGOSIOSVNSRLRNGDKOTLAPLAVKRISVVRLLDALTKCAOIDRIKGAEDGDANTVFKOLVVSLE



**SEQ ID 2757**

SEQ ID 2757

ATGTTGAACAAATAATTTTCTCGGTCGAGTCGCCGAATCGAACCCCTACCCCGAAGCCGCGCGCGAAAAAGCCCGGAAAAAGGCTTGTGCCGGTTTGTCTGGAGCAGTATGGACGGGGTGGCGA  
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CGAAAAAGGTTGGGAATGGCGGCAATGGCGGCGATGATGGTGTTTTCGTCGTGTCGGCGTTTGC CGCTGCCAACGTGCGCGCTCAAACCCCTTCAGGGCGGTGTTCCTTATGCGCTCGCG  
TGGAACTTCCACCGCCGTGATGCTGAACAGAGCCTCGGTTTTATCAGGACGAATTTGCCGCGCCGCTGTGCGCCAAAGTCATGCGAGAACCCGCGTGGCGTTTGGCGACGCGGTGATGACGG  
TTGCCGATATGGTGCTTATGTGTGTCGGTGATTTTCACTACTCGGGCGGTGATTTCTCGCCCTCGCTCGACTCATGGCTGCTGTCGCCCTTTATCGGCTGGATAATCGGTTTTCCGTTCTGGTAAAT  
CGCGCTGTGATTCOCAGATTTGGGCAAAACCGCGCACGCGAGCGGAATGCCCGCTCGCTGATGACCGCGCGGATTAACGATTCGCTTATCCAGTATGCCCAATGCGGCTCAAACTCTTTTTCAC  
GGCGCGCGGAAGCCGTCTATGCCAAGCAGTCGATGGCAAGAAATTTATGGTTACGGTGGCGCGCGGCTGCGGCTGCGGACACCGCCACCGCGATGGCGTTTGGCGCGCAACGGGCTGTGGCAATACATTATGTG  
CCCTTCCACCGCGCGCTACTGGGCACTTGGCTTTGGCAACAACCGGACAGGTGCGCGGGTGCGGTGCGGACCGCCACCGCGATGGCGTTTGGCGCGCAACGGGCTGTGGCAATACATTATGTG  
GGAATCCCGCGCGCTGTTGGAAGAACATCGCATTCGCTCAACGACGGCATGGCGACCTGTGCCAAACCGCACACCATCTCTCGACAAGCCCAAGCCCTTGGCGCTGAACTGGCGCAAGGGCGCA  
ATCAAGTTGCAACACGTGATTTTGTCTAGCAAGCGCGCAACCGCTGCTCAACGGCTTTAACTGAAATATCAAAACCGCGCGAAGGTCGCGTTGATCGGACGCGCGCGCGCGGCGCAAT  
CCACCATCGTCAACCTGCTTTTGGCTTTCTACGAACCGCAAGCGCGCACGGTTTCGATCGACGGGCAAGCATTAAGCGCGGTTACCCAGAATCTTTACGCGCCCAATCGGTTTGTGTCAC  
ACAAGATACCTCGCTGCTGACCCGTTTCGTCGGCGACAACTATTATTACGGCGCGCCCGACGCGACCGATGCCGAATGGTTTCCGCGCGCGCAACGGCGCGGAAGCGCGCGCTTCATCCOC  
GACCTTTCGATGCCAAAGGGCGGAGCGGCTACGACGCGCACGTCGCGGGAACCGCGGCTGAAACTTCCGCGCGGACAACGCGACGATCGCCATGCGCCGCGGTGATGCTCAAGACGCGAC  
CCATCTGCTGCTTGACGAAGCCACCAACGCGCTGATTTCGAAGTTGAACGCGCATCAAGAAAGCGCTCGACAAATATGATGAAGGCAAAACCGCTCATGCGCATCGCCACCGCGCTCTC  
CACCATTCGCGCGATGGACAGCTGCTGCTCTCGACAAAGGGCGGCATCATCGAAGAAGGCACACACGCGGAACCTCTCGAAAAACGGCGGCTTTACGCCAACTCTGGCGCACCGAGAGC  
GGCGGCTTCTCAGCGAACACGCTCGAGTGGCAGCACGAC

**SEQ ID 2758**

SEQ ID 2758

MLNKLISWPFSEIDDPYPEAAPKTPKEKGLCRFPWSSMDGVRKWIAALALTAGIGIMEALIFQPMGKIVEHGLKYAPAEKPAEKGWELAAAMAAMVPSVVWAFAPASNVRILQTLQGVFPHRLR  
WPHFRMLNMQSLGFGYQDEPAGRVSAKVMTALALRDAVMTVADMVVVYVSYVYFITSVGILASLDSWLLLEPTGTWIIGFASVMRLILPLRGQTAAARQANARSLMTGRITTDAYSNPATVVKLFPH  
GAREAVYAKQSMEEFPMVTVRAQMRLATLLHSCNFIVNTSLFLSTAALGTLWLNHNGQVGVGAVAPATAMALRANGLSQYIMWESARLFENIGIVNDGHAFTPLDKPQALPLMWPGQA  
IKPFHVDFCYEAGKPLLNGFNLIKPGKVLIGRSGAGKSTIVNLLRFPYEPQSGTVS IDGQDISGVQTESLRAQIGLVQDTSILHVSREDNIYIGRPDATTADHVSAAERABEAGFTIP  
DLSDAKGRSGYDAHVGERGVKLSGGQQRQIALARVMLKDAPIILLDEATSLDSEVEAAIQESLDKMMBEGKTVAIAHRLSTIAAMDRLVVLDRGRIITEGTHAEELLEKGLYAKLHAQS  
GGFLSEHVEHQDH

SEQ ID 2759

SEQ ID 2759  
ATGTTCTGAACGGGTTCGCAAGCAGGTTATACCTGTTTTCAAAGTTGAGATGCAGTCTCAAATTTATAGGGTTTCATATATACATACACGATTGCACGGATAAAAAAGTCCTTTTTATAAATCGC  
CCTCGTCAAAACCGGACCGGAACGAAAAAGCCCACTA

**SEQ ID 2760**

MFERVAKQVIVPVFKVEMQSQFYGFHYTYTLARIKSLFYNPPSSNRPETKTPPL

**SEQ ID 2761**

SEQ ID 2761  
ATGTTCTGGCTTAAAGATGGTTCGGGTGCCCGGAAAGACAGTTTGTTTGAAGTTGATTACATTTACGGTGCAGACGGTTGCGGGTTCTTCCGCTCAAATTTACCGGAGTTCAGAAAATATT  
GCCGGAAGAAAGCACCAGAAAGTTTAAAGCAGATGAAGTTTGTAGTAAACCCCTACCGGTCGATTTTGTGGTCCGAAGGAACCCCATATGACACCGCCATGTGACTTCAGTCAAATATT  
TGT

**SEQ ID 2762**

SEQ ID 2782  
MFWLKDRVARKDSLFEVDYIYGADGCGFLPSNLTEFRKYCRKKHQKFKDDEVLVNRYAVDFLGAKRPFYDDRHVTSVKYFV

**SEQ ID 2763**

SEQ ID 2763  
ATGATTTTTCGAAGCCGTGGCTGCAAGTCCGGAATTTATGCGGGGCTGACTGTGTGATACGGCGCAATTTGTGCCATAAAGTTTTTGAAATCGTGAAGCATCTGGTCATGAATTTGGAGTGTG  
CGGACGAAAAACGCCATCATGCTCGCTGTTTTAAATCTGATTGATGTGGTTATGATTTCGCAATTTGCTGACCAATGGTGAGATTGGCGGGGTATGAGTCGTTCTGATATCCCGGTTGCGTATCGA  
CGACCATCTGACGGCCCGGAGTGGTTGAGCCATGTGGAATGCACCGGTATGAAGGTGTCGATGTGCGATTATCGGTATTCATCCATCCATTGCTCCAAACATTTATCAATTCCG  
CCAATCTGTTCGAAAAAGCAGC

**SEQ ID 2764**

SEQ ID 2764  
MIFASRWLQVPITYAGLTVVRAICAYKFLKSLKHLVMNLDVSDENATMLAVLNLDVVMIANLLTMVQIGGYESFVSRLRIDDPDRPEWLSHVNAPVLKVRLSMSITIGIHPSICSKHLSIP  
PICRKS

SEQ ID 2765

SEQ ID 2765  
GTGGTGTGAGCCATGTGAATGCACCGGTATTGAAGGTAAGCGTGTGCGATGTGCAATTATCGGTATTTCATCCATCCATTTGCTCCAAACATTTATCAATTCCGCCAATCTGTGCGAAAAGCAGC  
TGATGTGGCAGTGTCTGGTGCAATGTCTGCTTTTGTGATTTCGGCGATTGCGATGCGCTTGGCCGGATAAAATCGTGTACGGCAGCAGGCACAAAACCGCAT

SEQ ID 2766

SEQ ID 2766  
VVEPCECTGIEGKAVDQVDYRYSIIHLQTFINSANLSEKQLMHCCLVHVCFLLSALAMANADKIVYGTTHKPH

SEQ ID 2767

SEQ ID 2767  
ATGAATAACGCTTTCGCATTACCGCCATCCAAAGCGGCACAGCGAGCCTCGAACAATACATCCACACCGTCAACAGCATCCGATGCTGTCCAGGAAGAAGAAACCGCCCTCGCCGAAC  
GCCGGAATAAAGCGGACCTCAACGCCGCCAAACAACATCATCTCTGCCACTCGCGCTGTGCTGPTTCCATCGCGCGCGGCTATGACGGCTACGGGCTGAATCAGGCGACCTGATTACAGGA  
AGGAATAATTCGGTCTCATGAAGCGGTCAACCGCTACGAGCCCGGTGAGGTGCACGCCCTGTTTTCATTTCGCCGTGCATTGGAATTAAGCGGAATTCAGCAATTCATCTCGAGGAACCTGG  
CGCCTGTTCGGCTTGCCACCAACCAACCGCAAGCTGTTTTCAACCTCGCGAGCATGCGTAAAAACCTTAAATGTCTGTCTCCCAAGAGGCACAAGACATCGCCGACGATTGG  
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CGATTCCGAACCGAGCCGACAACATATCGAAACAGGCGCATTACGCCCTCGAAACCGAAGGCCCTGCAAAACGCGCTTGGCGCAATTGGACGACGAGCGCGCGCATGTGCTGTGGAAGCGCGCTGG  
CTTCAAGACGACGCGCGACTGACGCTGCACCAAGCTTCGCCCGCGAATACGGCGTATTCGCGAGCGCATTCGCGCAGATTGAAGCGAAAGCCATGCAGAACTGCGCGGTTTCTGCACCGAAG  
AAGCCGAAGCGGTT

SEQ ID 2768

SEQ ID 2768  
MNNAPALPAIQSGNGSLEQYIHTVNSIPMLSQEEETRLAERRIKGDLNAKQLILSHLRVVVSIARGYDCYGLNQADLIQEGNIGLMKAVKRYEPGRGARLPSPAVHWIKAEIHEPILBNW  
RLVVRVATTKPQPKLFPNLRSMKNLNLVLSPKBAQDIADDLGVKLSEVLEMRQMTGHDIAIMADNSDDDESPAFIDMLADHDSEP SRQLSQAHYALQTEGLNALAQLDDR SRRIRESRW  
LODDGGI/TLHOLAAEYGVSAERIRQTEAKAMKLRGFLTERAEAV

**SEQ ID 2769**

SEQ ID 2769  
ATGGCGGGTAATGCGAAAGCGTTATTCATTGGGGCATTTCTTTCCGGCTGAAACTCGGTATCGCGGGTTTGGTGTGTGGGATGCAGTATATCACTGCTTGGCTTGTATTTTGTATGTTT  
GGCAGGAGATATACGCTAAGGTT

SEQ ID 2770

SEQ ID 2770  
MAGNAKALFTWGISFRLKLRIGGLVCWDVAVHCLACILYVWQETYAKV

## SEQ ID 2771

ATGTTTCCAACTGGACAAATCTGGCAGCACCCGCTCTACTGGCCTTTGCTCATCTCTTTTTCGCGCCGACCCCTTCGCTTCGACCCCTACTACACTTTTGGCTGATGCCCT  
TGATTTTCGGCGCTTCGTCGCGCTCATCGAACTGCGTCCGCGTTTTCGCGCTTCGCGCTACCTGTTTCGCTTCGACCGCATACACGGCAGCTTCTACTGATACACTGCGCTGCA  
CGACGTTTCGCGCTGCGCGACCTCTATGCCGTACCGCTGACCTTCTGCTGCCGCTTACCTTGCCCTTTATCCGGCATCTGTTTCTGGCTGTGGAAAAATTTACCTGCCCGAGGC  
ATAAGACCGGCTCTGCTACTGCCATCTCTGTGGACGCTGACCGAGTTTCCCGCGAGCGCTTTCCTGACCGGATTCGCTGGCTGGGGCGCAATCGGCTACTCCAAATCACCCGACAGCCGC  
TGGCGGTTTCGCGCTTCGGCGGCTCCACATGGTTACACTGGCAACCGCTTCTCGGTGCTGGCTGTTTTCGGCATCGACAAACCGCAGCTTCGGGCAACGCTGCTTCGCGC  
CAITTCGATTTGCCGCTGCTTTCGCGGCTACACCGCCCAACAAACCGACTTACCCGCGCGGCGAGCGGACCGCTGCTTCAGGGCAACATCGCCCAACCCCTCAA  
TGGCGTGAAGACCAAGTCTATCCGACCATACAGAAATATTAGCAACAGGTCGGCAAAACCACTGCGGACATCTCTGCTGCGGAAACCGCATCTCCATCATGCGCAAAACCTGCGG  
AAAACATCTGCGCAATTCGCGGACAGCGCAAAACAGCGCGCTGCGCGCTGCGCATCAGCAATACACTTCGGACGCAACGTTACGAAACCGCGCTCATCAACTGACCG  
CTATCAGGAAACATCAGGACGCGATCCCTTACTACGCCAAACACCACTGCTGCTTCGGGCAATACAAACCGCTGCGCTCTGACCAACCGGATTCGGGACGAACTGATTCGCGCGCAAG  
CTTTCGACTTCGCAAGGCGCGGCAAGCAATCCGCAATGATGATGAAAAACCAAAATTCGCTTCAACATCTGCTACGAAAGACGGATTCGGGACGAACTGATTCGCGCGCAAG  
ACGCCACACTGCTTGCATATGTCAGCAATATGCGCTGATGAAAAACCAAAATTCGCTTCAACATTCGAGGCGCGGCTATGAACTCGGACGCTATATGCTCGCGC  
CACCAACCGCGCAACCGCATCTCCCGCAAGGCAACATCTGCGCAACCGCAACCGGATACGAAACCGTATTAGAAGGACACATCAAGGCTACATCGCGCAAGCGCTAT  
ATGAAACCGCGCATCTACGCTGATGCTGGCATATTGACCTAGCGCATGATCTTTTCTCTTCGAAACAAAGAAC

## SEQ ID 2772

HFSLDKYWHQHPALYWPILLFAAATPFAFYHFWLMLIFGAFVRLIELRPRFAASSAYLFGLTATYAFYWIHTALHDVSGLPDLYAVPLIFLPAFLALYALCFWLKFKLPLQ  
IKTGLVLPILWLTETAFERERFLTGFGWGAIGYSQITPDSPLAGFAPLGGIHMVLTATLFGVWLVAIDMTARSGRLLPAILIAALLAAGYTAQQTDFTRPDGSRSTVALLQGNIAQTLK  
WREDQVITIQKYEQVQKTTADIVLPETAIPIMRQNLPENILAQFAEQQNGSALAVGISQYTSNGYENAVINLTGYQENQDGIPIYAKNHLVPPGETKPLPLLTPLYKMDMP  
LSDFRKGGKQSAMMMKNQKIAFNICYEDGFDLILAAKDATILLANVSNMAYGKSNAMYQHLQSSQARAMELGRTMVRATNTGATALLSPKGNILAQAPDTEFTVLEGHKIGYGETFY  
MKTGSSWMLMGLITLAAILLIFIPRNKEH

## SEQ ID 2773

TTGGCTTGGCGGATGATGTTGCTTTCGGGAGATGATGCGGCTTTCGCGGCTTTCGCGGCGGACCATATAGCGTCCGAGTTCCATAGCCCGGCTCGGATTTGAGAGTGTCTG  
TACATGCGGTTGGAATTTCCATACACCGCATATTTGCTGACATTGCGAAGCAGTGTGCGCTTTCGCGGCGGCAATCAGTTCTGCTCGCGCAATCCGCTTCTGAGCAGATTTGAAGCGA  
TTTTTGTGTTTTCATCATATGCGGATTTGCTTTCGCGGCTTTCGCGAAGTTCGGAAGGGGATGCTCCATCATTTTGTAAAGCGGTGTGTCAGAGGGGACGCGTTTGTATTCGCC  
GAAGGGACGAGTGTGTTTTCGCGTAGTAAGGATGCGCTGATTTTCTGATAGCGGTCAGTGTGATGACGCGTTTTCGTAACCGTTGCGCTCCGAAGTGTATTTGGCTGATG  
CGACGCGGAGCGCGCTCGCTTTCGCGCTTTCGCGCAATTCGCGCATGATTTTTCGCGCATGATGGAATGCGGTTTCGCGGACGAGTACGATGTCGCGAC  
TGGTTTTCGCGACCTGTTCTGAATATTTCTGATGCTCGGATGACTTGTCTTCACGCAATTTGAGGGTTTCGCGCATGATGGAATGCGGTTTCGCGGACGAGTACGATGTCGCGAC  
GCGGTTGAAGTCGTTTGTTCGCGGCTGATGCTGCGGCAAGCAGGCGGCAATCAGAAATGCGCGGAAGCAGCGTTTCGCGCAACGTCGCGGTGTGTCGATCGCAAAACAGCGAGCA  
CCGAGAAAGCGGTTGCCAGTGTAAACATGTTGATGCGCGCAAGGCGGCAATCAGAAATGCGCGGAAGCAGCGTTTCGCGCAACGTCGCGGTGTATGCGGTCAGGAAAGCGGCAAG  
AAGCTCGCGGCAAACTCGGTGACGCTTCCACAGGATGCGGAGTACCGAGCTGCTTATGCGCTGCGGCGAGGTAATTTTTCACAGCGCAAAACAGATGCGCGGTATGCGGTCAGGAAAGCGGCAAG  
GTAGGCGGCGCAGGAAAGTTCAGCGGTACCGCATAGAGTTCGCGGAGGCGGCAAGCTGCTGCGGCGAGTGTATCCAGTAGAACTGTCGCGGTATGCGGTCAGGAAAGCGGCAAG  
GCGGAAGAGGCGGCAAAACGCGGACGCGATTCGATGAGGCGGCAAGGCGGCAAAATCAAGGCGATCAGCCAAAGTGTATGAGGTCGGAAGCGGCAAGGCGGCGGCAAA  
GGATGACAAAGCGCATAGAGGCGGCTGCTGCGCATTTTTCGAGTTTGGAAACATATTCGCTGCTGTTTCGGAAGATGCGCTGACGCTTTCAGACGCGATCGGTATT

## SEQ ID 2774

LGIGDDVAFGGDDGGCAGVGADHIAEFHSPRLRLLEVLVHGVFSIPRHIADIGKQCVFVGGNQVAVSVFVADVEGDFLVFHHHGLLAAAFVVGKGVHVFVRCQGGQRFVFA  
EGDEVVFGVVRDAVILVFLIAGQVDDGVFVTVAVRSVLADADGERAAVVLRLFGELRQYVFRQVLAHDNGGFGQDDVDVSGFADLFVFIPLYGRDLVFTPFEGLDVALKQGDGAAAVG  
AGEVGLLGGVACGQKQGNQNRQAFARTCGVVDQNPQDTEKGCQCNHVDAAQGGETQRAVRGDLGVADCAPAESQETLAGLKGRQPDQYQTLGLYALQKGFPPQPEQCRKIGK  
VGGQEQGRYQIEVGQAGNVVQGSVYPVELCRVCGGTQVGGGKTRTQDEADBEAENGQHPKVVVVCGEBEGGGGKKDEQRPEGVLPVFPVQPKHILRSVRKMPSERLSDGIGI

## SEQ ID 2775

ATGGAGACGAGAACAGCTGTGAAATCCCGTTTTCATCTACAATTTGATATATCTGTTTGTGAATCATGACATCCTCAGATTAGTATTCAGAAATGATTTTAAAAAGAACTTTCT  
GCTTTACGACTCCGCGCGGATTCCTTCAACCGGTTTTCGCGCTCTTCAGTTGCTGATACAT

## SEQ ID 2776

MEFETICEIPVFIYFNDLSWPNHDLRPSIQNMILKRTFCFTTTPPIPSNGFPRSSVVH

## SEQ ID 2777

TTGGTTTTCATATAATGCGCTTTCGTTTCGGGTCGGTTTACGAGGCGGATTATAAAAAAGCTTTTATCCGTGCAATCGTGATGTATAATGAAACCCATAAAATPGAGACTGCAT  
CTCACTT

## SEQ ID 2778

LVFLIMAFSFRVGLTRADYKDFLSVQSCMYNETHKLETASQL

## SEQ ID 2779

TTGCAGATTTCCTGCAACGCGCAACACTGGAACGCTGGCTGGACAGATATCCGCCAACCTCGTTGTCGGGCGCTTTCGGTTCGATTCGCTGCGCGCGCTTTCGCTG

## SEQ ID 2780

LHDFLHAQHWNAGWTEYSANLVVGPLSGSIACAPPCR

## SEQ ID 2781

TTGGACGATGTTGCGCTGATGACCAAGCGCGGCAAGAAACCGCGCGCTGCGCGGCGAGATTTCGCAACCAATGCCAACCGGGTTACAGGCTATCGGCAGAACGCGAGTTGCCGA  
TTGTTTGGCGGCTGGCGAAAGGTTCTTTTGCACAAAGCGGTTTGGGTCTGTCGCGCTCTGCTGCTTTCGCGCTTCTGCGCAACTCATACGCGCTTTTTCAGCGCAGCGGGATTTA  
TTTGTGCTTTGAGGCGCTGGAAGAGTGTGTCACAGTTTTCGCAACGACATGACGCGCAGATGACGCGCGGCAAGCGCGGTTAACGAGCAGGCTAAATCAAGGTGCAATCCGTACC  
GACTTTATCTCTCGCGAGAAATCATCATCTGCGCTGTCGCTGTCGCAACATACAGCTGATGACGCGCTGCTGCTGATGCGCGCGGCAAGCGGATCGGATCGGATGACTGTTTGGGTGACG  
GAATCGTCGCGCTCATCTGCAACTGACGACTTGGGATGCTGCTGATGCGCGCGGCAACCACTCGCGCTTTTTCACGATTTCTGCGACGCGCAACTGGAACGCTGCTGACAGAGT  
ATTCGCGCAACCTGCTGTCGCGCGCTTTCGCGTTCGATGCTGCGCGCGGCTTTCGCTGATGAACTGTTTCGCGAGCAT

## SEQ ID 2782

LDDVALMTKAAAKTAGVAGDDLAPNANRVTVSAERELPIVWPVAKGSFANKFVLVSAALLLSAFLPQLITPLLTAGGIYLCPEGVKLLKFLHRHDAHDDGGSTAVNEQAKIKGAIPT  
DFILSAEIIILALCVVQYSLMTRSLVMAAIGMTVLVYGVIVAVIKLDDLGLMLMRRPQPRFPARFAPARATLERNLDRVFRQPRCRAAFRFDCLRPALSLMNRFRH

## SEQ ID 2783

TTGGGAACGCCATCACCAGCGCATCTCCGAGGAAATCGGTACGCTCTTCGCAAGCCCAACCACTGATATACGCTTTTTCACGCGAGCTG

## SEQ ID 2784

LGTPTSGILIASIGTAPRKNQILYAFSRL





CCCTGTATCCGCAATATGCCGCTTCCAGCAGCGGAGCGGGTAGATAAAAGTGTGCGCAACACTGCTGCTGCAACGCAACCAATGAGCGTCCGCACCAATTTTCGCGCTTTTATGATGATGC  
CGCGTACATTGATGCGATGAAAAACCACTCTCCGATATTTGGCGGGAACACGGCGGTGGGAAAAAAGTATGTTGTAGTTTTCACGGCGTACCGCAGAAGCACTACGACCTCGCGGAACCC  
TATCCCGCAGAGTGGCGGCCACCGCCAACTGCTTTGCGGAAGCACTGGAAGTACCGGATGCTTTCCAAAGCCAAATTCGGCAGGGGCAAAATGGGTATACACCGAGCA  
CGCGAGATTGTGTCGCGAAACTGCCCAAACAGGGGGTAAACGAGCTGGAGCTATTTCTGCCCGGGCTTTTGGCAGACTGCTTTGGAAACCAATGGAAGAAATCGCCTGATGGGGCGGGAACA  
GTTTTATGAAGCGGGCGGAAAAAATACCCTACATCCCTGCGCTCAACGCAACCCCGACTGGATAGACGCACTCGTGCACCTTCCGAAGAAAAACCTTTGGCGGCTGCGCT

**SEQ ID 2796**

SEQ ID 2796

MPSEAASDSILPLYPACTIIFQKPIHLPLFLPEPSLSYTPQNRITAVLLNLGTPDAPTAQAVRPYLKSLFTDRRIVELPKNLWYPIILHGLVLTFRPKKSAHAYEKIWFKEGSPLEVYTAQAA  
ALAEKMPDLIVRHAMTYGNPSIADVLAELEKSKQSGVGRLLLAIPYQYAASSSSGAANDKVCEQLLQRNQMSVRTISRFYDDAGYIDAMKNNILLRTWAEGRGKKMLSPHGVPQKHLYDLGDP  
YPDECRHTAKLLAAEALTEDEYTVSFQSQFGRAKWTPTSTQDLFGKLPKQGVTELDVFCPGFLADCLEMEETALMGREQFYBAGKKNYRTIPCLNDNPWDIALVALAEENLGWR

**SEQ ID 2797**

SEQ ID 2797

ATGAAACCCGCAAAACCTGCACGACATCAAGCGCAAAATTATTTTGGGCAACACTTATCATTTGTGGCTGCGTCCGGTGTGGAGGTCGTGCAACAGTTTGGAGGGCTTCACGGTTTATACG  
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AGCTTCGCGCTGGCGGAACGGAGCAAAAAGCCTTTGAAGATTGAAAAACCCGAACGCGCTGTTTCGGCATCGTCAAGCGCGCATGTATGAGGATTTGCGCGAAGAAATCTTTGCGCGGTT  
TGGAGGAATTTGATTTTCCCGGCTTTGCGCTGCGCGGTTTGTGCGCTCGCGGAACCCAAAGCCGGAATGTACCGTATGCTGCACGCGCGTGGCGCCGATGCTGCCCAACGCAAAACCGCATTA  
CCTGATGGGCGTAGGCACGCGCGAAGACCTCGTGTACGGCGTGGCGCGCATCGATATGTGCTACCTGCTGATGCCACCCGCAATGCAACGCAACGGCTGGCTGTTTACCGGTTTTCGCG  
GATTTGAAATCAAAAACGCCAAACACAAGCCGACACGCGTCCGATAGACGAAGCAATGCTGCACTGCTACGCTGCCAAAATTTACGCGCGGCTTACCTGCACCATTCGACCGCGCGCGGCG  
AAATCTTGGGCGCGCATTTGAACACCATCGCAACCTGCAATTTCTACCAAGTCATCATGCGCGAAATGCCGATGCCGTGCAACAAAGCAAAATTTGCCGACTGGCAGGCGCAATTTCCACGA  
AAACGCGCGCGCGCGGTGGAC

**SEQ ID 2798**

SEQ ID 2798  
MNPQNLHDIKAQIILGNTYHLWLRLPGLEVVEQPGGLHGFIGNDKPILTDSCGFQVFLSDMRKLFEBCGCTTKSPINGDKLFLSPETISMKIQTVLNSDIAMQLDECTPGGETTREQAQKSLQM  
SLRNAERSKKAPEFDLKNPNALPGIVQAMYEDLREESLRGLEEDFPGLAVGLSVGEPKPEMYRMLHVGWMLPERKPHYLMGVCTPEDLVYGVAGHIDMFDCVMPTRNARNGLFTRPG  
DLKIKNAKHKPKRPIDESCTCYACQNFSAVILHHLHRAGETLGAQLNTIHLHFYQVIMAEMRDAVEQGKFDWQAQFHNARGVD

**SEQ ID 2799**

SEQ ID 2799  
TTGCAAGAGAGAGTGTGCATTTCTTTATGCAACATTTGGGCAAGATTGGGGATACCGTCTGAAAAACCGTGGGAATTCATTTATAATGCCGCTCTTT

**SEQ ID 2800**

LQERCAFLYATLNQDLGIPSEKPWEFIYNAVF

**SEQ ID 2801**

SEQ ID 2801

ATGCCGCTATTATTTTAACTCTTCGCAGACGGTTTGATGTTGAATATTACCTTGCCCGGACATGTTTCAGTCGCGCAATACGAAATCCCCCGTTACCGTGGCTCAAATTGCTGGGCTCTATCGGTGCCG  
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CATCCGCCATCTCTTGCGGCATCTTTCGTGGCGATCGCGTCAAGCACTCTATCCTAATGCAAAATGGTTATCGGCCCGCTCATTTGAAGAGGGCTTTTATTTACGACATCGCCACGGA  
CGGTTTACACCGAGATGTTGCGCCATTGAAGCGCGTATGAAAGAATTGATTGCCAAGATTGATGTGGTCAAATCATGATCTCCGCGTGCAGGAGCGGATTAATAATTTTCAAGAGC  
CGCGCGAAGAAACAACTGCGCCTGATTGACGATATGCCGAAGTGGAAAGCGATGGGGATATATCATCACCAGGAATATGTCGATATGTGCCCGCGTCCGCACTGTCGGAACACGCTT  
CCTGAAAACTTCAAGCTGACCAAGCTGGCAGCGCATATTTGGCGCGGCAGACCAATAATGAAATGCTCAACGCTATTTATGCGCATCTGTTGGGCGACGAAGACGAATTTAAAGACTAT  
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TGTGGCAGCATATCGAGCAGCATATGCGGTAAGAGCTGAACGCGCGCGGTTATAAAGAGCTCAAAACGCTCAAAATATGGATAAAACCTTTTGGGAAAAATCCGCGCATCGGGCAACTA  
CAAAGACAATATGTTGCTAACCAAGTTTCGGA AAAACCGGAATATGCGGTTAAACCGATGAACGTGTCGGGTCATGTTCAAATTTTCAACAACGCTTTGCGCTTCATATCGAGATTGCGCGATG  
CGTTTGGCGGAATTCGGTCTTGCCACCGCAACGAGCGAGCGCGCGCACTGCACGGTCTGATGAGGGTTTCGCGGTTTGTGACGAGGATGATCGGCATATTTTGTACCGAAGATCAAATCG  
TCAGCGAGGCTCGTGGTTCAATGAATTGTTGGTTCCGATCTACAAACAGTTCGGTTTCCATGATGATCCGTACGGCTTTCCTTCGCCCTGAAAAACCGCGAGGTTCCAGACGACGTTG  
GGATAAGGCAGAGCAGGGTTTGGCGCAGGCATTGACTGCCGTGCGCGTGGAAATGGGGCGAATTGCGCGCGAGGGTTCGCTTTACGGGCTTAAATGCAATATCAGCTGCAAGAAATGCCTTG  
GGTCTGTTTGGCAATTCGGGTACATTACAACCTGGATTTTGTCTGCCCGAAGCGCTTGGATGCGAGAAATGTAAGCAAAACCAACGACGAGCGAGCGCGGCTGTTATGTTGCATCGCGCAATT  
TAGGTTCTTTGGAGCGGTTTATCGGCATCTGATTGAGAACCTCAGGCTCTTTCGCTTATGAGGCTTCGACCGGTTCAAATGGTGATTATGAACATCACCGBAAATCAGGCAGATTATG  
TCGGGAAGTTGCTGCCAAATTCGAGCGCGAGGCTTTCGCGCGAGTGGATTTCGCTAATGAAAAATCGGTTACAAAATCCCGGACACAGGCAATACCGTTTCCTCTATCAATCGTT  
ATCGGTGATAAAGAGAAACAAGAAAAGTTCCGGTACCGCGCAAGCGGAAGACTTGGGTCTTTGGATTGATGATTTCAATGCGCAATTGACGACGAAGAACTACTGATGCGCTCG  
TCAATCAT

**SEQ ID 2802**

SEQ ID 2802  
 MPLFPHLSERIMLNIHLTPDCSVRQYESPTVVAQIAASIGAGLAKAAVAGKVGKGLVDACDPIVEDSAVQIITPKDQEGEILIRHSCAHLVGHAVKQLYPNAKMVGIPVIEGFPYDIATEK  
 PFTPEDVAAITEARMKELIAQDYDVVKIMTPRAEAIKIPQERGEYKLRLLDDMPVEBAMGIYHQEYVDMCRGPHVPNTRFLKNFKLTKLAGAYWRGDSNNELQRIYGTAWATKDELVDY  
 IQRIKEAEKRDRHRKLGKQLDLFLHQDEAPGMVFWHPKGMALWQTI EQHMRKELNAAGYKEVKTQPIDMKTWFEKSGHWNDYKDMFVTSSEKREYAVKPMNCPGHVQIFNNGLRSYRDLPM  
 RLAEFGSCHRNVEPSGALHGLMRVRGFPVQDDAHIFCTEDQIVSEARPNELLVRIYKQFGPHDVSVRLSLRPEKRAGSDVDVWKAEGQIGREALTACGVENGLPGEAGFYGPKEIYHVKDAL  
 GRSWQCGTLQLDLFVLPERLDAEYVTENNDRARPVMLHRAILGSLERFIGILIEHAGSFWLPLAVQVMVHNINTEHQADYCREVAAKTQAAGFRAKDLRNEKIGYKIRDSQYRFPFYIV  
 IGDKEQENKAVARRKAEDLGSLDLDDFIAQLQQEITDALVNH

SEQ ID 2803

SEQ ID 2803

GTGCGTTTAAATCAGTGAGTCAGGCGAAACAGCTTGGTGTCGTTTTCAGTTCGTGAAGCTTTGGCTATGGCGAAGGGCAGGATGTCGATTGGTAGAGATTTCCTCAACTGCTAAACCTCTCTG  
TGTGCAAACTGATGGATTACGGTAAATACAAATACCAACAGCGCAAGAGCGCGACGAGCCAGAGAAAACCAAAAGCAGGTGCAAAATTAAGGAAATTAATATTCGGTCCGGGTACAGATGA  
GGCGGATTATCAAAATCAAGATGCGCAACATCAACACGCTTCTTCCGACGGCGGATAAAGTCAAAGTGACATTCGCTTTCCCGCGCCGTGAAATGGCTACACAGCAACTCGCGCGCAACTT  
TGGGAACGCTGAAAAGAAGATTGGCTGAAGTGGCGCAAAATCGAGTCCTTTCCCAAAATGGAAGGCCGTCAAAATGGTGATGATGATTGCACCGAAGAAAAA

**SEQ ID 2804**

SEQ ID 2804  
VRLISESGEGLGVSVREALAMAEQDQDVLVEISPTAKPPVCKLMDYGYKYQQAKKRDEAKKNQKQVQIKEIKFPQGTDEGDYQIKMRNINRFLADGDKVKVTLRFRGEMAHQQLGAQL  
LERVKEDLAEVAQIESFPKMEGRQVMMLAPKKK

SEQ ID 2805

SEQ ID 2805

ATGCCACGGTTTTTTGCGCGCAATTGAAAACCTTACTCCGAAGCGGCAATCGGAGTAAGCGGAAAAATTATAGCTTTTATTTTTCTTCGGTGCAATCATCATACCAATTGACGGCCTTCCATT  
TTGGGAAAGAGACTCGATTTTGCGCCACTTCACGCCAAATCTCTTTTACACGCTTCCAAAGTTGCGCGCGAGTTGCTGGTGAGCCATTTCACGGCCGCGGAAACGCAATGTACATTGACTT  
TATCGCCGTGCGCAAGGAAGCGGTTGATGTTGGGCATCTTGATTTGATAACGCGGCTCATCTGTACCCGGACGGAATTTAATTTCCCTTAATTTGCACCTGCTTTTGGTTTTCTTGGCTC  
GTCCGCGTCTCTGGCTGTTGGTATTGTAATTTACCGTAATCCATCAGTTTGACACACAGGAGGTTTAGCAGTTGGGGAAATCTCTACCAAATCGACATCTCGCCTTCGGCCATAGCCAA  
GCTTCACGAAC



## SEQ ID 2806

MPRFFAATENLRSGNRSKRKI LALFFLRNHHHLTAPHPGKGLDLRHP SQIFFYTFQKLRAELLVSHFTAASTQCHPDFI AVGKEAVDVAHLDLIALICTRTEFNFINLHLLLVFLG  
VALLGLLVFVTVTHQFAHRRPSSWGNLYQIDILPPGHSQSTFN

## SEQ ID 2807

TTGCGCAAAAAACCGTGGCATTGTGGGTCAAGTGTGTTGAAACCGATGTTTTAAAAACCCCTAATGCCCTATCCGATAACGAATGGAGTTTTCCCATGCCATAAATGAAACCAAGTCTA  
GCGCGAAAAACCGTTTAAAGTACTGGGTAAACGCGGTGTGAAACGCGCTCATGCGTTCAAACGCCACATCTTGACTAAAAAGACCACCAAAAAACAAACGCCAAGTGGCGGTACCTCTAT  
GGTAAATGATCGGATTGGCTTCTGTGCTAAAAATGTTACCTACGCT

## SEQ ID 2808

LRQKTVALWQVFETDVLKPPNALSINWSPFHPKMKTKSSAKKRFKVLGNGGVKRAHAFKRHLTKKTKNKRQLRGTSHVNDRLASVAKHLPYA

## SEQ ID 2809

TTGCCGACCGGGCGGAAAAATGCCGCTGAAGCCGATTGGGTTTCAGACGGCATCCGTTTGC AAAAATGCTACAATCCGCTTTTTACCGAACAACCCGAAACTATGAAGAAAAACA  
CCCCGAAATCGTTGAAGAGGCTTGTGCGGCTTGAATCGCTGACCGAGTCCATGACGGCGGAAATGCCCTTGGAAAGACGCGCTTGGCGCTATCAGGAAGGCAACGAGCTGGTCAGGTA  
CTGCCAAACCAAGCTGGCCCAAGTGAACAGAAATTACAGGTTTTGGATGCGGACGGGACGAAGAGTTGAACCTTGAATCCGACGAA

## SEQ ID 2810

LPTGAEMKPSAEGFGPTASVLQKCYNPLFTGTPETMKKNTPKSPREALSRLSITQSHQEMPLDALAAYQEGNELVRYCQTKLAQVEQKLQVLADGTEKLNLESDE

## SEQ ID 2811

ATGAGAAAAACCAAAACCGAAGCCTTGA AAAACCAAGAACACCTGATGCTTGC CGCTTGGAAACCTTTTACCGCAAAAGGATTGCCCGCACCTCGCTCAACGAATCGCCCAAGCCCGG  
GCGTAACGCGCGCGCGCTCTATTGGCATTTC AAAATAAGGAAGACTTGTGTTGACGCGTGTTCACACTATCTGCGACGACATCGAAAACGTCATCGCGCAAGATCGCGCAGATGCCGA  
AGGAGGTTCTTGGACGTTATTCGCCACACGCTGCTGCACTTTTTCGAGCGGCTGCAAAAGCAACGACATCCTACTACAAATTCACAAACATCCTGTTTTTAAAGTGGCAACATCGGAACAA  
AACGCGCGCGTTATCGCCATTGCCCGCAAGCATCAGGCAATCTGGCGCGAGAAAATTACCGCGGTTTTGACCGAAGCGGTGGAAAAATCAGGATTGGCTGACGATTGGGACAGGAACGG  
CGGTCACTTCATCAAAATGACGTTGGACGGGTGATTGGCGTTGGTTCTCTCCGCGCAAGATTTCGATTGGGCAAAACCGCGCGCATCATCGGGATAATGATGGAACACTTGA  
AAACCATCCCTGCCCTGCCCGCGAAA

## SEQ ID 2812

MRTKTEALKTKFHEMLAALETTPYRKGIARTSLNEIAQAAGVTRGALYWHFNKEDLFDALFQRICDDIENCIAQDAADABGGSWTVFRHLLHFFPERLQSNIDHYKPHNIFLKEHTBQ  
NAAVIAIARKHQAIWREKITAVLITRAVENQDLADLDKETAVIDFKSTLDGLIWRWFSSESFDLGKTA PRIIGIMDNLENHPCLRK

## SEQ ID 2813

TTGCTGTTGTTCCAAAGTCCGGATTCCCGCTGGCGGGAATGACGAATCCATCCGTACGGAACCTGCACCCGCTCATTTCTACGAACCTACATCCCGTCATTCCCAAGAAAGTGGGAAT  
CTAGAAATAAAAAGCAGCAGGAATTTATCGGAAATAAC

## SEQ ID 2814

LLLFQGPDSRLGNDESIRTECTTSLRTYIPSPFKWESRNKKQQEFIGNN

## SEQ ID 2815

GTGCGAGGCCCCAAGGCACTCACTATTCGGTAATCTGTTTTGTTAAAGAGCGTTGCGAAATTATAAAGTATCCCTTCGCGCTGTCTAAGATATCTCTCGATATTTCCGACATTCCGTGCT  
ATACTTTTCAGTTGCTCGCGCGCTTCGCGAGCGCGGAAGAACCGCAACTATACGCTTAAAGAGATTTCGCGTCAACCGTTTTTTGAAAAAATTTTA

## SEQ ID 2816

VRGFRSHLSVICFVKERCEI IKYFRLSKISLDSIDPCYTFQVFRFGSGEEPNTYKICGQPPFEKIL

## SEQ ID 2817

ATGCCACCGGTA AAAACCGGTGTACCGCCGCTGCCCGTCA CAAAAAATCTTCGCGTTAGCCAAAGGCTATCGTGGTGGTGTGTA AAAACGTTTACCGCGTTGCCAAGCGGCGTAATGA  
AAGCTGGTCAATACGCATACCGTGACCGCGCCCAACGCAAAACGCAATTCGCTCAATTGTGGATTGTTGCTATCAATGCAAGTGCGCGTGAAAACGGGTGTCTTACAGCAAAATTTATGAA  
CGGTCTGAACCGCGCTCTATCGAAATCGACCGCAAGATTTGGCTGATTTCGCGGTGTTGATAAAGCGCTTTTGCACAATTTGTTGAAAACGCAAGCTGCTTTGCGCTGCT

## SEQ ID 2818

MPRVKRGVTARARHQIKIFALAKGYRGRKNVYRVAKQAVEKAGQYAYRDRQRQRQRLWIVRINAGARENGLSYKFMNGLKRASTIEDRKVLADLAVDFKAAFAQLVEKAKAALAA

## SEQ ID 2819

TTGCGGAAATCTATGTGATTGATTCTTTCTTTTAAAGTCTATTTTTTAAATAAATTTGCGTTAAATAACAGAAAAATTTATCCAATGGATTGGCGGTGAAGAAAAATAGGTCGTC

## SEQ ID 2820

LRKPYVIDFLSLKIFLNFALKYRKPIQWIGREENKV

## SEQ ID 2821

TTGCGCGTGAAGAAAAATAGGTCGCTGAAGAGTCTGATATGTCAGGCTATACAGCGCGCTCGTTGTTTCAGGTGGCATACTAATTTGACAGGCTTGATATTATGAAAAATGTAAAC  
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GCAAAATGTCGCTGAAGAGCGCAAAACCATAGGTGCGCATATCAATGAATGCAAAAACCGGTTTCAGACGGCTTTAATGCCAAACCGGATGCCCTCAACGAAGCAAGCTGCAAGCCGGA  
CTTGC CGCGAAGCCCTCGACATTTACCTGCCCGGACGCGCTCAGGAAGCGGCGAGCTTGCAATCCCGTAACCTGACCTTGCACACGTGTGTGCAACTCTTTACGGAATGGTTTCGAAG  
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TACGCACACTTCCCGGATTCAAAATCCGCTATATGCTCGATAAAAAAGAGCGCGCCATTCGCAATTATCGCCCCCGCGCGCTTACCGTGTGGACAGGATGCCACGCACTGCCTATGTTT  
CATCAGCCGAGGCTTGTGGGTAGAAGAGGGCTAATTTTGGCGACTTAAAGCAGTGTTCAGTACTTTATCCGTGCTTCTTTGAACCGGATGACCTACAAGTGGCTTCCGTCCGT  
CTTCTTCCGTTTACGAGCCTTCTGCCGAATCGACATCATGGGAGAAAACGCAATGTTGGAAGTAGCGGTTCGCGTATGTTACATCTTAATGTGTGAAAAATGTCAATATCGA  
CCCTGAAAAATATACCGGTTTCCCTTCCGTATGTTCTCGACCGCTTTGCCATGTTGCGCTACAAACGCTCAATGACCTGCGCTTGTCTCGATAACGATTGAACCTCTTGAAGCAGTTT  
GAA

## SEQ ID 2822

LAVKKIRSEESDMGYTGGLVVSGGISLIDRLDIMENVNRIVAEGIAVEAAQDFNALEQIKARYLGTGELTGLLKTGLQMSPEERRTIGAHINECKNRFPQAFNAKRDALNEAKLQAR  
LAAEALDTTLPGRAGGSGSLHPVTLTQRVVELFHGMGEVADGPEIEDDFHNPALNIPANHPARAMQDTFYVENGDLRHTSPITQIRYMLDKKEPPIRIIAPGRVYRVDSDATSPHF  
HQAEGLVVEGVTFADLKA VFTDFIRRRFFERDDLQVRFRSPFPFTEPSAEIDINGENKWLLEVGGCGMHPNVLKNVNDPEKYTGPAFGIGLDRFAMLRVNDRLRFPDNDLNFLOF  
E

## SEQ ID 2823

TTGAATAAATCTCAAAATAACCCAATGGATAAATTAACCCCGGAGCAGCGCAAAAAATGTATGCAGTCCAACAAAAGTACAGGACGAAACCCGAGCTTGTGTTGGCGAAGCAATGTGGG  
CTTTGGGCTCAGGTATCGGAAAAATAGCGGAAGCAATTTTGGAAAACTGATTTTTCATTTAAAAAATAATAAGTTGCCGTATTGTGCGATGGGGAATCTGGCACGGTAAGGATTGGGA  
ACAGAAAAAGCGGTAATAAGGGAATCTGAGTTTGGATTGCCAAAATGAGCGCAATATCCAAGGGATATAGAAGTAACAGCGCGCTGAAAGCCGAGGCTGGACGGTTTACGT  
TTTTCGAGTAACGATGCTGCAAAAATACAACCTGTGCGCGAAAAGTCAAGAAATCATCCAACAAGA

**SEQ ID 2824**

SEQ ID 2824  
LNKSQLNPKDLKTPQRKKCHQSNKSTGKPELVLA KAMMALGLRYRKNSSGSLPGKPDFSFKKYKVAVPVDGEFWHGKDMEQKKAVIKGNREFWIAKIERNIQRDIEVTGRLKAEGWTVLR  
FWSNDVVKNTTCCAERVKELIQTR

SEQ ID 2825

SEQ ID 2825  
GTGCCGAAAAGTCAAAGAAATCATCCAACAAGATGAATTGATTACAAAAACAAGATTAAAGGAAGATGGGCAGGATGAACGGTTAAAGGAAAAAGCAGCACAAATACCGCCTTTTGGAA  
ACAACGATACCTTTTCAGACGCGCTTGAAACCCAAATTTACCTTTATCGACTTGTTCGCAGGTATCGGGGGCTCCGCATCGCGATCGAGAAGTGGCGGGGAATACGTGTTTTCGAGCGA  
GTGGGACGAAAAAGCCAAACTGACGTACGAAGCCAATTTTCGGGAGAAGTCCCGTTTGGCGATATTAGCTTTGGAAGAAATCAAAACAATACATCCGAAGCAATTTGATGTGCTGTGTGGGTTT  
ACCTTATCAAAA

**SEQ ID 2826**

SEQ ID 2826  
VFKSKSSKQDELITYKNKIKEDGQDERLKEKAAQYRLFENNDFQTALKPKFTFIDLPAIGGGFRIAMQNLGGETVFSSEWDEKAKLTYEANFGVEVPFGDITLERIKQYIPKQFDVLGGF  
TISK

**SEQ ID 2827**

SEQ ID 2827  
ATGTCTGTGTGGTTTACCTTATCAAATAAAGATTTTGAATAATGAGGCTTCTGATTATATTTGAAATAAAATAAATATAAATAATTATCTGATAAACAGGTACAAGAAATTA  
TTGACTATTTTTCTCAGAAATAGACGACTGGTTATTGGCAAGCGAAGGAGTTAAAAGATTATGATGTATACCTATACAAATTACTACTAGATGGACAGCAATATGTTCCGGGAATAAG  
AAAATCTGTATTGTACGATTTCCTTATGGAAAATCAGAAAGATAGC

**SEQ ID 2828**

SEQ ID 2828  
MCCVGLPYONKDFRMRSLSDYTLANKININNLSDKQVQRIIDYFSSEIDDWLLASEKELKDYDVLYLKLVLGQQYVQGIKRSVLYDFLMENQDS

**SEQ ID 2829**

SEQ ID 2829  
ATGAAAAAATGGACTAGAGATGAAACCGTGGCTTTATCTTTATTACATCATTCCTTTTCAAAGGTTAGTAAGGACAATCCTGTTATTCAAGAAATATGCTGAAATACTGGGCAGGA  
CACCCGTCGCCCATCGGTATGAAGATAGGAAATTTGGGTCGTTTAGATCCTACGCTGAAAGTCAAAATATTTCCGGGATTAGTAATGGCAGCAAAATGSGATGTTGTCGTATGGAATGAGTT  
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TTTGCAAGAATATCAGTACCGCTCAATCAGGGCTTTTTCGCTCCAGTGTTTGGCAGCATACAAATCAATGTGTGATTACTGGAATTAACCAACCTGAATTTGAGTCTAGTCATATA  
TCAACCCCTGGGGGGAAGATAAAGGATTAACCGTTTAAACCCAAGGAATGGGCTATGTTGAAATGCGTTCATACGACAAAGCTTTTGATAGAGGGGCTGTAGGAATGAGATGAAATTTCAAAAT  
TATATTTTCTCCACTACTGGCAAAAACAGAAGGATTGATGATTTATTTAAACCATATGAAATCTGGGATGATGAGACTGCCTGAAAGACTAAACCCAAGCTGCGAATTTTAAAAATTTCC  
AGAGAAAAATATTTTTCAGAGT

SEQ ID 2830

SEQ ID 2830  
MKKWTRDEFTLVLYLYIIPFKVSKDNFVIQFYARILGRTPSALGMKIGNLGRLDPTLKVKNIISGLNNGSKMDVVVWNEFSGDWEQLNKEFGVLSQYQSDNDSNIEIESPEIKGRER  
PARISVRVNGQFFRSSVLAAYNNQCCITGLKQPELLVASHIKPWGEDKDNRLNPRNGLCLNALHDKAFDRGLLGIDENFKIIFSPILLARTEGFDDLKPKPYENRMIRLPERLNPSLEFLKPH  
RENIFOS

SEQ ID 2831

SEQ ID 2831

ATGCAATTCTCTACTCATGGCTGAAACCCCAAGCCAATCTCTGATCTTTCTGCGCGATACCTTGAACATCTTTTGACCATGGCCGGTTTGGAAAGTGGAAAGAAATCGATACTGCGCCCGCT  
CTTTCTAGTGGCGGTGTTGTTGCCGAAGTAAATCTGTTGAAAAACATCTCTGATCGAGATAACCTTTGAACGTTACTCAAGTTGATGCGCGGTACGGCGGAGTTGGTTTCAGATTGTTTGTGGTGC  
GCCGAATGTCAGCCGGGCAATAAAGTGCCTGTTCTGTTGCCCGTTGCCCGTTTGGCCGGGCAATTTTAAAAATTAAGCCGACATAAAATGCGCGCGTACCATTCAACCGGTATGCTGTGTTG  
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CATTAACGCGCGAGCTTCCGTTTTCGATCATGAAATTGAGGCTGATTGATTGAAGAAATCGGACGCGTTTACGGCTATGAAACATATCCCGACGATTAACGTCAGGCGCTCTGAAAAATG  
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CGTGCCTGTTTGAATTCGCTTGCCTGCTGCTGCGCAAGGTTTTCAGACGGCGGTTTGTCCAAAAACGAAACGATCGGCGCTGTGTGATGCGCGCGGATCCCGGCAATGCGGCTGAGAA  
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TTGGTACGAAATTCAGCGTGTGTTGACGTGTATCGCGCACGGGCTGCGCGAAGGATGAAGAGCGTGGCGGTTTAAAGTGATTTTGTCAGGATATGAAAAACACGCTGACGGATGAGGCGG  
TCGAGCGGCTTTATTGGAACACTGATTGCGCTGGCAACGAGGCGAGGCGCGCTTCGCACT

SEQ ID 2832

SEQ ID 2832

MQFSYSMLTKQANPDL SADKLEHLLTMAGLEVVEEIDTAPAPSGVVVAEVKSVEKHPDADRLANVTQVDAGTGLVQVCGAPNVKPGIKVPCSLFVAVLPGNFKIKPTKMRGVPSPNGMLCS  
TNELGLPLDDGVGLHLLPEDAPVHTNIREYLDLDDMLFTLKITPNRADCLSVKGIARVSALQCAFTPVIEITAPAGSEKKQAVRIDAPADCGRPSRVIEINNVAKAAPTDMKQRLEBS  
GIRISALQADVGNLMLIGOPHHVDKDLKSSLSLIVRRQQNGETLACLNEKTVTLADNTLVVADEKAGLSLAGLGGAAASVSDGTQNVLEAAWFEPETIVGKSRQYGFSGDSSSFRFR  
VDVRIQLADATERATELVLQICGGAAGEMVEAQKGLPEAKQVGLRGLRKLTVLGVDIPAEQVETILQHLGLQPKRTABGFRIITAPSFPRDIETADLIEIRI GGVYGIENIPDDYTSGRMLR  
SELPETRPRPFAVNVNMAARGYREVISTAFVDSQMELOFAANAPARIRLQNPLAAQYAVMRSTLIGGLVETLQNNLARQNRKRVVFELACVFGKSGDGRFVQNERIGLMLYGAAMPQGWKEK  
TRNADPYDIKADVENILKNKAVEFVTKGHPALHPGRAANIVSDGKVI GFVGEIHPKWLQVLDLPQAPLWFEIDMAVLECGKTRTRYRANVSKTRQPVRRDLFAVMPEVMHDDLLVLKGAANK  
VMDSTGNNVVEGGLPEKMGSAVKVILQMDLNTDEAVEPLIGKLI GVATEAGARLS

SEQ ID 2833

SEQ ID 2833  
ATGCCAATTACCTTCCGGCTGATCCACTTTTAGGCATACCTCTGAAAATGCTGATTGTGAGAATCATCTTGCACAGGCTGCACATTCGTAACCTATGCCGGGTATCTCGCCGCACTGG  
AAAAGTTCAAAGGCTACACGGCAATCGCATCAATCCATGCCCTCCGACATATTGAACCTCTCTTTAAATTTCGGGATTCGGTCAGGGGTGGGCTGCCGTTCGGCGCATTCCTCGTTCTT  
CATTGGTATGCACGCATTCAAAAAAGTACGCTTTGTCTTCCGGGA

SEQ ID 2834

SEQ ID 2834  
MPLISGLIPLIGTLLKMLIVRIILATGLTFVTTYAGYLAALKPKGYTANAINSMPSDIIALLLLISGFGQGLGCLFGAPSFFIGMHAFKRLTFVFPFG

SEQ ID 2835

SEQ ID 2835  
ATGCACTAACTAAAGCAGAACTGGCCGATATTTTGGTGGATAAAGTCAGCAACGTCACCAAAAAACGATGCCAAAGAAATTGTCGAACCTCTTTTGAAGAAATCCGCAGCACTTTGGCAA  
GCGCGAAGAAATCAAAATTTCCGGTTTCGGAATTTCCAGTTGCGCGACAAGCCGCAACGCCCGCGCGCGTAATCCGAAAACCGCGGAGGAAGTGGCGATTACCGCCGCGCGCGTGGTAAC  
TTTCATGCCAGCCAGAACTCAAAGGCATGTTGGAACACTACTATGACAACAACAGCT

**SEQ ID 2836**

MEATKAEIADTIIVKVSNTKNDKKEIVELFFEEIRSTLASGEIKISGFGNFOLRDKPQRPGRNPKTGEEVPIITARRVVTTFHASQKLKGHVEHYDKQR

**SEQ ID 2837**

ATGACAAACACCGTTGATTTCACGATTCCTGCAAAACGCTATTTCACGCTGGACGAGTTGTGCGGACTGTTCGCAAAATCAGCCCCATGCGTTTTCGCGAATGGCAACATGATCACCGTGTGG  
TGTGTCGGTTACGGCGGAGAACGCTACACCCGTTTGGATGTGGTGAAACTGTTGAAACTGAAGAGCACGTTTGCACCGTATGCAGAAGCTGCCGAATCGGTTTCGGACGGCAACCGTCCGGT  
TAGCGCTTCAGGAANTCGGAGACGGTCTGAAAGACCTGTTGGAGGATTTGGATAAGGAGTTGTGC

**SEQ ID 2838**

MTNNVDI.TIPAKRYFTLDELGLLOISPYGFAOWOHDHGVVVGYGGERYTRLDVVKLLKLSFPYAEGAESGSDGNRPVTLQEIGDGLKDILLEDLDELKELC

**SEQ ID: 2839**

TTGCGTGATTTCACATGTGTTTCGGCTTGAAGCACATGGTTTTGTAATCATTTACAGGCAGCTCGCTTGAATCCTGTTGGGGCGGTTTGCTGTTTACTTAAATATAAGGATGACGGTCAA

SEQ ID 2840

LRDFTLFRLEAHGFVITYRQLAHNPVRAVCCLLKYYKDDGO

SEQ ID 2841

ATGAGATTCTTTCGGTATCGGTTTCTTTGGTCGTCGTCGTTTTGGAAATATATGTCGATTGTGTGGGTGCGGATTGGCTGGCGGGGGTGGAGCGCTGTCTCAATGGCGGCAACCTTTGCCG  
CCGGTGTCTGATGCTCAGGCATACGGGGCTGTCCGGTCTTTATATGGCTGGCGCGGGGTAAAAAGTAGTGGGAAGGTATCTGTTTATCAGATGTGTGGCCATACCGTTATACGGTGGC  
CGGGGTGTCTGATGAGTCCGGGATTCTGATCCCTCGGTGTGGCGGTATTGCTGCTGCTGCCGTTTAAGGGAGGGGCAAGTGTTCAGGCAGGAGGTGCGGAAAAATTTTTCAACATGAAAC  
CAATCGGGCAGAAAAGAGGGATTTTTCCACGATGACGATATTATCAGGGAGAAATATACGGTTGAAGAGCCTTACGGCGGCAATCTGTTCCCGAAACCCCATCGAACACAAAAAGACGAA

**SEQ ID 2842**

MRFPFGIGFLVLFLBINSIVWADVLGGWTLFLMAATFAAGVLMRLHTGLSGLLLAGAAVKSSGKVSYYQMLNPIRYTTVAAVCLMSPGFVSSVLAVLLLLPFGGAVLQAGGAENFFNNH  
QKPKKEGFFPHDDDLIESEYTVPEEPYGGNRSNAIEHKKOE

SEQ ID 2843

ATGAGCTGTTTGGGATATATGGGACAGGATGGTGGAAATCTATCATAAAGTATAAGAAGCCGTCCTGGTTTTAGCAGTGGATTTTGTGATGGGTATCGTATTTCATAGAGCCGAANTGAGGACC  
CGTCGATCGGCAGATGCTATGGGCTATGGCCGAGTCCCTGATTTTGCCAAACGCTGTGGCATGGCTGTTGCTATGACCTGTATCGCTATTTTATCTATGAT

SEQ ID 2844

MSVWDTWDRMVEIYHKYKKPCLVLAVDFVMGMVFIEPNKEPCIGRCYAPHPESPDPANAVAMAVAMICTVFTYD

SEQ ID 2845

TTGATTGAACCGTGTGGCGGAGGCTGTGTGAAACGGTATTGGGCGTTGGTCTGTCGATCCAATCAGCGTTGAGGAATGCGAAACGGTGTGCGCTTATGTTGCGGACGATTGTGTTTCGGG  
GTTTTTCGCCCGGAAACGGATGGAAGAGTGTGGGAACGGGCTCTGCGAGTAGAATACGCTTTTTCGGTTTGAATGCGACTAATAAGAAAAGAGAGAACTTATCGCTCTGAACATCAACAC  
ACATCATCATTAATTACTTAATTTCGACCGTACCCATCTGCTTCATCCCTATACTTCCA

SEQ ID 2846

SEQ ID 2840  
LITEALGGGVKRYWALGRILPTBLEECETVCAYVADDLFRGFSPETDGVWEAVCRSRIRFLRLNAVIRKERNLCRLNDNTHHHYLSTVPICSIPLP

SEQ ID 2847

ATGACCGATCCCGCTCCCGTTTATCCTGTCAAACGTGCAGAAGGGGTGTTTATCGAATTGGCGGACGGCAGCGGGCTGATTGACGGGATGTCGCTCTGTGTGTGTGCGGATACACGGTTACA  
ATCATCCCGTTTGAATCAGGCGGTTGAGAATCAGATGAAACAAATGCGGCACGTGATGTCGCGGGCTGACGACAGAGCGCGGCTGGAGCTGGGCAAGTTGTGTGTGCGGGATTTCGCG  
GCAGGGGCTGGACCGTATTTTTATGCGGATTCGGGTTCGGTTTCGGTAGAAGTCGCGTTGAAATGCGCGGTGCAATACCAGCAGGCGCGGGGTTCAGCGCGAAGCAGAATATTGCGGAC  
GTACGGCGCGGGTATCAGCGGATACTTGGAACGCCGATGTCGCTTTGTGATCGCGAAACCGGGATGCACCATATTTTCGCGCAGCGCTGCGCCGCGATTAITTTGTGCGATAATCCGAAAA  
ACCGTTTCAGCATGATGAGACGGGCGGGATTTCGACGCTGTCGCGCGCTTGTGTGAAGCGCATCATCGTGGAATTCGCGCGCTTTATTTTGAAGAACCGGTGTGCGAAGCGCGGGCGCAT  
GTATTTTATCATCCGACGATGTTTCGCGCGCTTTCGCGGATTTCGCGCAGCAATTTGATATCGTGTGATTTTTGACGAAATCGCCACCGGATTTCGGCGCACGGGCAAGATGTTTGCCTGC  
GAACACGCGGAGGTCGTCGCGGATATTATGTGTATCGGCAAGGGTTTGAGCGCGCGCTATATGACGCTGGCGGGCGCAATCACTTCGCAAAAGTTACCGGAAACGATTTCACGCGCGGAG  
CGGGCGGTGTTATGACGCGCCGACATTTATGCGCAACCGCTGGCGGTGCGCGTGCCTGTGCTTCGGTCAAGCTGCTTTTATCCCAAGACTGCGAGGCAAAATATCGCCGTATCGAAAG  
CATCTTAAAGCGCGTCTGAAAGCCGCGTGGGACATTCGCGCGGTGAAAGACGTGCGCGCTTTTGGGTGCTATCGCGCTGATAGAGTTGGAAGAAAGCGGTGGATATGGCGCGTTTTCAGCG  
GATTGTGTGCGCGAGGCATTTGGGTACGCCCGTTTCGGCAGGCTGGTGTATCTGATCGCGCCCTATATCATTTTCAGACGGCATTTTGACCAAACTTCGCCGATAAAGCTGCAATCTTGA  
AGGAACACGACAAA

SEQ ID 2848

HTDPLFPVYPKRAEAGVFIELADGTRLIDGSSWMCALHGYNHPVLNQAVERNQMKQAHVMFPGGLTHEPAVELGKLLVGLIPQGLDRIFYADSGSVSVEVALKNAVQYQQARGLTARQNIAI  
VRGTHGDTVKNAMSCVDEPETHHIFGSALPQRYFVDNPKNRFDDEWDGADLQPVRLFEAHFVDIAAPILEPVPVQAGGMYFYHPQYLRGLRDCDEFDITVLPFDEIATGFGRTGKMFAC  
EHAEVVPDLMICIGKLSGGYMTLAAAITSQKVYTTISRGEAGVFMHGPPTFMANPLACAVACASVKLLLSQDWQANTRRIESILKGLRKAANDIRGVKDVRLVLAIGVIELEKGVDMARFQA  
DCVAOGIVVRPFGRLVVIAPPYIISDGLITKLADKTVQILKEHSE

## SEQ ID 2849

TGAATCGACGAAATGATTTGAAAGCGGTGCGCAACAGAGGGCGCAGGCGCAGACAGAGCTGCTGCTGGAACGCTTTTTCGCGCTGGAAGACGAAATCCCGCACAAGCTGCACGGAAGCGATGC  
 GCTATGCGGCTTTTGGACGGCGGCAAGCGCTCTGCGCCGATGCTGGTGCTGGCGGCTTCGGAATTTGGCGGGGCCATGGCGGATCGGCTCGGACAGGCAATGCGGCGCAATGCAATGATGATCA  
 CGTCTATTCCTTTGGTTCACGACGATATGCGCGGATGGACAACGACAGCCTCGGGCGGGCAACCGACCTGCCACATCAAATATGGCGAAGCCACGGCCCTTCTGACCGGGCAGCGCTTTA  
 CAAACCCAAAGCCTTGACGCTGTTGAGCGCTCCGACAGAACTGCCCGGCCGACGCGCAGTTGGCAATGTTGTGCGGTGTGGCAAAAGCGGGCGGCAGCGCGGTATGGCGGGCGGACAGGCAA  
 TCGATTTGGCAAAATGTCGGCAAAACAAATGGTTCAAGCGGATTTGGAAACGATGCACAGCCTGAAACAGGGGGCGTTGATCCGTGCGCGCGTTTATTGGGGGCGACGGCGCTTGCCCGATCT  
 GTCCGACGCGGAACCTTGCCGTATTGGACGCTTACGCGGCAAACTGGGTTTGGCGTTCCAAGTCATGACGATGTGTTGGAATGTGAAGCGGACACGCGGACCTTTGGCGAAGACGCGCGCGG  
 AAGATGCGGACGACGACGAGCCGACTTATGTGAAACTGATGGGCTTGAAGCGGGCGGCTATACGACACAAACCTGTTGCCGAAGCAGTCGCGCTGCTCGGCGACAAAG  
 CGTTGCGCTCGCGCAGTTCGCAAGAATTTGCACTGCGCAGCAAAATAT

SEQ ID 2850

INPTNDLKAWQORAAQTELLERFLPSGNEIPTHLEHAMRYAALDGGKLRPLMVLAASELGGAMADAVGQAMAATENTHVSYLVHDMAMPNDNSLRRGKPTCHKYGEATALLTGDAL  
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SEQ ID 2851

TTGTTTGCAGAAATGCCGGAGAAAAATCGAATTTCACATTTCGAATGGTATTTGTTATTAATTGTGAATAAATATTGGAAGGTAAATGATATGAAAAATGAAATTCAA AAAATCATGGATAAAT  
ATGATCCATGGCATTGAAGATGATTTTAAGTCGTATGAAGACATTGCCAAGATGTATCGTTGATGACAGATAAAACCTTCATTGAACATTATTTTGTTAGAAGTTTATTTCAGAAGAAAACGG  
ACATTTTGCACCAAGCAATGTTTCATCGCATGATAGGGGAAATTA AAAATGCAATT

SEQ ID 2852

1.FARMPEKNAVYTRVLJ.LJVNKYWKVNDKNETOKIMDKYDPWHEDDFKSYEDIAKOVSLATDKTF IEHYLLEVYSBENGHFDQDNVHAMIGETKNAI

## SEQ ID 2853

ATGAAAGCGCTTACTTGTGTCAGCGGTATAGACACGGACATCGGCAAAACCGTCGCCACCGGTATGTGGCAAAACAATTGTTGCAGCAGGGCAAAAGCGTGATTACGCCAAAAGCCGTCG  
AAACCGGTTGCGCAAGACATCGCCGAAGACATCGCCGTCCACCGTAAATCATGGGCATACCCATGCAGGAAGCTGATGAACAGCGCTGTGACTATGCTTGAATCTTTCAGCCATCCCGCTC  
GCCCCACCTTCCGCGCCGACTGGACGGCAGGGGTTTGGACTTGGACAAAATCCGACCGCCACACAAGAAATGGCGCGCAGTACGAAGTCGTTTGGTCGAAGCGCGCGCGGGTGTATG  
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TCAACAATACGCGATTTCGCGCTGCACAGCTCGTGTTTAACCAATCCACGACGCGCGCAGCACAAGTCGCGCAAGACAGCTGAATATCTGCAATGCCCTCTGAAAGCCGATTTTCC  
CGAAGCGGAATGGATGGAGTTGGCAAAACAGGCGCGGTA

## SEQ ID 2854

MKGVYVPSGIDTDIGKTATGMLAKQLLQCGKSVITQKPVQTCQDIAEDIAVHRKIMGIPQEADEQRLTMEPEI PSHPASPHLAARLDGRGLDLKIRTATQELAAQYEVVLVBGAGGLM  
VPLTEKLLATIDHIQQQYAPVILVTSGRIGSINHLLSFVVLQYQIRLHSLVFNHIDSRDAHVAQDSLNYLQCRLLKADFPPEABWMLAKTGA

## SEQ ID 2855

ATGGATGGAGTTGGCAAAACAGCGCGGTATAAGATTGGGAAGATATGGAACACCTATTTGGGAAATGGCTGCCGACTTGCCTGCCCGCTTTCAGACGGCATGACCTGCCGATGA  
GCCGTTATTGAAAGCCCGGTGCTGACCGCGCATTTGTCGCCCTTCCGCATACATTTTCGGTGAATGCTGAAATGGGCGAAGCGGAAACGGAAATACGGACGGCGAGGGTCCGCGA  
TGTGCTTCTGAAACTGACGCGCTGCTGTGTGTCAGGCACGAAGCGCGTGCAGCTCGGCTTCCGCTTTGGCAAAACATTTGGACTGCGGCACACGCGCTTGGGCGAGCGTCTGTT  
CAAGCGGATTGGGAAGGGCGCGTTCGCGCTTGGCTTTCAGTTGCGCTTTCAGTGAAGGATGCGGACGGTACTTTGCCGCGCGCGCTTCTCGGTTTCCCATCAAGCGGAGGAAATGCTGCTGA  
CCGAGTATTTCTGCCCGCACTGAAACGCTTTATCGGA

## SEQ ID 2856

MDGVGKNRRGIRIKDKMEHLFGKWLDPAPVSDGIDLPMSRLKARSITAAALCALPHTFVRLKLGEABTEYGRRRVRDVLKLDGTAVVQARSACSVGSFQWNLDCGTRPLGERLF  
QADLEGARSAPFVAVSSEGGRYFAARRSRFSHQEMLLTETPLPELKRFIG

## SEQ ID 2857

ATGAATATAAGAAATAAAGTAGGAATCGTTTCTAAACAAATATATCTAGTGGCATAATGGATATTTCACTAGTCTCTTTTCAACTGACTGTCTAATGTATTTTAACTATCC  
GAACAGGTACAAAGCCTTCTGTAGAAATCGAAATGGGGCTGTGGCTAAAAGATTATGATACAGTTGAAATGAAATAGAGTATTAAGAAATAGCTTTATTAAGGAATGAAATGTCAAATGTGCT  
GCATAACAATAGAAATATATGCCAAGTAGAAATAAGAACCAAGAGATGCTTAAATAATAAGATTTTACGACAATAATCAAATGGTTATGGAAGTAGAAGTTTATGATTAGTT  
TTCAAAGGGTGAAGCATTTATATGAAGAGGGTTATGAATCT

## SEQ ID 2858

MNIIEIISNRRLKQIYPSGIMDISLVSPSTDLNLCILITRTSTKPSVEIEKWLGLKDYDTVEIELNSFIKMKQNWSENNRNICQVEIKNGEDGLKIRFYDNNSNWILLELEVYGLV  
FQCKTYMKGVES

## SEQ ID 2859

ATGAATCTTAAATCCCTTTATTTTACGACTGTCCGATCGTTTGGACGCTTATATCAGACTGATGAGGCGGACAAAGCCATTTGGGACGCTGCTTTTACTGTGGCGGACCTACTGGGCAT  
TGTGGCTGGCTTCAGACGGCATTTCCCGATTGGCGGTATTGGCGGCTTTAATCGGCAGTCCCGCTGCGTCATCAACGACTTTGCCGACCGGATTTTGACGG  
TGCTGTGAGCGCACAAAAACCGTCCGTTCGCACAGGGCAGGGTCAAGAAAAAGAACGCCCTGCTGTCAGCGCATTTTGTGTCTGCTTGGCGCATTTGCTGATTCGCTGAATCAT  
CTGACATGGCTGATGAGCTTGCCTGCGCTGCTTCCCTGCGCTGACTTACCGTTTACCAACGCTTTTTCGGATTCCCAATTTTATCTGGGATTTGCTTTTCTTCCGCTATCCCGATGG  
CGTTTGGCGCAGTGGGCAACAGCGTTCCCGTTGAAGCGTGGATACTCTTTCGCCCAATGTTTATGGACACTGCTTACGATACCGTCTATGCAATGGCGACAAAGAGGACGATTTGAA  
AATCGGCATCAAAACCTCCGCGCTCACGTTCCGCGCTTACGACATCGCCCGCTTATGCTGTGTCATGGCGGCTTACCGCTGCTGATGGCAGTATGGGTGCGGTTATCGGTCCGCGCATGG  
GCATATTGGACGCAATCCCATCGCTCTGCTGCTGAATACCGCAATATGCGCGCAATCAAAAGCCGCGTCCGCGCAATCTGTTTGAACCGTTTTCGCAAAACAAGATCGGTGGG  
TGTGGTTTGGCGCTATTTTGGCCATACGTTTTTCGCGAAA

## SEQ ID 2860

MNLKSPFLRLISRLDVYIRLMRADKPIGTLILLWPTWALWLDGIPDLAVLAFTTGTPLMSAGCVINDFADRFDAVERTKNRPFAQGRVKKKEALLTAFICLLAALCLIPLNH  
LWMLSPALFLALTYPTTKRFFPIQFYLGFAFSPGIPMAFAVGNVSPVEMILFAANVLWTLAYDTVYAMADKEDDLKIGIKTSAVTFGRYDIAAVMLCHGGFTLLNAVLAGAVIGAAM  
AYWTAPIVLLQLQRYAAIKSRVRQICFETPLANNRIGWVFAAIFAHFTFAK

## SEQ ID 2861

ATGAGCCTTATCGCGGCAAAATTTGCCCTTGTGCCATATGTTTGGATATGAGGTTGGGAGTAAAAAAAGCGTGTGAGGAAGCGGCGCTGCTTTGGAACCGGAATCTCATTTGTCCC  
ATGCTGATGTTTTCGAATGCTTTTTCGCCGTGAAAACTGGGTTCCGACCGGTTTGGGCGAGGTTGCGCATCCCCACGCGCGCCACGCGAGCGTGAACAGCGCGAGCGGCGGCTTAT  
CCGTACGCGCGAACCCTGCGGATTCGACGCGCTGACGCGCAACCGGTTTACTGGTTTATCTGTGCTGGTCCGGAACCGCAACGCGCGAGCATTTGGAAGTCTTATCCAACTGGCC  
GGCAAGTTTCCCAAAAAAGCATCAGAGAATCGCTGATGACGGTTGCTTCTCGGAGAAAGCCCGCCATCTCTGACCGAAGAA

## SEQ ID 2862

MSLIGKILPLSHIVLMEVGSKRLFEAGLLERESSLSHADVFELFAREKLGSTGLGQGVAPHGRHASVKQATGAFIRTPVGFDAFDGKPVSLVIFILLVPENATGEHLEVLKSLA  
GKFSQKSIRESLMTVASAEARAILTEZ

## SEQ ID 2863

ATGCTTTTGGGAAACATGCGCGCCAGTTTGGATAAGACTTCCAAATGCTCGCCGTTGCGTTTTCGGCACAGCAAGATAAAAACAGTGAACCGGTTTGGCGTACGGCGGCTGCA  
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AAGACATTGCAAAACATCAGCATGGGCAATGAGGATTCGCGTTCCAAAGCAGGCGCGCTTCTCTCAACAGCGCTTTTTCAGTCCCACTCCATATCCAAACAAATGGGCAAAAGC  
AAAATTTCCCGGATAGGCTCATAGCTTCTCTTTTCAGACATCGCAAAACAGAAAGATTGTACCGACTGCGCGGGCAAACTCAATCCCGCATACGGTACGGG

## SEQ ID 2864

MLFWENLPASLDKTSKSPVAFSGTSKIKTSETGLPSGASNP TGSRVRMNPVACFTLAWRPWGMATPCPKPVEPSFRAKRHSKTSAMDWEDSRKSRPASSNSLFLIPTSLKFTWDRG  
KISPIRLISFSFQTSQNRRIPTAGANLNPAYGTG

## SEQ ID 2865

TTGCTTGTATTATCCCTGTGCGCGTGTGCCAAAAATACCGCCGACGAAACAGGGAAGCGGAAAAATGAGGTACAGGCAGACGAGCGTGGG

## SEQ ID 2866

LLVYSLLRVQKYRRTHGKAKMRYRQTTVA

## SEQ ID 2867

ATGCACTCAATATATTTTAAAGGAGAAGCAGATGAGTCAAAACGACGCGCGTGTAGCGGACGATTTTACGCACAGTCAATGGCTGGGCAATATGTTGCCGACCCCGGTTACGCTTT  
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GAATAAATTGGGCAGGCGTGGTGTTTGTGCTTATCCGCCCTATGGCTGGGAGCATCGTCCCTGCGGAGCGGTATTTTGGCTCATCTCTGAACAGGATTGGTTGCCGGTTCCGCCGTTTT  
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GGCCGGCTACCGCGCCGAAGTCATTCAAGCCGCTTACCGCATCGGTGATTCGGTTACCAATPATTTATTCGCGCATGATGAGTATTTGCGGCTGATTTATGGCAGAGATTAATCAATACACAA  
AAAGATGCGGGCGTAGGCACGCTGATTTTCATGATGTTGCCGTATTCGCTTTCCTTTCTTAATTGCATGGATCGCCCTTATFTCTGCATTGGGTATTGTTTTGGGCTGCCCGTCGGTCCCG  
GCACACCCACATCTCATCCGGTGCT

**SEQ ID 2868**

MHSYTFPFKEKQMSQTDARRSGRFLRTVWLGNNMLPHPVTLFPIPIFVILLIISAVGAYPGLSVDPDRPGVCAKGRADGGLIHVVSLLDADGLIKLILHTVKNFTGFAPLGTVLVSLLGVGIAE  
KSLGISALMRLLILTKSPRKLTFTFVVVFCTLSHTFASRLGYVVLIPLSAVTFESLGRHPLAGLAAAFAGVSGGYSANLFLGTIDPLLAGLQTOQAAQIHPDTPVWPGEANVTFHAASTVIAL  
IGYVTFTEKIVEPQLGPQSDLSQEEKDIRHSNETTPLYEKLINAGVVFVLSALLAWSIVPADQILRHPTGLVAGSPFLFISVTPVIFLPAFGIVGYRITRSIGREVEVNNMAESTS  
TLGLYLVIIFFAAQFVAFPNWNTIGQYIAVKGAVFLKEVGLGGSVLFIGFILICAFINLMIGSASQAVTAPITVFVMLILMLAGYAPEVIQAYRIGDSVTNIIITPMHSYFGLIHTATVIKYK  
KDAVGVTLSMMLPYSAFFLIAIALFCTWVFVLGLVGPGRPTTFYFVP

**SEQ ID 2869**

ATGCCAGTATPCTCCGTCCGCGCGCTGTTTGACGACAAACCAATPACAAGTTGCAACTTGTGCTGGGCGCCGCGCAATTGCGGTGCGGACAAACCGTATPCCGCGTAGAGGGCGGACAAAGCCCGTCC  
TCGCCCTGTGTCGGACACCTGAATTTCACTCATCCCAAACCAATPCCAAGTGGTTCGGTTTGGCGGCGCGGAATATCTGAAACCGCTCGAATCCGGGGGAGCAGGTTTATCAGTTTCGGAGACCT  
TGTGCGATATTTCCATGCTTTGTGCTATCTGTGCGCAACCAAGTATTCGCGGTTTCCCGGGGTCGCGACATCTGCCAAGAACGACATCCCTTGTGACTTTCCAAATCTGAAGACCTCCCTTAT  
CTGATGGAATGTGTCGGGAATTTACCTGCAACGCACTTGGCAGCATCTGCGTTCGCTGAAACCGCGCTATTTCCTCGATGTGTTTGAATTCGGCGTCTGATTACCGGACATTCGTTTGGGTA  
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CGGTACGCAATPACATTTTGCAGTTCGCGCGGCAAGACGATGACGCGCAATTTTGGAAACGCAATCAGACGCAACCTTAAGAAACGAAACAGATCATGAAATTCGCTCGAT

SEQ ID 2870

MPISIVRRRLPDNQYKQLQAWAAGNSGADNRIGVEADKPVIALVGHNLTHPNQIQVVGLAESYTLNRLESGETGYQFGDLDFISMSLVIVANDLPVSPGLRDYCHKNDIPLTTSKLESFY  
LMDLVIRIYLQRTLAASSVKGHVFLDVFEGVLITGHSGLGKSEIALELISRGHSLIADDAVELFRIGPETLEGRCSPMLRDFLEVRGLGILNRHIFGETSIRPKKIQLIINLVEADDEY  
MKQLDRLSIRTEFESILNVNVRSVTLPAVAVGRNLAVLVEAAVRNYTLQIRGKDSITREFLERHQTLQKENEQNHENRPD

SEQ ID 2871

TTGCCCGGAGCCGGAAAGCCCGCTAATCAGGACGATTTTCATGATTCGTTCGTTTCTTTAAAGTTCGCTCTGATGGCGTTCACAAAAATTCCGCGCTACTGTCTTTTGCCGCGCAACTGCACAA  
ATGTAATTTGCGTACCGCCGCCCTCAACCAAAACGGCAAGGTTCGCTCCGACGGCGAGCGGACGCCTAACCGAACCGAGCGTGTACAGTTTGAGGATGGATTTCGGTTTCGGTCCGGATGCTCAACC  
GGTCGAGCTGCTTCATATCATCTGCTGTCGCCCTCGCCCAAAATGATAATGAGTTGACGAGGATTTTTCGGGCGGATGGAAGTTTCCGCCAAATATGCGCGATATGAGTATGCTCCCAAGCC  
CGCGCACTTCACAAAATACGGCAGCATAGGCCAGCAACGCCCTTCCTCAATGTTTCCGCGACGATCGGCAACGCTGCACGCCATCGTTCGGCAATTCAGGCTATGGCCGCGAAATCAGTGTCC  
AATGCCAATTCGCTCTTACCCAAACCAAGATGTCGGTAAATCAGCAGCCGATTTCAAACACATCGAGAAATACGCCGTGTTTGACGGACGATGCTGCCAAGTTCGCTTCGAGTAAATCC  
GCAACACATCCATCAGATAAGGCTTTCGAGTTTGGAAAGTCAACAGGSGATGTCGTTTTCGTGGCAGTAGTTCGCGCAGCCCCGGGGAACCGCGCAAAATCGTTTGCACAAATGACCAAAAG  
CATGGAATAATGCAACAGGCTCGCCCATGATAACCCGCTTCGCCCGATTTCGAGCGGCTTCAGATATATTCGCGATCCGCCAACCGACCACTTGGATTTCGTTGGATGGATGAAATTCAGG  
TGTCCGACCAGGCGGAGGACGGGCTTGTCGCCCTCTACGCCGATACGGTTCGCGCACCCGAATTCGCGCGCCCGCAGGCAGTTCGCAACTGTATGTTGGTGTGCTCAACACGCGCGCGGA  
CGGCAACTATCGGCACTATTTTATCTTCGGTTCAGGATGGCGCGGGCTCTTCCTGCGAGAAGCAACCGTCATCAGCGATTCTCTGATGTTCTTTGGGAAAACTTGCCGCGCAGTTTGGGA

SEQ ID 2872

LPEPESPLITITIFMILFVFFKLRLMAFQKFARTVFAAQLONVIAYYRLNQNGKVASDGDGQNRRTDVVDVEDGFGFGADAQFVELLHILVVRLAQIDNLEQDFFGADGSPAENHADIKYPOA  
 AHFQKIAQHRRTTFFQCFRTDABQLDRIVGNQAMARNQFCCQFALTQFRMSGNQHADFKHIEKYAVFDGRCCQGALQVNPQHIIHQIRAFEPGSGQGDVVVFVAVVAQPRGNRQIVCHNDQR  
 HGNIQVSELIITRLPRFEAVQIFRLRQTDHILDLVGNDEIQVSDQGEDGLVRLYADTVVTRTIAGGPGKQLVLVVKVQAADGDTGHILFFQCGDAGCFRRSRNRHQRFSDAFLGLLAGQFG

**SEQ ID 2873**

ATGAAATCTGCTCTGATTAGCGGGCTTCCGGCTCGGGCAAAATCCGTGCACTGCGCCAAATGGAAGATTGGGCTATTTTTTCGCTGGACAACCTGCCCTTGGAAATGCTGCCGTCGCTGG  
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GGTGGAAATTTTGTGTGTGTCGAGGCGGAAGAGCGCGTGTCTGTGTCGGCGCTTTTCCGAAACCCGCGCGGACATCCTTTGAGCAATCAGGATATGACGCTGTTGGAAAGCCTGAAAAAAGAG  
CGCGAATGGCTGTTCGCCCTTAAGGAAATCGCCTACTGTATCGACACTTCCAAGATGAATGCCAACAGCTCCGCCATGCACTGCCGACGTGGCTGAAGGTTGAGCGTTACCGGACTGCTGTG  
TGGTTTGGAGTCTCTTCGGGTTCAAAATACGGTGTGCGGAAACAACGCGGATTATTTATGTTCGATATGCGCGACTGTGCCCAACCGGTTATTACGATCCCGAGTTGAGGCTTACACCGGTATGGA  
CAAGCCCGTTTGGGATTATTGGACGGACAGCCGTTGGCGCAGGAATGGTTGACGCGCATGAAGGTTGTGATCGGCTGTTGTCGCGGTTTGGAGGATGAAGACAGGAGCTACGTTACC  
GTCCCATCTGCGCTGTACCGCGGGCAGCATCTGTGGTCTATATTGTGCGAAAACTCGCCCCGAAGGTTGAAAGGCGCTTATGAATTGCTGATACGGCACAGGCAGCGCAAAACCTGTCTCG  
GCCGC

SEQ ID 2874

MKTVLISLSSGSGKSVALRQMEDLGYPVDNLPLEMLPSLSVSYHIERADETELAVSDVRSIGDIAQAREQIAYLRGLGHRVEVLVFAEEAVLVRRPSETRRGHPLSNQDMLLESLSLKE  
 REHLPLKEIAYCIDTSKMNAAQLRHVARQWLKVERTGLLVLEFSFGPKYGVPPNADFMFDMRSLPNFYDPEL&PVTGMDKPFVWDYLDGQPLAQEMVDGIERFVTRNLPLEDESRSYVT  
 VAIGTCGGQHRSVYIVKELARRLKGRYTELLIRHQAOQLSGR

**SEQ ID 2875**

TTGACGGGATTAGCGGCCGACAGGTTTTCGCGCTGCGTGTGCGGTATCAGCAATTCATAAGCGCCCTTCAACCTTCGGCGGAGTTTTCGACAATATAGACCGGAACGATGCTGCGCGCGGTACACGCCGATGGCGACGGTAACCTAGCTCTGCTTTCACTCTCCAAACGCGGCAACCAACGCGTAACAAACCTTTCGATGCGCGTCAACCAATTCTCTGCGCAACGGCTGTGCGTCCAAAT AATCCCAAACGGCGCTGTGTCATACCGGTGAAGGCCCTCAACTCGGGATCTGAATACGGGTGTGGGCAGACTGCGCATATCGAACATAAAATCGCGCTGTGTCGGCACACCGTATTTTGAACCC GAGGACTCCAAAACCAACAGCAGTCCGGTAGCTCAACCTTCAGCCACTGCCGGAATGCATGGCGGAGCTGTGTGGGCATTCACTTTGGAAGTGTGCAATACATAGGCGAATTTCTTTAAGC GGGAACAGCCATTTCGGCTCTTTTTCAGGCTTTTCCAAACAGCGCTATATCTGATTGCTCAAAGGATGTCCGCGCGGTTTCGGAANAACGGCGGACAGCAGCGCTCTTCGCGCTCGA CAAACAAAATCTCCACCTCTGTGCCGAGTCCGCGCAGATAGGCAATCTGCTCGCGCGCTTGGCCAAATGCTATGCGCGAAGCACATAGCGCTGACCGCAATTCGGTTCGTGTCGCGACG TTCGATATGGTAGCACAACGACGCGCAGCATTTTCAAGGCGAGGTGTGTCAGCGAAATAAGCCCAATCTTCCATTTCGGCGAGTGCACACGGAATTTGCCGAGCGGAAAGCCCGCTA ATCAGGACGATTTTCAAGTTCGTGCTGTTTCTT

SEQ ID 2876

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BGLQNHQSGVFLANQLPLPDCMAELLGLTHLGSVDVTGDFLKRQEPFALFPQAFQQRHILLIAQRMSAPGFGKAADQHLFRLDKQNFHPVSESAQIGNLLARLGNVYAGTHIDADRQFGFVRT  
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SEQ ID 2877

ATGCCGCTCTGAAACCCCGTCCGCGTTTCAGACGGCATTTCAAATATTGAGAAGAAAGAACAGACATGGCAATCCAATGGTTTCCGGCCATA

**SEQ ID 2878**

MPSETPSAVSDGISNIEKKEQTHQSNQFPAL

**SEQ ID 2879**

SEQ ID 2879

ATGGCAATCCAATGGTTTCCCGGCCATATGAACAAGGCAAGAAAAGCCATCGCCGAGCGTGCCAAAAGCGTTGATATGGTGATTGAAATGCTGGACGCGGATATGCCCGCTCCACGCAA  
ATCCACTGTGGCGCAGCTTTCCAAGGTAAGCCCAAACTCAAATTTTAAACAAGCAAGACCTTGGCGACCTGAAACGCACAAAGGCTGTGGCTTGACACTACAACAGCCGCCCCGCAC  
CCGGGCGATCGCCCTCGATTCTTCCGAAACCGGCGCACACGGCAAAATCAACCACAGCTTCGCGCGCGATGATTCCCCACCGGCAAGGCATAGACAAACCCCTGCGCGTTTGTATTGGCGG  
ATTCCCAACGTCGGCAAAATCCACCTTCATCAATGGAATGATAGSCAAAAAATCCGCGAAAACCGGCACAGAACCGGGCATTAACAAAGCCGCAACACGCTTTTCCTTGGCGAGACTTCT  
GGCTGTACGACACCCCGGGAATGCTGCTGGCGGAAATCATCGTGAAGAAGCGGCTACAACTTCGCGCCGCGCGCGCATGTGGACGCAACGCATTGGAGCAAGAAGAAGTGCCTCGA  
ACTTTTAGACTACTCTCGCGCGCACTACCTCCCTATGCTGCAAGAAGCGCTACCAAGCCGACAAAGACCCACAGACCATCGGGACGACAACCTCGTGGCTCGAATGGATAGCAAAAAACG  
GCGCGAGCTCTCAGCGCGGACGGGTCAACTACCAAAAAGCCGCCGAAAACATCTTCACGGACTTCCGCGAAGGCAAAATCGGCAGAAATACCTTGAACACCGCAACATGGGAACCTT  
GGCTTAAAAAAGCAGCTCAGAAAGAAGCGCAACTCAAAGCCATTCGCGAAGCCAGAAAAGCAGAGCGCAAGGGCAGAAAGCTTCGGAAGCA

**SEQ ID 2880**

SEQ ID 2880  
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GAVLSGGRVNYQAAENILTFREGKIGRITLETTPNQWETWLKKARQKEAKKATREARKAERKQKQPSGA

**SEQ ID 2881**

SEQ ID 2881  
ATGACCGACAAAAATTTCTCCGACGCGCTGATTGAAGCCGCACATGTCTGACCCAAACC GAACCGCTGACCGAAAAATCATATGCGCGAACTGTGTGTGCCGCGCTTGTGCGAAGACAAACTGA  
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AGAACAGCGCTGCGCGCGCTACTCTCCGCGCGGTGATGGAACACCTGGCGATTATCGCGCTACCAGCAGCCGCTAACGCGCGCGGCACATCGAAGGTATACGCGCGGTGGCGGTGTGCGAGAAC  
GTGATGTAGACAGCTTTCGAGGATCGGGGGTGATTGAAGTCATCGGACATCGGGACACATTGGGAAAAACCCGCAFTGTGGGCAACCAACGGCAACTTTTCTCAGCGATTGTGCGCTTGGACGGTT  
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**SEQ ID 2882**

SEQ ID 2882  
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VHQTLQDRGWIIEVIGHRDPLGKPALWATTATFLSDLALDGLSELPPLTELGLVLPLDIEMPTTDEEPEPTVPSDTLWN

SEQ ID 2883

SEQ ID 2883

TTGGCTTCGCTTGCCGAACACGAGGGCGACTTCGGTATAGTCTTTCGCCCTTTGCTGACTTTGCTGCCGTAATAGGCGGTTCGGGCTTTTTCAGGGCGGGCTTCCCAATCTGTGTTTTGG  
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CCGCGCAATACTCTGTGTTCTTCGGAATGAGCATAAAAGTTTTCGCCGCTTTGCGCTTCAGACGGCATAACGGCGCAAAATATCAGGTGTCCAAACAAAAAGCCACAGTTGCGGGCGCAATT  
GGGTTTCGCCGTAGGCGTAAAAACCTGACCCGACGGGTACAGATTGCCAAAGCTGCCCTTCAGGATTTGCCCTCCGACGGTATGGCGTATGGAAACGGGGGCGAGTTGGGGCTGT

SEQ ID 2884

SEQ ID 2884  
LACVAHEGDFGTIVLPFADFAAVIGGLGFPQGGPFIILGKRFGGKRGFGKQRRAVLPEIEKRHPFROQLQCVLRDFRQYPCFSGLLDKGLPRFCFRRHNGAKYQVFPQKSHFLRRI  
GFVGVKHLTAAVQIAQAAPQDLVRRYGVWKRQGFQAV

SEQ ID 2885

SEQ ID 2885

TTGTTTATTATCTGCTATTGTTGCAATGCCGTCTGAAGCAATGTGCGTTTCAGACGGCATTTGGAAATTTCAGTGGCGCAGGATATCGGACGGTACGGTTTCGGCTCTCTTCATCCGTA  
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GTTTTCCCAATGTCGCCGATGTCGATGACTTCAATCCACCCCGATCTCGAAGTGTCTCATACGGTCTCGACACCGCCACGCCGCGGTATACCTTCGATGTCGCCGCGGTTACGGG  
CTGCTGCTAGGCGATAATCGCCAGTGTTCCTACGACGGCGGGAGTAGCGCGGCGGCACGCTGTTCTTGCAAGGTGCCACGCCGCTCGAATGCCGCTGCGAACAACTCTGAACACGCCAGCCC  
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GGAAGTAGAGAAAGCTGCCGAAAAATATTTTTCAGACGCCATCTTTATGCTTCCGAAGGCTTTCGCCCTTTCGGCTCTGCTTTTCGGCTTCGCGAATGGCTT

SEQ ID 2886

SEQ ID 2886  
LFLISAYLLQCLRLKQCAFQTAFGISVGQIGIRYGFRLFFIRRRHFYQIGNQFAQFGQRRQFFQTVAQIAEKSCRCPCQCGFSQCVPMSSDDFNPPPILOGLHHVLRHKHAAFTFDVAARYG  
LLVGDNRQCPHHGAGVARRTLFLQAAQPLECLRNWLKTPALLRMHQLQRPILPTRFQLRQHINQFVLRQRNRHTQFAHRFFGQRFGGLGQQCGFNQVRVGRNFVGHGTGIRAEATAWWICRLKSV  
GVERSCLKNIFQTAPFMLPKASALCALLFWLREWL

**SEQ ID 2887**

SEQ ID 2887

ATGCTTCTAACACTTTCCTTGCCTGATTTGTTCATGTGTCGAAAAATCTGAATCTGGAATTTTCAAAGCGGTTTACCGTTTGTACCGCGGAGACCGGGCGGGCAAGTCCATTACTTTGGATG  
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CAACGCGCATATTATCAATGTCAAAAAGTATTTGGCCAAATGTCGCAAACTCGAGACCGCGCTTTGCCGAGAGCTTGAATATGTTGGCAAGCATCGAGGCGAATTGGGCGAAATCAGTGTCCA  
ATAATGGCGAGTGTGGCAGGACAGTGACATCAACCCCAATGAATTGGCGGCACAGGAACAGCGTATGGGCGAAGTATGGGGAATGGCGCGGAATACCGGAATTGAACCCGAAGAGTGGC  
TGCCAAGTTGGCAGAAATCGAAGAAGCGCTGCAAAAGTCTTCAAGCTGCGCGCTGATTTGGAGCGCGCTCGAGCATTAATGTTCGCCCAAAATTTGGCCAAATATCGAAGATTCAGGACCTGCCCATCTCT  
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CAGCGCAATATACCGGATTCACCACTGTATTTTGTGATGAGGTGCGATACCGGTATTGGAGGGGGAGTGGCTGAAATGCTGCGCAAGGCATTACGTGCTGTGGGCAGAAAACATCAGGTGCTT  
GCGGCTTACCCATCTTCCGCAAGTCGCATCTCTGCGGAGAAAACTAGCTGCGGGTCCGCAAGCACAGCGAGGAGAGCAACCGTCAGCGGAATCAGTATATTGGATGAAATACAACGGATCG  
AAGAGGTTGCCGTATGTTGGCGGAGAAGTTATTACCGATACGACCGGCAACATCGCGCAGAAATTGCTGCAACTTGCCTCGAAAAATAGTTTATT

... SEQ ID 2888

SEQ ID 2888  
 MLLTSLSRPFIIVENLNLDPQSGPTVLGTETGAGKSTITLDAIGLLGLDKADYSQVRSKAQAQLSALFDISHLPALKAELREQGLLDGGSELSIRRIIDAKGKSESFINNQAAITLAQLKA  
 VGGQLIDIHGQNDHHSINQEAAQRELLDAFVGGRVQAEVRLQYQWANAKKALQEAQEHADAVTIERERLEWQFNEINQDLIDKQGEWAFSQSHDSLASHSAELLQAAEEVGSKIDGNGI  
 QRHIYCCQKLLANLQNIERPFAESLANLAEIABELGEISANRDRVAGHSNDINPELAAQEQRMGELMGMARKYRIEPEELPAKLAETIERLQSLQAAADLDALSHVHNHFAEYQEAHITL  
 SAMRFRQAAGRLSSDITTERMQHLANKGARFDIVLLPSSPTAHGLBQVQFQVAANKGNPPRPLANKVASGGELARIISLALQVVASQYTVPTLTFIDFVDTGIGGGVAENVGKALRALGRKHQVL  
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SEQ ID 2889

SEQ ID 2889  
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## SEQ ID 2890

LLHTSNRAFSLLPYLTGGTETEAAGRVKEVFECYKFLDSKGNLLGIPYSLFWEENVKGVFDILP

## SEQ ID 2891

GTGTTTTGATATTTTACCGTGAGGATGGTATGTTTATTTGAATATGATTTTTTGTGGTCGGGACGGCATCGGCAAGGCTTAAGGAATCAGGTTTCGCTTC

## SEQ ID 2892

VFSIFYREDWYVYVNIIMPCGRDGMRLKESGSAF

## SEQ ID 2893

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## SEQ ID 2894

IDQATQCLQFDSINLIHEHLPDVRFWLVPSPRRLHEHFHHISQTEAIPTQESKDXPWFALPQTSERKPEHVLVIGAGIAGASTAHALASHGISVTVLEARKAAQASGNRQGLLYA  
KISPHDPTGQTEHLLAGYTRKLLGHILPDSDTGGNGIHLNYSRTBQJRNHELGLQKHNLHLYRSITSAAEKIAGIPLNTPYAEPLCGLYWHGVNLPAPVTRTLLSHPLIELYENT  
TLTGSHDGEKWLASTPNGTPTATHIYCTGAHSPCLPEFNLAALPLRQIRGTGLTPTSPFBSQLECAVSGESYISPSNHLHLYGASFI PNSSNTGWNAAEASNRQALAHNLPALAES  
LFAANPNPKHQHGAIRCDSPDHLFVVGALGDIAMRQTYAKLALDKNYRIDTTCFYLPAVNTAHGTGLATAPICAAVAAEILGLPHLPSQLRHLALHPNRTVIRATVRRQNLIP

## SEQ ID 2895

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CGACCAACCAATCCGCAACACGCACACCGGCTCAACC

## SEQ ID 2896

VPLNGATFNSFIPIPKPLTQALITWISYGTAPFSAHSTKPSANTHTST

## SEQ ID 2897

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AATCAGTTTTTTCGAGCGGCGACGACAGCGGTCTTTACGATTGGCGGTATCTGCACAGACTGGCATACGATACGATGCGATGTGCGAGGAATATTTGACAAATTTGGCGCGCGCGCGCG  
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## SEQ ID 2898

LYAEPRCLNNIPVEIRLLKNRAVLVLTGYDEPKNLPAEFLRVYSPSAEVRHGQVQDVLQTKADVQITDLQPVGQVALKISFSDGHDGLYDWAYLHRLRAYGDAMWQBYLDKLAAGA  
SRPEKQSDC

## SEQ ID 2899

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GTGAAATTT

## SEQ ID 2900

MGGQKTHFGFSTVNEDEKAGKVAEVFHSVAKNYDINNDVMSAGLHRVWKHPTIHTAHLKRGDKVLDIAGGTGDLRSGWAKRVGKESEVWLTDINSSMLTVGRDRLLNEGMILFVSLADAER  
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VKP

## SEQ ID 2901

TTGTTTGTCTGTTTATTCCTGTTGCGCGTGTGCCAAAAATACCGCGCACGAAACACGGGAAGCGAAAAATGAGGTACAGGCAGACGCGTGGCTAAAACTCCCAACCCGTGATGTGT  
ACCGCTCCCGCACGGGATTTCGAGGATGTAGGCAAGAGAGCGCGTACGCGGAAACCTGCGCGCAGCTCGATCAGGTGTTGTCGAAATGTTTGGCTTGGAGCGCGGCGACCGCAACAGT  
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TCCGCAACCGCATATCTTAAACAAAAACGGCAGCTC

## SEQ ID 2902

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## SEQ ID 2903

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**SEQ ID 2904**

MFYLYQSNRLBSIALFARIQKVKLKCALQPEQIVVQSQGRRYLNTCLARDLGVAAFLSPFLAGLAWKMLKKLPGIPELSPFAPFVYMRWLLDQFSAEQNGAEFQDVENVLQDYL  
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SEQ ID 2905

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CGGAAAAAATCCCGTTTGCCTACTGCTCGCCTTTATCATATATGTCGGCTTTTGTGCTTTTCGGTTTCGTTGGGGGGGGAA

**SEQ ID 2906**

LDWNNPVLNRCFTDWNNGGCAVNGKDDFRAGASPSLGRNPKYKEMDAKPKKILSLKVDADPDKTIATGTPGYSEKVEVAPGTVKNGSPVTDNRNGAPVQVAATPGRDAGQNTIADQVVI  
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SEQ ID 2907

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GAGGGAGCTCGACCCGCAAGGATAATGCCTACAAACCGCCCTGTCCGCGTTGTCCAGAAAGCTGGGGCGGTGTAAAGCAAGCTGCATACGGCGGTTACGCCCTTTTGTGTGAGACTGGTG  
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**SEQ ID 2908**

MPESIFKQI SSDILRLHRDSVSYLLATSGCNCQVHEAAYWNIDGKYIYALSCEPVEGVEVETGILLI EDESRNLRLSWVGSARELDRKDAYKRALSAISRKLGRCKDKLHTAVQPFLLLV  
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SEQ ID 2909

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SEQ ID 2910

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SEQ ID 2911

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CACGAACGCGAGTTTCGTCATACGCCCTTTGGCAGAAATCTCCCTGATTTTATTTTGGGAAAATACGGAAAGGTTGTGCAATTTGTCAAAACGGCTGGGCAATCAAGGCATCCGCTCTTTTAC  
CGGACAGG

**SEQ ID 2912**

MONRHFVAVIALGSLNDNPAQQIRGALDALSSHPDIRLBQASSLYMTAPVGYDNPQDFINAVCTVSTTLDGIALLAELNRIEADPGRERSFRNAPRTLDLTIIDFDGSSDDPRLTLEHFA  
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**SEQ ID 2913**

ATGCAGTATCTGATTGTCAAATCAGCCATCAAATCTCGTTACCATCAACATTTTGGTATTCAACATCCGTTTTCCTACCTTTGGAAAAATCCAGAAAGCCCTTGGTGGCTTTGGAA  
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CTGCCAFTC

## SEQ ID 2914

MQYLIVKYSHQIFVTITLIVFNIRPFLWKNPEKPLVGFWKALPHLNDTMLLFTGLWLMKITHPSFPNAPWLGTKILLFAYIALGHVHRRARPRSTKPYTVYLLAMCCIACTVYLARTKV  
LFF

## SEQ ID 2915

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TCCTGCTCTGTTTCGCTTACATCGCACTGGGCATGGTAATGATGCGCGCCGTCGCGGTTGACCAAGTTCACACCGTTTACCTGCTCGCTATGTGTGCATCGCTGCATCGTTTACCT  
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## SEQ ID 2916

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CQNSPAILKHCHEQDTFCRHLRGQP

## SEQ ID 2917

TTGCCGTCCTTATCCGGGACAGAAAACCGCAACAGGAGGAGAGCCGTCGGACAATGGGCAAAAAACCTGCCTCAAGAACAGTTTCCGCTTTTACGTTACGGCTTTTACCAACCGGAA  
GAATAGCCACCTATCTTTTGGCATTTGAAAACTGCGTCAAAAATAACTGTTTTCGG

## SEQ ID 2918

LPSSIRDTKTANRRQKPSDNGQKTCCLKNSLFFVTALPTGRIAHPIFWHLKNCVKNECLR

## SEQ ID 2919

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ACCGGAAGATAGCCACCTATCTTTTGGCATTTGAAAACTGCGTCAAAA

## SEQ ID 2920

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## SEQ ID 2921

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GGCGCTTGGCAAGATGAGTCCCAAGACCAAAAGGATGTACAT

## SEQ ID 2922

FPVARVPKIPFHETREGENEVQADDGVKLPPLIVVRSRTGFEDVGRGGQRETQRLDQVVSZPALERGHABQSGREGGVGKDEQDQKDVH

## SEQ ID 2923

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## SEQ ID 2924

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## SEQ ID 2925

TTGCTCCGCATTCCGGGCGCGGAGCGCTGTGGGACACCCCTTCGCGCTTATGCCAAATCCCCCGCGCTTCTCGGCTGTTTGGGCTTCGCCCGCAAGTGGGTACTTCGCTGCTT  
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## SEQ ID 2926

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## SEQ ID 2927

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## SEQ ID 2928

VSRIDGKNTVFFQQGEGCSKGNAGFLVGGQILVASGQPAETENGCTQRLRNILLQVMSVQDEPYIAVTCFLQTASGVVQGLRLDVECPHPFPVACGLCEKGVVSVAGGAVQRIAP  
GKCLPQKANGWKDVFQ

## SEQ ID 2929

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GAAGCAATATATTCGGGAGCGCTGGATGACGCGTTTTCAATTTGCGCTGTTTCCCGGAGGCGACAAGAATCTGACCACCGACAAGGAAACAGCATTCGCCGCTT

## SEQ ID 2930

LKNILFFARCLREALPEGGNALDGTAGNHDTLFLAQTAGNRGKWFADIQPQALNTRCLRQBAQYSNVRLILDGHENLKQYIPEPLDAVFNFGMLPGGDKNLTOKETSIPAL

## SEQ ID 2931

ATGCCCGCGGAAAAACGCCCAACAAAAAATGTTAATTTTTCTATTCCAGGCTACAATTCAGACGACAGGGCATCTGCCGATTTCACANTATAATAGCGAGTTAAAAAAT  
ATGACAGC

## SEQ ID 2932

MPGKPKPKHKIGNFSYSLQFDTHRASARFHNHNSGVKKYDS

## SEQ ID 2933

GTGGATGCTGCAGCAACGCTCTGACATACAAATGCCCGCGGAAAAACGCCCAACAAAAAATGTTAATTTTTCTATTCCAGGCTACAATTCAGACAGCAGGCGCATCTGCCCG  
ATTTCACAAATCATAATAGCGGAGTTAAAAAATATGACAGCTAAAGGACAAATGTTGAAGATCCCTTCTGAAACGATTGCGTAAAGAGCATGTTCCGCTTTCGATTACTTAGTTAACGG  
TATCAAATTCAGGTCAGGTGGAATCTTCGACCAATACGTCGTTCTCTGAGAAACACTTCGTAACCCAAATGTTTACAAACAGCCATTTCACCATCGTACCGGCTCGCTCGCTC  
AACTCCACATGAAACAAACCCCAAGCGCACCGGCTTCGACCTTGTCCAGTGAAGAACCTCCAGCAGCTGCCGAA

## SEQ ID 2934

VDAAATLLYKCPAENRNPNTKKLVIPPIGYNSTRTGHLDPFTIIIAELKNMTAKGMLQDPFLNALRKEHVPSIYLVNGIKLQGVESFDQVVLNRPVTONVYKHAISTIVPARSV  
NLQHENKPAAPASTLVQVETVQPAE

## SEQ ID 2935

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GCGCGATGGTCTGTTTGGATGCAAACTTGGACATGAACGAAACCGTTTACCATCACACCCGACGAAATCGACCCCTCAAAGGGACCGGACGCGCTCTTGGCATAGGTACGGCACTTACAG  
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CGAGGACGGCAGGCTATGGTTGTCAAAGCCAACATTCAAAACCAACCGCTTACCATGCTATGCTGAATCGCCACATCCGCCACACGCGTCAACAGCGCCCGCAAAATCGAATCGTGG  
ATGCTGCAGCAACGCTCC

## SEQ ID 2936

MSNHKICSDLKTECYKTQLQKHNTARLRVSCQTYTPTDGCFFNKITPILKNTEPKMSIRTLKRLPSSLLGLCLSLPSAHLFADNDILQFLQNL/TSSDPIKIFAESTIYPADTQAI  
TGLILSSQSALVNNKTGQILYQKNADRIPIASISKLMSAMVLDANLDMNETVITTPDEIDRLKGTGSRILAIGTALTRKELLHLSLMSSENATHALGRITYPGMGAFVAMNRKAQS  
LMYGRSFYEPTGLNFQNVSTAKDLSLMVNAAYPQIRTNSTSNYASVQTKNGQNYKNSNALVREGMNIELQKTYIREAGRSMVVKANIQNPVTIVLLNSPTSATRVNDARKIESW  
MLQORS

## SEQ ID 2937

TTGGTACAGGTAAAACATGGCTTGCCTTTTCAAAATGACAGTATGCGGAATTATATAGCTTCTCGGCAAGCCGCCGCAACAAATGCCGTCTGAACGCTTCAGACGGCATCGGGTCA  
TT

## SEQ ID 2938

LVQVKHLLFPQNSDAELYSFGKPKANKMPSEFRFRHVT

## SEQ ID 2939

TTGAGGCGCGCCGCTTATGCTATGGGTATCGCCTGTTGAAAATGGGCTGCCAATCTATCTACACCCGCATAGGTAACAGCCATCAAGCC

## SEQ ID 2940

LRRARYAMGYRLLEMGCSITTRIGNSHQA

## SEQ ID 2941

TTGGCAATTCGCGCGTCTGCTGCGCGCTTTTGAATAATGGGAATATCGGGAGTAGGACTATGGATATGAAATATGAATTTACCTGCTTCGAGCAGCGGTGCGGATTTTCAATTCGG  
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AAAAAATGATGCGGAAGAGTCTGTAGGATCGAGCGCAGTACGTTCTGCTGTAACAAGGACGCGGAAATGTCGCGGAGTGCGGAAAGTCAAAGTGGCGGCTCATGCACAGGAAGT  
TGGAAACGCTTTCCCGA

## SEQ ID 2942

LALAAVRLRAVLNNGNISRTMDMKYEFTLPSSSGADPHSAHLPLVVVYFPKDPSTPGCTTEGLDFNARLEQFEALGYTVVGISRDGVKAHQNFCAKQGRFPELLSDKDETVCRLFDVILK  
KKLYGKESLGIERTFVLNKGDEIVREWRKVKVAGHAQEVLESLR

## SEQ ID 2943

TTGGTTTGGAAACGCTATGGAACGCTTTGATTGACAGGCTGCTGGAACCTTTGTGGTTGGATCGCGCGCTCAGTCGGAATACTTTGGACAGCTACCGCGGGATTGGAAAAGATCGCCC  
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AGCCTGCGCCACGCTTTCGACGCACTGCTGTCGCGGACGAGTGGATTGCGCGTAGTTCAGGATATGTTGGGACACGCGGATTGAAACAGCACTCAGATTATACCCATGTTGCCAATG  
TCCGCTGCTATAGCTGGTAAAGAACCACTTCCCGAAGC

## SEQ ID 2944

LWNAMENGLIDRLLETIMLDRRLSRNTLDSYRDLKILARRLSLCGRITLDADEADLAAAVYVDGEQRSSQARALSACKRLYVWMBEGRADNPTRLKPKIDRNIPTLITEQOISRL  
LAAPDTTPHGLRDKALLRLMYATGLRVSEAVLNFGNVDLDRGCTTTLGRGDKQRMVPMQGESAYWVERYTTEARPLLLKGRSCDALFVSQKGTGISRLQAWMIVKEYAGRAGIGHISPH  
SLRHAPATHLVRHGLDLRVVDMLGHADLNTQITTHVANVRLHSVVKHHSRN

## SEQ ID 2945

ATGTTTGTCTGCACTGCAATGCCGTTACCGACCATCAAAATCAAGGAAACCATCGCTGCCGCGCGGACCAATGGGCGATTTCGAGTCGCAATGGGCGTGGCGAGCTGCTGCGGCTGCT  
CGCGGAGCTTCCGCTTCTGACGCGGCAATGCGCAACCGACGCTTACGGCGGATCAACGTTCAAGCG

## SEQ ID 2946

MFVCIENAVTDHQIKETLAAGATTMGDLQSLQGVASCCGCGELAASFLTAHNAQPTVTAGINVQA

## SEQ ID 2947

TTGATAAAAAATTACCAAGACAAACCGTGTATGCCGACCTTGCAATGCGAACCGTTTTTATTTATATTTGCTACGATAATAAAAGCCGCTATCGGTACGATAGTTTGAACACACCGGAG  
CACAAAATGTTTGTCTGCACTGCAATGCCGTTACCGACCATCAAAATCAAGGAAACCATCGCTGCCGCGCGGACCAATGGGCGATTTCGAGTCGCAATGGGCGTGGCGAGCTGCTGCG  
GCTGCTGCGGGGAGCTTCCGCTTCTGACGCGGCAATGCGCAACCGACGCTTACGGCGGATCAACGTTCAAGCGTAAACGCTTTTGGAAATGCCGCTGCACTGTTTACAGC  
GGCAATTTGCTGTTTTCGAGGACT

## SEQ ID 2948

LIRNYQDKPCMPFLQCEPFLIFAYDNKSRYRYSRLRTHGAQNVCLHLQCRYRPSNQGNHRCRRDHNGRFVAIGRGELLALLRGACRFVSDGAQCATDGYGYQRSSVKRFWCRILNCSD  
GIFAVFGRT

## SEQ ID 2949

GTGTCAAATGACAGATAAGGAAACGCGGATGAAATGACCTTGATGTTTGTGTAATTTGACGCTTGTGCCACAAAATGCCGATGCACTCAAACCTTTTCAGGATGAATACGGGTTGG  
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GAAACAGTTTCTCGAACCG

## SEQ ID 2950

VCKLTKETRMKLTLMFREYCSLCHKMRDALKPFQDEYGFGLVVDVDENPVLEEKYNELIPVLLAGDERICHWFLEDRLKQFLER

## SEQ ID 2951

ATGCTTCGAGGAGATGATACTCAAGTCTGCCAAAAACAGCAAAATGCCGCTGGAACAGTTTCAAGCGGCTTCCAAAACCGTTTACGCTTGAACGTTGATACCGCGGTAACCGTC  
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CCTGATTTGATGGTGGTAAACGCGATTGAGATGACAGACAAACATTTGTGCTCGGTGTCTCAAACTATCTGACCGATAGCGGCTTTTATTTATCTGATGCAAAAT



## SEQ ID 2952

MSSRKNILKSCQKQKCRNLSSDGLSKTVLRNVDTNRNRLRIVRRQKRSKLPAAAAARHAQLRLQIAHCRAGSDGFLDLNVGNGIADADKHFVLRVFSNYRTDSGFYRQI

## SEQ ID 2953

GTGCTTCCTTTACCGGCAGGTATCAGCCCCACAAAACGTAAGAAGCTTGATTGAAAAAATGCCGCTCGAAGTCTGCTTCAGACGGCATTTTTACCGTTCGAGAACTGTTTCAA  
CCTGCTTCATCCAAAACAGTGGCAATTTCTCATCTCCGCCAACAAAACGGGAATCAGCTCATTTGATTTTCTTCCAAAACAGGATTTTCATCCACATCGACCACTTCAGCCCGG  
AACCGTATTCATCTGAAAAGGT

## SEQ ID 2954

VLPFPAGHQPHKNVNDLKKMPSEVLLQTAFTTVRETSTCPHPTSGKPHLPPTKRESAHCIFLPKQDFPHRPLPARTRIHPEKV

## SEQ ID 2955

TTGACCTTTCTTTATTTTATTTGTCGGTGGGAGAATCTTAATTTATTGATTTTTTCAATAAAAAATTAGAAAAATTATTGTGAGATGTCATGTTGGCAATCATATCATGTTTGTCTGT  
TGATGGAAGCA

## SEQ ID 2956

LTLFLPYLSVGRILNLLFSIKIRKFIVRCHNQSYHVLLLEHA

## SEQ ID 2957

ATGAGGCAAAAGTGCCTTTTAAAGAAAGGAGAGCAAAATGAAATGTTGGCGCATTGATTCGCCTCTTGATGAGCGTCGACGGCCGTATATGACTGCATTAGGCTTGATGGCTGTTACCT  
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TCTTTTCGGCGCAATCGCTTTATTTCTGCTCTTTAAACAAATGACAAAACTCGAACCTCAATCGGGAAGAAAAA

## SEQ ID 2958

MRQTCILLRKGQMKLLAALIPLMSVAGRILFALGLNAVITYAGVDRLAANFQQAITHSTGAPQAMLQFYISGGGTVLNIFLGAIAFILSPKQMTKLATSIGKKK

## SEQ ID 2959

ATGAGAATCCTATTGACAGGCTCGAAAAGCCAACTGGCACATGCTGCGGACCGCTCTCTGAAGACTGGGAAACCAATTGCGACGGATTCCGCATCCTAGACATTACCGATGCCGATG  
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TTTCAAGCTGCTC

## SEQ ID 2960

MRILLTGSQSLAHLRDLRDLPEWETIATDSASLDITDADAVCNMVKSPQDAIVNTAAVTAVDKAEADAAAFVNASAVYNLALAAHRAHARFIHISTDYVFDGKGIPIYQESDFTNPS  
NVYQSKTAGELLALANPDSLILRTSWLSEYGNFVFTMLNLAERSPLSAVHNQIGCPTYAGDLASAIIRLLQSNPVRGIYHYAGGKSVSWYEFARHIFQALQDASPVPFELKAV  
SDEGSAAPRPAISILDCRKLINDPFIKPSDWQKALAQVSKLL

## SEQ ID 2961

TTGCTGAAAGTGTATTGTAGGACTGTCTGCTGTTATATTAGTGCCAAACTTTGCCGACGGTTGACGGGTGGCTTTTGTGCCATGGGTATTGTTTGGCGCCGACTTCGGCTAGAAATATC  
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CTGGCGCATATTATGCCCAACCAATTCACGCGGATACCGGTGACGATGTTTGCCTGAAACGAAGCCAAAGCTTTGAAAAACCGCGCTGTAGCTAAAAACCTCACTCCGTTGAAAG  
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ATTGAGCCGCTTCTGCGCGGATCAATATGAAGTCGCGACCAATCCCGCTCTTTTGAACAAATTCGTCGCGACTGGCTGGAACAAAGCGGTGGAAACAAAAAGCCCTTGCAGGCT  
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## SEQ ID 2962

LVKVYCRCTCRYYSAKTLPTVDGLAPCAMGIVLRRLLEYRFATQTCRVGIFKIFSGGCEMSEIGLVKISGKVRDLYEIDDKRMLMVASDRLSAFDVLIDAPIPKGEILTQISNFWFKK  
LAHIMPNNHTGDTVDVLPENEALEKRAVAKKLPVKVEAIVRGYLAGSGWKDYQKTSVCGIRLPEGMREAQQLPEVLPSTPKAAVGDHDENISFEECGRIIGKLAEEVRDKAVR  
LYTEAAEYAKSRGIIICDTKPEFGLDEBGLTLMDEVLTDPSSRFWPAQDYEVGTNPPSFDPQFVRDLQSGWNNKAPAPKVPADVIRKTVKEYQALFTLLTQD

## SEQ ID 2963

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GGCTGAAACCTTAATATGACATTCGGATTTTAGTGTGATTTATTAGTGTTTAGCAGTGGGTATTTTGAAGGAACAATGATGTTTCAA

## SEQ ID 2964

MFQTAFLLYQYHILRMVAFIIRNCFQRPKRLKACLQPAARSETLTMHIRILVCLISVLAVRYPERNDVQ

## SEQ ID 2965

TTGAAAGGAACATGATGTTCAATAAATACGTTAAGACCTTCCAAATACGTAATCAAAACGTTACTTTGGAAACCGGCAAAATGCGCGCAAGCTGCCGCTGCCGTAAAGTATCGATGG  
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TCAGCGTGATGCCGGCAAGACGGTTTGGTACACATCAGCCAAATCGCACAGCGCGTACGCAATGTCGGCGATTACCTGCAAGTCGGTTCAGGTGGTGAACGTGAAAGCATTTG3AAGT  
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**SEQ ID 2966**

LKGTMMFNKYVKTQYGNQTVTLETGEIARQAAAAVKVSMGDTVVFVAVTINKEVKEQDFFPLAVDYLERTYAAGKIPGGFFKREGKQSEKEILTSRLIDRPIRPLFPEGFYHDIQIVAM  
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TSRDEQIIDLALSGEYTDRLHYNPPYSTGEVGRMGAPKRRREIGHGRLLAKRALLAVLPKPEDFSYTHRVVSEITTESNGSSSMASVCGGCLSLLSAGVPLKHAVGIAMGLILEGNKFAVL  
TDILGDEHLDGMDFKVAGTTEGVTALQMDIKIQGITKEMQIALAQAKEARLHLIDMQKAAVAGPQELSAHAPRLFMKISQDKIRDVIGKGETFIRSTIATETGTEINIAEDGTTITAAAT  
TQEAAGAAKKRIEETAEVEVGKVTYEGTVVKILDRNVGAIIVSMPKGDGLVHISQIAHVERVNVGDYLVQVGVVNVKALEVDGRVRLSLKALLDAPVRENAAE

**SEQ ID 2967**

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TCGCGCATTTTTCCTCGCACTGAAAAAATCATGCAAAACCGATATATCGCGCTGTGTACAGGATTATCGGTATCATATGGGCATTTATGGAAGCTTGGCGCTCTGTGGCTG

**SEQ ID 2968**

MCGGLSSAFALQLPPHNRFWLILLNTGRISSTYTAIGMLIGLIGQLGISLSDQTRVLQNLITYTASNLILLFLIGLYLSGSSSLAAKIEKIKPTWRNLNPLNRLPIKSIPIACLAUGILNG  
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**SEQ ID 2969**

TTGTTACCCCTTACAAGAAACAAATGTCCCGCTGTCTGCTGCTTTTCCCTTGGGCAACCTTGGCGCTGCACCCGAAACATACCGGCAAGCCCGCGCTTCAAATTTGCGCGCATC  
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TAACAGCAGCGGGAATGCCCTCGTCAACCCATTTGGTGGGACTGCCGGAATTTGCCGTTTCCCCGACAAACATCTGACCATGAGCCATCCA

**SEQ ID 2970**

LPLITRMYSRILFLLLFPWATLAACTRNIPASPAVSNCAHLNRTVLYFDAHGPADSTAKGGFYRTVEIHDNRIILIQDFNSTGNALVKPYWSDCKRLSVFPDKHLTMSHP

**SEQ ID 2971**

TTGCTTCCGAATCGAAATCCCCGAGCCGAGGGAAATGCTTCCATCTCCCGCCGCTGAGGATTAATAGACCATTTACTGTTTGTATACCCCTTACAAGAAACAAATGTCCCGCT  
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GGCAACCCCGCGACAGCAGCAAGGGCGGATTTTACAGGACCGTCAAAATTCATGACACAAACCGCATCTTATTTCAAGACTTTTAAACAGCAGCGGGGAATGCCCTCGTCAAAACCCATTT  
GGTGGGACTGCCGGAATTTGCTGCTTTTCCCGGACAAACATC

**SEQ ID 2972**

LPLNPKSPSPKGNASISRLRIKMSHYTVCYPLQETQCPACSCCFSLGQLPFPAPETRYQAPPQIARIFTTAPSCILTHTANPPTAQQRADFTGPSKFMPTQASLKFILTAGMPSSNPI  
GRTAGNCFPSPTNI

**SEQ ID 2973**

TTGTTCCGAAATCCCGTATTGTCTGTGCTTCCGAATCCGAAATCCCGGAGCCGAGGGAAATGCTTCCATCTCCCGCGCGCTGAGGAT

**SEQ ID 2974**

LFRNFVLSVASESRIPPEPKCFHLPFPED

**SEQ ID 2975**

CAGCGTGTCTTCCAACGCCCTTGGCGCACCAGTCGATAACGGTTTGGGCATATATGCCACAGCACCACAGCAGCGCGTGAAGCTTAAGAGGGATTTTGGGCAITGTGTCCGCCCGGCG  
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CAAGCAGGGCAAAACATCAGAGACCATGTCATGATGACAGGTTCCAGCGCGTAAACCGCGTAAACCGGATGCGGAAGCGAAACAGCGCGCGGATTTTGGGGCAGTGGCGCAAGCGGTAAACAG  
AGTGGCGCGCGTGATACAGCTGCGGCATCCCATATGGAACGGTACCGCGCGGATTTGAACGCAACCGCGCAGCATAAACACAGACCCAGTTTCAACAGCCATCTGTTAGCTTCT  
TCATTTAGAGAGAGGGGAGCAGCGCGCAAAATTCACGCGAACCGGTTCGCGCGTAAACCATAGAAATACCGTAGAGCAGCAGCGCGGATGCGAGCGCGCCAGAACAAATATTTCAAG  
CGGCTTGGCGCGCAAAACCGGAATCGCGCGCAGGGCAATCAGGGCGTAAAGGGGAGCGACAAGAGTTCCAAACCGATATAGGCGAGTAAAAAAATGCCCGCGCTCACCATCAGCTCAT  
GCCCAAGAGGGCAACAGCGGACAGGGGTAAACCTGCGCTTTGAAATACCGCGCAGCTTGGTTGTAGGGCTTGGCATAGACAAACAGGACAAACGTCAAGGCATATAAAACCATTTTTCGC  
AAACCGGACATACCGTCCGCAATATACATCCCGTTGAACGAAGCGTGTGCTGCTTCCACAGCGCAAGCTGCACCGCGCGGTAAACCGCCAGCTTGCACAGCGCGCGTAAATCGGTCC  
AACGGCATTTGTCTACTGTCGCCCAAGTCCGCGGCAACAATAACACAGCAGCGACAGCAGCGGACTTCCGGCAGTGGCGGCATTAAATTCAAATCTGACCAATTCAT

**SEQ ID 2976**

QRVLQRLGAPVDNGLRHNAPOHQQRVIDA\*EGFCGIVAAGGGTGAAGFVKIHDFDHAQVVERANQRHHDGKHRQPYIALPQKRHNNAEFVKTHQRRNARHREHNQHQKGPYAVLVQPC  
QLADVFALVVPVRQHHAEPERRHRQVGVNGVIEARRKADRARHKRQDDETHMYRGGIEHTFIDILHDDGKVADQQRGGGKQKHQRPVPMHGSQPGNEDAESENDGGDFRGSADQGGNR  
SGRAVIVHGHMERYRAEFERNDDDKHQTPQPPVVSFFIEGRGEHAGKFPQTGCAVNHNFTVQDQAGCQRAQNKIPQGGFGGKTGIAAQQNGVKGGERQEPQTDIGS\*KMPRAHHHAH  
AQEGKQKQGVKLAFFENTAHLLVVLGIDKQDKRQGI\*NHFCQTRHTFVRNHPVERRRALFPHGKLHRRNRHRCQRAVMRPTAFVITGPVRRQ\*HQQRQRPDQCGH\*IQI\*PIH

**SEQ ID 2977**

ATGGATACACAAATCAAATGAAGCCGCTCAGCAGAAATACCGGCATTATCTGAGCGTTTGGAGGTGGCATTTTTATGCCGTTTATTTGGTTATGCCCTTCTTACGCCCTGCTTGCCTTA  
CAGGTTTGGGTATGCTGTTGTTTGGCAATATTACCGGTAAAGAGGGAGAGCGTATTACAGCTCTCCCTCAGGCACTGGTGCAACCCCTCTCTGTTCAAGCAGAAAGCGGACGCGGTGCGAT  
TAATCCGAGACTTCGTCGTCGTCCTCAATATATTGACCCGCGTCCGATGATATGTTGCTGTGTTCCGTGTCAACAAATGAGGTAAAGCAACCATGTTGCGGTGGATCTTTATACGGCA  
AAAGTGGTCAACACCATTCGCGCAATCAGGGTTGATATCACTATGATGAAATACCGGCAATGATGCTCGGTGCGGCAAGGATTAATCTTTTGGAAACCGGACGCTTCACTGACCA  
TTATTATGTTTGTGACGCGCTTGTACTTTTGGTGGCGAAACAGCGCGGATTAAGCGATGCTGCTGCCGCCAAAAGGCAAGGCGGCTTCTTGGTGGCGGAATTCGACGCGCGGTTTGG  
AACTTGGGTGCTGTTGATTTTACTGTTTCTGCTGTCGCGTATGCTTGGCGAGTATTGTTGGGCGGCAAGTTCGTGACGCTTGGAGTCACTCCCGCGCGCAATGGGTGTGCGAA  
CCGAACCCGCTTTCAGTCTGCGGACCCACGCGGAGTTATGAATGACGGCAAGTTAAGGAAGTGCCTGAGTATTGAGCTTATGCTTATGCTTCTCAGGACGACTGTGGGTGAAA  
ACGGCATTAACCCAGCGAGCGGATGACATTTGGAACCGTTCGACCGTTTTCGCGCGGAAATCGGTTTCAAGAGGCGTTATCAGTTGAATTTGCCCAAGGCGAGGACGCGGTATGAGCATTT  
GTCCGAGGATTCTATGATTTATGACATGATCAGCCGTTTTCGCGACCGCAGGTACATATGACACAGTACAGCGCAAGATTCTTCCGACATCCGTTTTCAGCATTAACACCCGTTTCGCG  
AAATTTATGCGCGCAAGCATTTGCGTGCATATGGGACTTTGGGCTGGTGGAGCGTGTGGCGAAGCTGCTGCTGCTTGCCTTGCCTGATTTTATCGGCATCAGCGGCTGCGGTATGTGTT  
GGAAACCGCGTCCGTCGCGCGGCGGCGCATTTGCTCCGCGCAAAATCAAACTCCCGCTTGGTGGCGGATGGCATTCCCGCTGCTGTTGATGTCATGCTGTTTCCCGGACCGCGCT  
GCTTGCATTTGCCGTGATTTGGCTGTGGATACCTTGTGCTGTCGCGGATTCCTGTGTTGAGGAAATGGTTTAAA





**SEQ ID 2993**

GTGCTTGGGCGCCTTAGGGAAACCGTTCCTTTTGAGCCGGGGCGGGGCAACCGGTACCGGTTTTTGTGTAATCCGCCATATTGTGTGTAACACCCGCCGGAACCCGATATAATCCGCCCTT  
CAACATCAGTGAAAATCTTTTTTTTAAACCGGTCAACCGATATAAGGAGCCGAAAA

**SEQ ID 2994**

VIGRLREPPFLSRGGATPYRFLIRHIVLKHRPEPDIIRPSTSVKIFFLTGQTDIRSRK

**SEQ ID 2995**

SEQ ID 2995

TTGAAAAAATTTTATAAAATATTTATCATATTGTTTAAATGATTTATATCATTAACCTGCCTTTGCCATATAAAATCTTCAGTCATGAGAGATATTTTCGGCCTGCCATGCATTTTTCAGAGTGCCTGTAATTTTCGATTTCTTGTTGTTGATAGGTAAATGTAATTTTTCACGCATACAGGAACATAGTTTCGCGATTCTGTTCCTCTATACAGGCTGTCCCCAAATATAGAGAGCTGCCAGACTCTTCATTACCAACCCCTCACTGATGTCTCTACCCGTATGTGGCTCAAGGATGAACACGCCGCAATTTTTCAGTCTGATGCGGATAGCTGAAAACCCGGGTAAACCGCAATATTTTCCATATTGCGCGTCAGCTTCCACATCCCGCGCTGGATTTTTCATGCCGCCCTTTTATCCATCTCTTGTTTGTGGACAGTTTTCGCGTGCAGTACCAAGCCAAATAGCTTTTCTCTATTTTCCTTTTTCGCGAAATCTGTCGGCAAGAACAGCGGCCTTTTGGGAATATAGGGCAAAACAGCAATATGCTCCCGCTCGCTGTGTCCAACCTGTGCAGCAACCATACCTTTTCTACGCCCACTGTGCGCCAAATGTTTCGCTCAGACTGACTTTCGCCCGCGGAACGGTGGACGGATATGCTTTGAGGTTTATGTGATGCGCACAAAATCTTGGTGTCTGAA

SEQ ID 2996

SEQ ID 2996

LKKFYKNYIHYIVLIDLYLLTCFCHIKFFQCMRDIFGLPCIFQRCGNFDFLLIIGKLYPSRIQEHSPGFCSSIQAVPKYRAAQTLHYHPQLMCLTRMMLKDBQPHFPTDADTEKPGNGNIFH  
IAROLPHAPGFFHAAFYSLPFGFRFAVGQSQIAFLHIFPGKLGKNSGTGKIGKQYASGLLVQPVQQPYLYFQAQLCRKCCRQTDFAAGTVGDYALRFIDGDKILVSE

SEQ ID 2997

SEQ ID 2997

CCCTTCCGCGAGCCTTGC CGTAAATGCC TTCAAGACATACGCGCTATGCGGCGGAGGCGTCTTTTGC CGCATATCCCCGCAACACTTCGAGGGCTCGACGGATCTTTTCAGGATTGAACGG  
GTTTTCGTCGCCAACCGTCCACATCGTAACCGCTGT TTG CAGCGAGAGTGCCTCAGCGCGCGGAAACG TCTTTGCCCAATTCGATCATCCGTGTGCCGTAAATAAACCATAGCGGCAATGT  
CGCCGCAAGCGCTTGC CGCTTATGGGCAGGCGGGTTGCGGCGCGGGCAACGGTTCGCGGTTCGGGACTTCGCCGGGCCAAACCCGTGTGCAGTGTCAATGCGTGGACGTAGGGCGACGGCTTC  
GGCGAGTTTGTGCGCGGGGATGCC TTCGACGGCTTCGACGTTGAAGCGTTCGTGTATCATCTGTACCGGAGGAGTAGCCCTATGCGTTTGCGCCCGACAAAGCGCGGCAACGCCCGCGGC  
AATCCGCTACGGTTCGTGCGCGGTGGTTTTCGGAGTAATTTGGTAGCCGCTGT TTTTCGCGATTTCGAGGGATAACCTCTTCAATATCCAGTCTTCGAATTTGACGGCTTCGGCTTCGGTG  
AACGGAAGATGACTCGGTAGAGATTTCGGCTCGTTGATGAAAAGTAATCTTCGGTTCGCTTTT TTTTGTTCGCAACCGTTCGAGATTTTGAATGCCCTGTGCTTTTAATGCAACTGACGGGCATT  
TTGAATTTGAAGAAATTTCCGCAACATCGCCAAAGCAAAACCAAGGTTTCAGCCCCAAGATTTTGAATTCGCAACATTTCGAGATTTCGAAAGAAAATACAGAAATGGTGTTCGATTTTAAAGC  
TCCACGAAAGTTTGAAGCCCTCTCTCTGACCAAGAGAGGTAGCGGACGTTTCAGGTTGGTTCGACTGCTCGTGGAAACAGCACATCCGGAGATGTCCCGAAAGTCCGCGCGTTCGCTTTT  
TCAGCAAGGGGTGATGTTTAAACATACAC

**SEQ ID 2998**

SEQ ID 2998  
PCRSLAVNAFTKCYAAGGVFVRISQPHFEGCDGSFQD\*TGFFVNRPHRNRLFAEELLQRRGNVFAQFDHPCAVINHSGNVGQSVAAATGGGLRRRQQRFAVGDFAGQTRVQCQCVDVDGDF  
GQFVGGDADGDFVRLVIHTVRGGVAYAPADPKRGNRPAQSGTVVGGGGSNLAACFADLRDLNLFKYPVLEFDGFGFA\*TEDDSVEIRLVDEK\*FLVAFFCCNAGFLNALVF\*WQLTGI  
LNLKNTFNIAKAKRPRSPQDLSTDLIRFERKYRNGVLHFKLHESLKASLRPRRGRTFQVGRLLVETAHPMSRKSARNLVQQGCMFNH

**SEQ ID 2999**

ATGCAAAAACGCAATTTTCCGGCAGCGCGTTACACCGATACCGAAAAATGCGTCTGAATGTTTCGACAAATCCGATTAAGACATTATGCAAAATCTGCAAAAAGTGGCGTAGAAGATAGCGTCTGCGCAATAGAGAGCGAGCAGCAGCACTATCAGCTTGCCTTCGCTTTTCAGGCTGTTTGGCAAGCTGCAACGCGCTCCAACCCCGCGCACCCGGAAGAAATGCCCGCCAAATGCTCTCTTTTCCGCCATTCGACGGGGCGTTTCAAAGCCGCTTCGCGCATTCTTGGCAATGCTGTCGTAGATTTTGGTATTCTCAAACCGTTCGGAATATAAACCTGCGCCGATACCTTGAATCGGTGCGGACCTTTTCGCGCGCGCTCAATACGCGGGGAAAGCTCAGCTTCGACGCGCAACTCTTAATTTGTTGTTATTTTTCCTTAACACTTTCGCGCCAGCCGGTAATCGTACCGCCCGTTCGCGACGCGCGCAACGAGACATCGACTTCACCGTCGGTATCGTTCCAAATTTCTCGCGGTTGTTTTCGCGTGACTTCGGGATTTGCCTCATGTCGAACTGCGCGCGCATAAATATAAGTGTCTGGAATGAGCGTCCACCAAGGATTCGCGTTTGGCAATCGCGCCCGCCATACCTTCGCGCGCGGGGGT

**SEQ ID 3000**

SEQ ID 3000  
 MKKRIFRHGVTPIPKNASECDFNPICALCQICKWRRKIAFAIRRQQHDYQLAFVFRILFGKLRAPNRRRTGRNARQNAFFFRHCTGGFKSRFVRHFGNAVVDFIGI QNGRNKTCADTLNRRV  
 TFFAAAYGGSLSPDGNLTILNIPVFFQHPAHAGNRTARADAGNEDIDTIVGIVPNFLGGCPAVDFIGICLIVELARHKISVMMVSHQGLRFGNRRARHTFGGGG

SEQ ID 3001

SEQ ID 3001

GTGCGGAAATGCGTTTGTGCATATATACCGAAACGCGGTGTGCTTTAATCAGGTGTTGGCGCCGCGCATTGCTTGAGGGAAATATTTTATTTCGGTTTATCCGGCAGGACGG  
ATTTTGCCCCAACGGAAATAGCCGGCTGCCCTAAAGTCAGCCGTTTGTCCGGGCGCAGCGGGGCTTTGGGCTTCAGACGGCATATTTTCGAATGCGCGCACATTTGCCGGCGGGCGC  
GGCAGCCATATGGGGAAGGGAGGGATATGTGGTCGGTAACGGAAAAAATATGCCGCACCATGCTGCTGCTGGGTTGCGCGGTGTTCCGATTGGGCAGCC

SEQ ID 3002

SEQ ID 3002  
VPEAFGLHIYKRRLCPNQVLAPPHCLREIFFIRVLSGRTDFAPTENSRPARKVSRLSGRSGRGLQTAYTRNGGTFAGGAAAIWGREGILWSVTEKNMPEHCNCWVARCSDMAA

**SEQ ID 3003**

SEQ ID 3003  
GTGTTTCGGGATTTGGGCAGCCTGATTGTCAGATCCGTCGCCCGTCGGCCCGTATGCAATGCATTTTGGCGGTGCTGATTTCGGTATTTGGTATTTTGGTCTTTTGGCACGGTTTTTCGGACAAA  
AATTCCTCCAAAAAACAGAAAAACCGTCGCGATATGCCCTGACGGCGGGCGTGTCTTCGCTTTTCGATTTTGGCACTTTTGGCAGCAAGCATACACGCGGTTCGGGCGGGTATTTCCACCGCTGCT  
CAACAGCCTGCAAATCTTTTCTGTCTGGCAATCGGTGTTTCTTTTCGCGCAGCGTTTGGCAGGCTCGAGGCGGCAAGCTTGATGTTCGGCGGTTTGTGGCGTGGCGGATGTTTCGGGCTTCGCGGT  
CGGGAATTCGGCTACACCGTAAATCGGTTTGGGGATTCCGACAGCGTTTGGTGTCTCGGGCTGATGCTTCGCCATATCTATGTGTGTCTGCTCGCAAGCATCTGAAGTGCAGACGTTGGGGCGC  
TTTTCCCTCAATGATGATTTTGAGTTTGGCGGGCGGGCATCGCGGATTTGTTCCGGCATTTGCTGATGGACGGCGGGCAGCTTTATCCGACCACTTGAAGAAGATTTCGGGTTTGTGCTTGT  
GTACGGGGCGTGG

SEQ ID 3004

SEQ ID 3004  
VFGGLSLIVRSVFGPYAIAFWRLILSVLVFWFLARFPGQKFPKPKRTVRYALTAGVFLAFDLALMHESIHAVGPGISTLLNSIQIFFLSAIGVFFFGERLGRLOAASLMSAVVGVAITAG  
AEEFYGNVAWVGFASGLVSGMLALSMVFFVRKTHEVEQVALFPSMILSLGGASPIVPAIIIDGGALYPPTWKDSGLVLVNYGAM

SEQ ID 3005

SEQ ID 3005  
GTGGTAGTCAGTGTTTTGGCTGGGCGATGGTTGCCATATGCGATTCCGCTGCTTCCCTGTGCGTGACGGGGCTGTGTCTTTGTCCGAACCGGTGCGGGCCCTGTTCATCGATTATTTCG  
GATTGGGCAAAACGATTGAAGCCGTCGACGTGGGCAGGGGTGGTCTGACGCTTTCGGCGATTATCACTCGGTTGCGTGAACAGCCGTCGCGAGCTT

SEQ ID 3006

SEQ ID 3006  
VVMOCFANANVAYAIPLLSLSLTGLLLLSEPVAAFLIDYFGLGKTIEGVQAGVVLTLSAIYLGSLKQPSL

SEQ ID 3007

SEQ ID 3007  
TTGGACTGGCAGGCAGTCAAAACCGGCAAGACCAAAACATGCCGACACCGCGCGGAGCGGAAAAATCCCGTCTGAAGCCCTTTTCAGACGGCATCGGGCGGGCAGAAATCAAAAAGCCGCT  
CCGCAGGAATGGCAATGCAACTAAAA

SEQ ID 3008

SEQ ID 3008  
LDMOAVKTKTKHADNGAERKMPSEALSDGIGAGRIKKAASAGNAMOLK

## SEQ ID 3009

GTGGCGGCATATGGAAATACGGACATTTATTTAGTTGCATTGCCATTCTCGCGAGGCGGCTTTTGTGATTCGCCCGCCCGATGCCGCTGAAAGGGCTTCAGACGGCATTTTCCGCT  
CCGCGCGCTTGTGCGCATGTTTGTCTTTCGGCTTTGACTGCTGCCAGTCCAAATCGTACGAGGTTGCCACGGCAGAAAATCTGATGCCGACCGGAGTCAAAGCTCGGACGGCTGTTT  
CAGCGAACCGAGG

## SEQ ID 3010

VGGIKYGHYFSCIAIPABAAFLILPAPHPERASDGIPIRSAPLSACLVLPLVLAQSNRTQVCHGRKSDADRSQSSDGCSEPR

## SEQ ID 3011

ATGTCCTGATTTCCATATGCCGCCACACCGTCAGTCGGACGAAATGCCCTTTATCAATGGGATGGGTTTCCACACAAACGGAAATAACCGGCTTTTCACTTGCOCGAGGATAAAATCAA  
CCGATGATTTAAACACAGGCAAAATCATACGCCGCCGACGACATCAATTTTCCAGGCAATCCATATGTGCCGCCATATCGATAATGCCGCAAGCGGTGCATATAGTGGAT

## SEQ ID 3012

MSVFPYAAHTVSRITKCPILFNGMGFHTNGNRLPTCRRIKSTDILATGKSYAARTHPRSQISCAAHIDNAGKAVHIVD

## SEQ ID 3013

TTGAATTTAATCCACTATATGACCCGCTTGCCGGCATTCATCGATATGGCGGCACATATGGATTCCTGAAAAAATGATCGCTTCGGCGCGCGTA

## SEQ ID 3014

INLIHYMRLAGIDMGGTYGLPGKMMRSGV

## SEQ ID 3015

TTGTCGGATGCAGAAATCCGGATTTCATATCGAATCCGGATTTTTTATTTTGAACGGAATCTGTTTTGATTATGCGCTGAAAGTGGGGATTTTGATGCTTAAGCAGTCAGACCGAC  
TGATATTTTGTATGTTTAAAGAAATGTCAGTTGGGTGTCGGACAGCATGTTTGATGCTTTTACAGCGCATATAGTTTGTTCCTTCAAAAT

## SEQ ID 3016

LSDAEIRIHIESGFFILNGNPFVFLCRLKVGILMLKQSDRLIFLYGLKNGAVGCRITALFDFARRHIGLFLQH

## SEQ ID 3017

ATGAACAAATGCTAATGTGCGGGCGCGCTGCGCGCTGCTTGCCTGCATCTCTTTATTTCAAAGCGACAAGAAACGGCAGGAAACCGTGAATGGAGTTCCGGCTCGAATACGCT  
ATATCTCTGACGGCGCTCGGTGTGTTTCCGCTTTGTCCTGTTTATGAGCTTTACCGCGCTTTCTGATTTTCTGTTGTAATGTGCGGTACGGCTTGGGGGTATATAAATACCGCTGAA  
GACTCATCCGGAATCTCGGAAAGCAGCCACTTCGCGGATTTATTCGGCAGTTTCTCCCTACCGTTTGTGATTTGTTCTCATCCGCTCGTTTATGCGAACCCTTCCAATACCGCTCC  
AGCTCGATGCGCGCGGATTAATCAAGGGCGATTTCATTTTGTGCGCAAAATTTTCTACGGCTGCGCGTACCGCTTTTAAACAATGATTTATCTCCACGGGCAAAATCGAACGGGGG  
ATGTCGTGTTTAACTATCTTTGAGCGCGGAGATGACCTACATCAAGCTATTGTGCGCATCCCGGCGGACATGTGCGAATATCGAGATAAAGTTTTCAGCGTAAACGGAACCGGC  
TTCCGACATTCCTGAGGACATACCGTTTATCTGACGATACCGACCATCCGAAATCCACAAACCGGATATGTTCCGAGCGGTCTGGACGGCAAAATCTTCAATATCTGAAAAAAGAA  
GGACAGCTGCGGTTTCCCTGCGGATTTGCGCAAAATATACCTCGGATTTATGCTGCAAAACGGATATTCATAGATCAAAGCGGTCTGAACCTTGGCAATATGCGGACGAGCGGAGCG  
GTTTCGTGTCGAAAGTTCCGGAAGGACGCTATTTCGTATGCGCGACACCGGACAAAGTGGCGATTGCGCTACTGGGGCTTTGTGATGACAGCTGTTTGTGCGCAAGGCAATGTT  
CATTTGATGAATTCGCGGATTTCGCGAGGCGGCGACGCAATCCGT

## SEQ ID 3018

MNTHMSGAAALLAGIILYFKSKRQENGWSSGLEAYIILAVGVFAALSIFMSFVAVFLIFVVLCTANGVYKYLKTHPISESSHFDGYGSPFFTVLVLFLIRSFIAEPFQIPS  
SSMRPLIKGDFILVUGKFSYGLRVPLNVPFIPTGKIERGDDVVVFNYPLOPENTYIKRIVGIPGDI VEYRDKVLFTVNGKPSADIIDGTIYRYPDDTDSRIHNTDMPRSGLDGKSPNLAKE  
GQPAVSLPVLGKYTSDILMSNGYSIDQSGIAHCQYADDGSGFVCKVPEGRITFAMGDNDRNSADRYWGFVDDKLVVGKAMPILNFGDPGRAGTAIR

## SEQ ID 3019

ATGAAAAATATCCGAAATTTCTCCATCATCGCCCATCGACACCGCAAATCGACGCTTGCCGACCGCTTCAATCCATATTCGCGCGGTTTGGATTTCGCGCAATGAGTACGCGAGTGC  
TCGATTCATGAGCATCGAAAGAGCGCGCATCACCATCAAGCGCAAACCGCGCAGCTCAACTACAAAGCAGCGGACGGGAGGTGATCAGCTTAATTTGATTGACACCGCGGACA  
CGTCGACTTCTTACGAAGTTTCCGCTGCTGCTGCTGCGGTTGCGAAGCGCGCTTTTGTGCTGACGCGCTGCGAGGCGTGGAAAGCGGAAATCGAAGACATCATCGGCATCGATGCGCTGCGGCGGTGAGTGT  
TTGGCGGTGGAAGTCTGTCGCGTTTGAACAAATCGACCTGCGCGCGCGGAGCGGTGGAAGCAGGCTGGAAGCAGGAAATCGAAGACATCATCGGCATCGATGCGCTGCGGCGGTGAGTGT  
TAGCCAAAGCGGATCGCGCTGGAAGACGTTTGAAGAAATCGTTGCCAAATCCCTGCGCGGACCGCGGATGAAACCGCGCGCTGCAAGCGTTATCGTCTGATTCGTGTTTGAACAA  
CTACGTCGCGGTGCTCATGCTGATTCGAGTGAAAAACGGCACCATCAAACTGAAGACAAAGTCCGCTTATGAGCACCAAGCGGAAACCGAGTTCGAACAGCTGGCGTATTCACACCG  
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AGCGCTGCGCGGTTTCAAGAAAGTACAAAGCCAAATTTGCGGCTCTTATCTGTTGAAAGCCACGATTACGAAGCCCTTGCAGCGCTTTGGAAGAAATTCGAGCTGAACAGTCTTC  
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ATTACCCAGCGCGGAGCGGTGTTTACGAAGTCTGTTGAAAGCGGCGGCAAAAAATCGAAGTTGAAACCGCTTGAAGACCGGAGTTCGACATGGATTG  
TTACCGCGACCATCTTGTGCGCGGAGGAATACGTCGCGCAACGTCATGACTTTGTGTAAACAAAGCGCGGCTGCAAGTCAATATGAGTATATGCGCGGCAAGTATGCTGACTTACGA  
CTTGGCGATGAACAGAGTCTGAATGGACTTTTTCGACAACTCAATCCACTTCGCGCGGTATGCTTCTGTTGACTACCATTTCAAGAAATTCGAAGCTGATTTGATTAGCTGCGAC  
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ACATCGCGTCAAGCGCGCATCGGACGCGGATTTATCGCCCGAGAAACGTTAAAGCCCTGCGTAAAGCTTTTGGCGAAATGTTACGCGCGGATATACGCGTAAGAAAAACTGCT  
TGAAAAACAAAGCAGGCAAAACCGGATGAAACAAAGTGGCAAGCTGGAATTCGCAAGCGCGTCTTTCGCGATTTCGAGGTGAGCGACAAA

## SEQ ID 3020

MKNIRNFSIIAHIDHGKSTLADRFIYQYCGGLDLREHSTQVLDSDIEKERTITKAQTAALNYKARDQVYQLNLIDTPGHVDFSYEVSRSLSACEGALLVVDASQGEAQIVANCYTAID  
LGVEVVPVLAKLIDLPADPERVEQIEDIIGIDAVGAVQCSAKSGIGVEDVLEIVAKIPAPTGDNAPLQAVIVDSWFDNYVGVVMLIRVNGTILKLDKVRPMSTKAETQVEQLGVPTF  
KSVQKQELKAGEVGLITGVKELGQAKVGDVTVLVANPATEPLPGFQEVQSVFAGLYPVESHDEYALRDALDKLQNDASLKFPEPSQALGFGPRCGFLGLHLEITVQERLEREPDML  
ITTAFTVYVYEVVLSKEKIEVENPSKLPDIGSIETILEPIITATILVPEYVGNVMTLNCQKRGVQVMQYMGROVHLTYDLPNNEVMDPFDLKTSTSRGYASLDYHFKFPQPSDLIKLD  
IMVNGEKVDLSLIVHRQSAVHKRELASKMRELI PRQMFDAIQAAGISRIIARENKALRKNVLAACVYGGDIITRKKLLEKQKAGKRRMKQVGNVEIPQSAFLAILQVSK

## SEQ ID 3021

GTGCTGCTGAAACCGTTTCAGACGGCAGGACAAACCGCTCCACTCAATCTGCGGTGTAGCGGTATTAATTCGCGCTTCTATCCGAAATTCACAGCAGGTAGCAATATGCTTTGA  
AAACAGTAGCGTTATTCGCGCGGATGGAACAGGAAATCGAGCTTTTCCGCGAGATGATGAAATATGCAAGCGCTCTCTTTCGCGAGATTTTCCGCTATGAAGCGAATTTGCGCGGAAA  
ACGCATAGTCTGCTGATGAGCGCATCGGCAAGGTCAACGCGCGGTTGCAACGCGCTTGGCTTATTCGCTCAATTCGCAACCGGACTGCGTCATCAACCGGACGCGAGCGGTTTGGC  
AAGGCTTTGAAGTTCGCGCAGCTGGTATCGGCACGGAACCGGACACCGAGTGTGATGTAACCGCATTCGCGTATGCCCGGGGGCAAGTGGCGCACTGCCGCAAGGTTCCGTTCAAG  
ACGGCATATGATTGAAACCGGCAAAACCGCGCGCGGACGTTTGAAGCGCGGAGGTAGAACAAGGCTGATTTGTCAGCGCGGACCGCTTCGTCACAGCAGGAAAGCGGTGGCGGAAAT  
CCGCAAGCACTTCCCGAAGTCAAGCAGCTGGAATGGAAGCGCGCGGATTCGCAACCTGTCATCATGTTGGAACCGCGCTTCGTCATCATCGCGCTGTTTCCGATTTCGCGCGGAGAA  
AAGGCAAGCATCAGCTTTGAAGAGTTTGAACCGCGCGCGGCAAGTTCTGCAAAAAATGGTGGCAGAAATCGTCAAACTCTTTA

## SEQ ID 3022

VLSFTVSDGTDKPPPLNPAVLACIIIRRSIRNSQVSNMSLKTVAIVGAMEQRIELIREMMENVKAVSPGRFSAYEGELAGKRIVLALSGIGKVNAAVATAMLIHQFAPDCVINTGSAGGLG  
KGLKVDVIGTETEHDDVDTAFGYARGQVPLPARFASDGIILETKRAARTFEGAEVQGLIVSGDRFVHSSBGAIEIRKHFPEVKAIVEMEAALAQTHOLEPFPVIRAVSDADE  
KADISFEFLKTAASSAKMVAETVKSIL

## SEQ ID 3023

GTGAGGCGGTTTGTCCGTCGCTGAAACGGTTTCAGACAGCAGCGCGGATTTTGGTAGAATGGGAAGGTACAGATGTTTGAAGATTGGGGACGAGGATGTTTACCGATGAAATA  
TGACTGCAAGGAAGAACTGTTCCGATGGCTGCGCCATATGAACAAAAAAGAGTTCGACCTGTTTGTGACGACCCATTTCCCGCCGCTATGAAGCTGGAGCGGAAATACCCCGCAT  
CACGGACGAACCGCTGACGGCGGAAAAATGTATGGAAATCGCCTTTTCCGATATGAGTGGGAAGCAGGCGGAAGAAATTTTCATGACCAACGAGTCAACTTCGCCATCAGCCTGCCGGAC  
ACCAGCGCTTCCGCGTCAATGCGATGATACAGCGCGGTGCGACGGCTTGGTATTCGCGCGATACACGCAAGATTCCTCAAGTTTGAAGCTGAACTGCCGCCGCGCTTGAAGGATG  
TTGCGCTGAAAAACCGCGGCTGGTTATTTTGTGCGCGCACCGGCTCGGCAAAATCGACTTCGCTCGCCTCGCTTATCGACTACCGCAATGAAATTCGTTCCGACACATCATCACCAT  
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GTGATCTTATCGCGGAAATCCGCGACCGTGAAACAAATGGACTACGCCATCGCCTTTGCGCAACCGGGGCTTGTGTATGCGGACGCTGCACGCCAACAGCAACCAATCAGCGCGCTCGAAC  
GCATCATCAACTTCTTCCCGAGGAGCGCGGCAACAAATGTCTGACGGATTTGCGCTCAACCTTCAGCGCTTATTTGCGCAACCGCTCGTTCGCGGAGCGCGGCAAGGCGCGGTGCG  
GGCAGTCGAGGTGCTGCTCAATTCGCGCTGATTTGCGAGTTGATTCACACGCGCAACATCCATCAAAAGAGTGTATGAAATAATCCACTACCTGGGTATGACAGCTTCGACCA  
CACCTTTACCAATTTATGAAAAAGCGAGATTTCTTGCAGGATGCTTGAATAATGCGGATTCGCGACATGATTTGCGTTTGGCGGTACAGTTGCGCAGCGCGGCGCAAAAGTTCCG  
ACCCGATTTGGAACCTGCTC

## SEQ ID 3024

VEAVCPRLKRFQTRRIFGRMGRYLPEDWGTMTDENMTAKEELFAWLRHMMNKGSDLVTHFPFAMKLDGKITRTDEPLIAEKCMELAFSMAKQAEFFSTNECNFAISLFD  
TSRFRVNAIMQRGATLVRATTSKIPKFESLNLPALKIDVALKRGVLIVFGGTGSGKSTSLASLIDYRNENSPGHITIEDPIEFVHEKNCIITQREVGVDTENMMAALKHNLRLQAPD  
VILIGEIRDRETMIDYALFAETGHLCMATLHANSTNQALDRIINFPPEERREQLITDLSLNLQAFISQRLVPRDGGKGRVAEVLNLSPLISELHNGNIHEKVMKSTTIGMTFDQ  
HLYQLYERKEISLQDALKNADSHDLRLAVQLRSRAQSSDPLELL

## SEQ ID 3025

ATGATTTATCCGTGGCATCAGGAACAATGCGCGCAGATTGCCGAGCAITGGACGAGCGCTCTAATGCGTGGCTGTTTGTGGCAAAAAGGGGACGGGAAGACTGCGTTTCCCGCTTGT  
CGGCAAGGCGCTGTTGTGCAAAAACCTGCGACCGGCTGCAAAACCTGTGGCGGAATGTATGCTTGCATCTGTTTGGACGGGAAGCCATCCCGATTTTACGAAATCAGCGCTTGGC  
GGACGAACCCGAAACCGGACGCAAACTGTTGCGGATCAAAATCGATGCGCTCAGGGAATCATCGAATATGTGTACTGACTTCGGTACGGGGCGGTTTGGCGGTGATCTGATTCATCT  
GCGGAAGTATGATGTCCAAAGCGCCCAACAGTTTGTGAAAGTGTGGAAGAGCGCGCCCAAGTGGTCTTTTGTCTGGTAAAGCCACGCGCGGCAAGGTTTACCGACCATTA  
GCCGCTGCCGAAGATGGTTTGGCGCTCTTCCGATGCGGAAGCATTTGCCGTATCTGCGCGACAGGGGTGTGGCGAGCTGAGGAACGCTTGGCTTTCATTCGGGTGCGCGCTGTT  
TCAGGAGGAAGCGGAGCTTCCGGAATTTGAGGCAAGCTGCTGGAGATATTGGCAGAGCGGAGATTTGGAAGATTTGGAATTTACGCGCGCTTTCGATAGGAAAACTTCCGCTCGC  
GTATTTGTGCGGTGGATGACGAAATGGCTGGTCAATTTAGGCTTGTGCTGCAACACATGAAACCGCTTATTTATCCCGCTTATGAAGACAGGCTGCTTCAGACGGCATCGGTTTCCGCT  
CGCGCAATGATTTTGGCGGAGGATATGCTCAACACAGCTTGCCTTACGGGTTCATACCTTTAATGTCAAAATGCGATCGAGCATCTGCTCATCAACTATTTGGAATGAAGAAGA  
GAACAGG

## SEQ ID 3026

MIYPWHQBWQRQIAEHWTSRPNALFVGKGTGKTAFARFAAKALLCETPAPGCKPCGCMCHLFGSGHPDFYEITPLADEPENGKILLRIKIDAVREIIDNVYLTSVRGGRLVILIH  
AESMNVAANSLIKVLEPPPVVFLVSHADKVLPTIKSRCKMVLPAHSGEALAYLRDRGVAEPEERLAFHSGAPLFQEBGELREIRAKLLEILAEPRILLKILDYAALFDKELPLA  
VFVGMQKWLVDLGLCLQHMFPVYYPAYEDRLLTASGFRPRNVFAEDMLQLAPYGFHTLVNMQIEHLLINYLELKKENR

## SEQ ID 3027

ATGTCAGACGGACAAAATATTCGGCAAAAATGATGTCGTTGACGCTGAAAGACATGAATCTGCTGTACAGCTCTATATGCGGTTTGTGGAACACGGCGGTGTTTGTGACAGCCGAG  
ACGTATTTTCATCGGGGACGATATTTCTGCTTCCGTAGAAATCTCAACTGCCCAAACTGTTCTCGCGACCAAGGTGCGCTGGATTAATCTCGGAGTACTTCTCTCAAAACCAAGG  
GGTGGCGCTGCGCATCAAAAACGAAACTGCTGAAAGTCAAGACCGAGATCGAAGTCAAGTGGCGAGCACAATCAGCGCGAGCAGACTAGCTTTACCATG

## SEQ ID 3028

MSDQNTIPAKMMSLQKMDNLLYSYMPFLEHGLFVQTDVFSIGDILLAVEILNFPKLFPTKVAWINPASTSSPKGVGLAFTKHENCLKVKDQIEVELGSTISGSRPTFTM

## SEQ ID 3029

TTGTTTCCGCGCAAGCAAGGCTAAGGCGAGTCAGGACGAAATCCCGCAATGTATTAACACAGACGCGTAGAAATGCCGCTGCTTTATCCATCTCAAAATGAATATCATCTAGCCG  
TATCAAGGCTGTATAAA

## SEQ ID 3030

LFRAKQGLRQSGSKSRNVLKQTRNAGCLYPSSKLNITLAVSRLYK

## SEQ ID 3031

AATCTTCTGTTTGCGCCACATGGGCAATCAAACTGTTTCCCGCTGATGACCACTTCGATAAATGCGTTTCGGATACAGGCCATCCCAAAACAGCAACCGCAAAACCGCCAGAATCGCA  
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AAAGAAGGATGAATACTCTCCCGCTCTTACTTATTTCCAA

## SEQ ID 3032

NLALRHMGNQIVCRILMHFDKCVRIQAHQNSNRQNRQNRKLAADIVFHPGNVIRVNRAENHALVHPQIRRAVNRQHSRQRAHPEIHPDRAHNHKLAEHAGSRRQAGVRHTBQHHKRRK  
LGHHDIAAVIGNIARVQAVVHADAHKRRRHEAVRNHINDRAFQRPVQVLPVKNQKHPKRYKTHMADGRIRHQPLHILGHQHGHFDINDYNGQAYDDYGGKIASRVHRNQDAQESTIR  
TQFQRNCRQHRTAGRRFVNGIRQPSVYGEHRFPYK\*QEERYKQLLYAQRLFDVLEIDNREAACTLIQVNHNGHQBERTQRRIEBQLDRDIDAARAAPPTDQVQRNQHTLEHILQN  
RILRGRAVNTQTRHQEQRHILRRITFLNDFTPGQYHQQRNKRIQDDKEH\*NTVHAQCVDVDFQKRNPLVELGKLIAAAQTVETGQQRVQSTGKRSHEGKHTBQRRTAVFTGRNQHACGD  
GYPYCQAE\*VVGRKSG\*PVVKIKNVVWGLYRQRFRKSSERRNEYSPPFFTTYSQ

## SEQ ID 3033

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CGAATCTGACCGATAGCGATTGGTTGTGGGGCGCGGATCCCGATAAAATCCACGAGACCATCGAAAAAGCGCGTGTGGGACTATGCTTGCCTGGGGTCTGCTTTGGGGCGAAGAGCGGT  
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ACCGGACCATCTGCTCTCGAGAAGCAGCACAAGCCGCTTCTGAAGCCAAACCTGCGCAGCAGAACCTTAAAGCCGAGGAAAAAGCCGCACTGCCGCCAAAGCGGATGGCAAAACAGGTT  
TATGAAACCGTTTGTGCGCGCTGCCATGGCAATGCCAATCCAGGTATTCCTCATGTAGGCACCAAGCCGACTGGGCGGACCGCATCAAAAAAGGTAAGGACACGTTGCACAAACACCGCA  
TCGAAGGTTTAAATACGATGCCCGCAAAAGGAGGTGCGCGGATTTGACGATGATGAGGTCAAAGCTGCGGTGACTATATGTTCAACGACTGAGCGGTAAAGTCT

## SEQ ID 3034

MNATSQPTSNFWNIYIAIVLISFIALANLILLSQNVKRPKKEEVQTTGHEWDGIAEYDNFLPRWFWNLVLTWLPFGIYLVNYPGVGDYKGLLWTSNHYQYKEVKKADEQYKLYAKP  
ADMPIEKVAKDPAQKQIAQNLNFTYCIQCHGSDAKSGKFPNLTDSMLWGGDPDKIHETIEKGRVATMPAHGPALEGBGVKDVAVHYVMSLSKPKQYDEBRAARGQALFSGPPANCFTCH  
GDKGQGIQGLGNLTDDVNLWGGTQKSIIEITNGRSSQMPAWGHFLDKDLHINTAVYVNLNKGDKAPVKKABPAPAEAPAPAPAEAAQAAEAPKAEKAAAPAAKADGKQV  
YETVCAACHGNALPGIPHVGTAKADWDRKKGKDTLHKHAIIEGFNTMPKGGGDLSDIEVKAADVYVNVQSGKFP

## SEQ ID 3035

ATGCATATCATGATTTCGCACTGCCACCTCAATTTTGAAGGTTTGAAGAAGCGCTGCCGGAAGTTTGTCCAACATGGAAGCAAGCGGCTGGGCGAGGCACTGCCATCAGCGTCAGTA  
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CGCGCGCCATCCGAAAGTGGTCGCGATCGCGGAGAGCGGTTTGGATTATTACTGGTCAAGGCGGATTTGTCTTGGCAGCACAAACGCTTTCGAGACCATCGAAGCAGCAATCAAAC  
GGACTGCCGTTATCTGCATACGCGCGATGCGCGCGGACACCTTGGCGAATTTAAAGAAATGTAAGAACCAATTCGGGTGTGATTCACTGTTTTTCCGAGGATGTCGGTTTTGCGCGG  
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GCGTTCCTTGGCGCGCTTCCCAAACGAGGAGGAGGAGCAAGCAACCGGCTTTTGTGCGTCACTACTGCCGAACATATTGCCAAATGCGGAATCAACATTTGGAACAGGTTGCGGCATATACG  
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## SEQ ID 3036

MHIIDSHCHLAFEGIKERLEPEVLSNMEANVSQALAIYSRESFSEVPAVAEAEHIEYCTIVHPSKEAEFPIAEHVEAAHPKVVGIGETGLDYVWCKGDLSSQHKRFADHIEANQT  
GLPVIVHTRDAADDTAILKECKTHSGVIEHCFSEDVGFARAAMDGLYISFSGIYVFNAPLVQEAARYVFDRIIVETDAPFLAPVPRGRQNEPAPVRHTAEHIAKLENTLEQVAAAT  
TENFYRLPKRVDERVV

## SEQ ID 3037

GTGCCGACGATAAGGAAACCATGAAGGCAATTCATCCGTATGCATGTCGCGCTGCTGCCGGCTGCCCTGCCAACACGTTTCGGACAGGATGGCAAAATTCGCTTCCAAATCTGCATTG  
CCAAAGCGCGGAGAGCGGGAAGTAAAAAGACGAAAGCGCGCGGATATGCGCTGTGCCAATTTGCCGACAGCAGGATTTGTCGAGGAGTGGGAATATTGCCGTTCCGAACAT

## SEQ ID 3038

VPTIRKTKAHPYACPRCCRLPANTFTRTGANSASKFCIAKGGREVKKDESGGYALCHLPDSRIVEEWEYCRSQH

## SEQ ID 3039

ATGCGTTCCATCCACGACCAAAATTAAGAAAGTAGTAACGACACACCGCGCTGTTATGTTTATGAAAGGTACGAAGCAGTTTCCGCAATCGCGTTTCTCTTCCCGCGCGTGCAAATCTCTGA  
ACGCGGAGCGTGCACCGATTACGTTGCTGTCAACGTATTGAAATATCCGGAAGTACGCCAAGGCAATTAAGGAATACAGCGACTGGCGGACCATCCCCAACCTTTATGTGAACGCGGAGTT  
TGTGCGCGGTTCGACATCTCTGATGGAATGTATGAGGAGCGGAGCTGCAAGAGCTGCTGAAGGC

## SEQ ID 3040

MASIHQIKIEVVTTHRVVLFMKGTQFPQCGSSRAVQILNAGCTDYVAVNVLENPEVRQGIKEYSDWPTIPQLYVNGEFGGSDILMZYBAGELQELLEKA

## SEQ ID 3041

TGCGGAATCCATCAGGCTTTTCAGCAGCTCTTGCACTCGCTGCTCATACATTTCCATCAGGATGTCGCAACCGCGGACAACTCGCGTTACATAAAGTTGGGGGATGGTCGGCCAG  
TCGCTGTATCTCTTAAGCTTGGCGTACTTGGGATTTTCAATACGTTGACAGCAGCAAGTAACTCGGTGCGCGCTGCCCGCTTCCAGGATTTGCACGCGCGGGAAGAGAAACCGCATTCGG  
GAACTGCTTCTGACCTTTTCATAAACAATACGACCGGCTGTGCTGTACTACTTCTTAAATTTGGTCTGGATGGAAGCCATCGCTTATCTCTTTGATAAAGTTGACAAATTTGTTCAGG

## SEQ ID 3042

LPNPSGQQLQLACLHHPQDVRTADKLAVHIKLDGRPVAVFLNALAYFGIFQYVDSNVI GAACRVQDLHGAGRETALRKLITPHKQYDAVCRIYFFNLVVDGSHRLFLLIKLTAFVR

## SEQ ID 3043

ATGGATTCCGCAATCGCGTCTGACAGCTGTTTCAGACGCAATTTCTTTCCGCGCAATTAAGAAAGTATAATGACGCGTCTCAAAATCACAACGCGGATGAACGT

## SEQ ID 3044

MDSAMPSEKVSIDGIFFGSKLKKSIMTRLIKITLEHRDER

## SEQ ID 3045

ATGAATATAATCGGCGGACATCTCAAAGACACCATAGACGCAACATTGCTAAACAAACGGAAGTATCCATTACATTAATTAAGAAATATGATGATGATTAAACAGTTTAGAT  
TGTGGATAAAGGGAACAGAAATCAGAAAGTCTATATCGCATGGAGGCAACAGGCACTATTACGAAAGGCGAGCAGATATGCTTTCTCTACTATACCGTTTACGTTTCAATCCCTT  
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## SEQ ID 3046

MNIIGPDISDPTIDATLHKTNHSIHYIKPKNNDGLKQFRLWIKGNIRKRVYIGMEATGIYKERAADLSSYTYVYINPLKIKDYKSRFNRTKDKADSNLIADYIKRHQDLPYQIP  
KNKALQKLNKLNQLOQQQKQIKNRIHSTEDFIRNIHQDLIDTIQDKMEQVKIAISEQIKKQTDNNHYNLQTPISIGKDTASVLYAQLTKEHFTANQPVSYAGLSPALIQSGTSVRGR  
GRLSRYGNRLKSTLYNPAFCAYRFNAPFLINLKKAGKPKMVIIVAMRKLAKPAYIIVTKTQPYDAERHRLNQ

## SEQ ID 3047

TTCCCAATCAATATCTGTACGATTGCGATATCTGCCGTACTAAACATCTAATTCAGCCAAATCTTTTATTCTGACTGCATAGCTAGTAAAGCTCTTAACTTCACTTAAATCAATA  
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AGCCCAAGATTGACTTTTATAAATCTCTGCTGGAATTTTAGTCAAAATATTGCTTCAATTTGCTATTAAACGCAATGAGTCAAAATTTGAAGAACCGATTAAAGCATTAATATCA  
TTCTTATCATCTTCCAAATACAGCTTTAGATGAAACCCGTAATGCGCTTACGATCACTGTAATTTCAATGGGAGCGGAGCCATTTCAACATTTCCGAATAGCCTCTTTT  
TAGACATCCGAAATCTTGTCCAAATAAATTTAAACTCTTGCAA

## SEQ ID 3048

FPINICTIATPCLY\*NI\*FSQIFYP\*LHS\*\*SS\*LHT\*INIPGAFACSPCRKFIFF\*KFFNGSI\*NRISINIFLTKHFRKN\*TTSGNPTFF\*PINLGNHIIISLSKWSIKN\*LDGNA\*PS  
KI\*RLTRPFPFRILKTIAYPFSIFAFPRP\*FIKPIKIIVVYFSCCTLLNKIP\*LIHSLMVSHLLSPCRNQFLIIIMHLHK\*LIH\*LSNS\*FLIVNFSFLILKPIFRYRDRPHRNF  
SPRFDYKILLGNFSQNICPIIAIKRMSQI\*RTD\*SIIFILILPKYSPRMTLNALSYHQCEQ\*GRKPFQHFNSLFFRQSEILSKNFKLLQ

## SEQ ID 3049

ATGAACGTTAACGTTATCAACCATCCGCTCGTCCGCCACAACTGACCCCTGATGAGGGAGGCGGATTGCGAGCACTACAAATCCGTCAGCTGACCACCGAGTTGGCGCGCTGATGGCAT  
ACGAGGCAAGCCGCTGATTGTAATGAAAAATACCTTATCGACGGATGCTGCGGACAGATTGAAGCGGACCGCATCAAGGCAAAACCCCTGACCGCTGCTCCCATCTGCGCGCGGCTT  
GGGTATGCTCGACGCGCTGCTCGACCTGATTCGCACTGCCAAATCAGCGTGGTGGTTGCGAGCGGAGGAAACGCTGAAGCCTATTTCCTATTGAGAAATTTGCGACAGTATG  
GACGAGCGTCCGCTTTGATTATCGATCCTATGCTGGCGACAGCGGTTGATGGTGGCCACCATCGACCTGTGAAAGAAAAAGGTTGCCGCAACATCAAGCCTTAGCTCTGGTTGCCG  
CCCCGAGGGCGTGAAGGCTGTTAATGATGCGCATCCCGATGTTACGATTTATACCGCGCGCTGGATAGCCGTTTGAAAGAAAAAGGCTATATTATCCCGCTGCGCGGATCGCGCGA  
CAAGATTTTCGCGACCGC

## SEQ ID 3050

MNVNINHPILVRKILTLREADCSTYKFTLTTELARLMAYEASRDFEIEKYLIDWCGQIEGDRIKGTLLVVPILRAGLGHLDGLDLIPTAKISVVLQRDEETLKPISYFEKFDVSM  
DERPALIIDMPLTGGSNVATIDILKEKGCRLKALVLVAAPBGVKA VNDHPDVTIYTAALDSRLNENGYIIPGLDAGDKIPGTR

## SEQ ID 3051

ATGAATTTCCAAGACTATCTCGCCACATTTCTTCAATCGACCATCTGGCGGTTTGGATGTTGAGGATGCCGAAGGCAAAACGTTTACCACATTTCCCGCGCTTACGGGCAAGCTCGGTT  
CGCTCAAGCTGTACAATGCCCTTGGCGGAACGTTTGTATGAAATTTGGTAAAGAGCGGCAAGACAGGTTTGTATGTTTGGCGAACAATGTTGCCGACGCGCGGCCATCCGGGGA  
GCATCCGAACATCGATTTGCTGGAATATGCTGCAAGCGGCGAAACCCCTCTGCTCAACCCCTTGGCGCGCAA

## SEQ ID 3052

MNPDYLAFTPSIDHLGGLVDQAEKTVHPIPAVQKGLSLKLYNALAERFDKGLKEABQGLWPAEHVADARAHGPKHPNIDLLNVQSGETLLKPLAAQ

## SEQ ID 3053

ATGCCGCTGAAACGAATTTAGACGGCATGCTCGAAATTTATGCGCGGCAACGCGTTGAGCAGGAGGTTTCCGCGCTTGCACGACATTTCCAGCAAAATCGATGTTCCGATGCTT  
CCCGGATGGCGCGCGCTGCGCAACATGTTCCGCAACCATATCAAAACCTGTTCTGCGCTTCTTACCCTAATTTCCATCAAAAGCTTCCGCAAGGCAATGTACAGCTTACGCGAAC  
CGAGCTTGCCTGAAACGCGGGAATGTGGTGAACCGTTTGCCTTCCGCAATCTGAACATCAAAACCGCCAGATGTTGAT

## SEQ ID 3054

MPSETNFRHGRKLLRGKRFEGFAALHDIQQIDVRMLPRMGARVGMFGKPYQTLRCRFFTPQFSIKTRQGIQVQLERTELALNGNVNRPAGILNIQTAMVD

## SEQ ID 3055

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## SEQ ID 3056

LIPALIFDKIPYNKLYKGFYNVGRNKRIRHFTTF

## SEQ ID 3057

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## SEQ ID 3058

LSDTDKQALTSVSSKEQVKVIEPRKVTFCPCQSTHFVKNKDCGNQRLCRDCKSFVEQTGTILYNTQKDIWVWKYIHCMIKPYLRKCAEICKINLATAFTWRHKILDALQNMN  
EVELDGLVQADEFTSYISYKGHKFNFLRPAHKGRTATRGISKEQVCPCGINLDGKSVARISNLGKPSLKNIN

## SEQ ID 3059

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GCTACTGGCTGATGACGTTTGAAGAAACCAACACTTGGGACGCTGATTATATACGACCGCTGGCAGGCGATTAAAGCGCGCTGGTTGGAACATTATATTAACCAACGAAGTTCACAC  
AGGAGAATCGGTAAACAGCATTTGTAACGATAACGATGAATGGGTGCCGAAGCCTATTTGGAAGCTGATTATTCAAAAATACCGAGCAGATTTTGAGCAAGCTGCTGGAATTTGCT  
TTATTCAACTACTGGGAGCGGAAGTAGGCCGACTGAAATTTGGATAATGAAGCTATGAAGCAGATGACAAATACGACTTCCGAGACAGTAA

## SEQ ID 3060

MFALAASMTLRGDKANLHQSSCFMTDFQDLINKPKPETGLKRPVNGPINPPYAQSKSDAELHELYFVKEMLDMLAEGGTGIAIIPVSCVIAPSKAKSEIVKYHRLKAVMSMPSLPYFV  
GTVTCIVVFEAHKPHFQTVVIDPDTQEEISTKKACRKTWFGYWRDDGFEKTKHLGRIDLIDYRWQGIKARWLEHYLNNEVHTGESVTAFTVDNDEWAEAYLETYDYSKITRADFEQVUREFA  
LPQLLGAEVGPTENLINESYEDDENNDPFGDDE

## SEQ ID 3061

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## SEQ ID 3062

MVELQEIFDVSYGSKLDLNMKSMNPNTINPVRSGKNNGVTSVDLLKNTKPYFAGLLTVALGGSVLSLTLQNKPFYTAQNVAVLNPKTEHTEQQLFYCAAIIFANAYRFSACGREANRL  
RQLFVPSGLDEIPSWVESVINLPAGVTEPKLRESLDLPVVRQSKRLDEIPTQNGIAATKLKEFEQRQKDTVVYIRPASTQARTLSYLARDSVDEKHLFPCHTLPTSTNGEGSHYTSVS  
TCEFVANSVDVAVLTPIQSDMPIEVKLYYAKCTTANRYLFSYGRKPKGEKLSIMLPYDQQRDPDYICRPIHTLLFSNNL

## SEQ ID 3063

TTGTTAAACACAGCCTTCTATTTCAGGATACGGGCAATGATGTTTCAACACACAGGACGACACATAAAGCCCGCCCTATGTTGTTGCC

## SEQ ID 3064

LKHSLLFQDTGNDVSTRHTTKAPPYVLP



## SEQ ID 3065

ATGATGAAAAAATGTTCTTTCTGCGCATGCTTCTGTCGGCTGCGCCCAACCGTGTGGGCGGATACGGTATTTCTGTAAAACGGACAACAACAAATACATAGAAGTTCAAAAA  
TCAACCCGAATCTTTACGAATATTCGTTGCGCAGTGGCGGCAAAAAAGAAATGCCATACGCAACAGCAAGCTGACCTGTGGGGCGTTCGACAGGTGGCAAGGCATGGCAGCGGACG  
CGGGCAACGATGAAATTCACAAACGGCGAATTTATGTACACCGTATGGACAGGCTTCGATTCGGTACTCATACGAAAGCAGCGGTGTCGTTGTGGAGCGTAGGGGCAAGGAAGTCGCA  
CGGTAGGCTGTACGCCGAAACCGCGCAGCGAATTTCAACGATGACGATTTTTCGCCG

## SEQ ID 3066

MMKMFPLSAALLLSAAQTFWADTVFSCKTNNKYIEVQKINRNLVEYSPGSAKKKEIAIRNSKADLLGRSDRWQMGSGRRATHKPFQNGEFHTVWTFDSVHTHTSSGVVVERRGKEVA  
RVGCTPKTAQANFNDDFSR

## SEQ ID 3067

TTGGTGTATCTGAATGTAAAAATAACTGTGTATCCCTTTTGACTCCTCTATATTGTTGAGATTGCCTAAAAAATTTAGSAAACAGATAATTTGCATGTGGCTATTTACGCTGTGG  
GTACCATTTTGTTCACCCCTTTGACT

## SEQ ID 3068

LVYLVNKLTVSSLLTPLYLLRLPKFRKQIICHLAISRLGLTILFPHLT

## SEQ ID 3069

ATGGATATTAAACGGTATTCGCGCTCTTTTCACGGTATGGATCTTTATCTGTTTCTGTTAGTACTCTATATCGTCTTCAACAGGCGGAATAAGAAAACTACGATGATGCCGCAACAGCA  
TTTTTGTGAAAACCAAGATGCGCAAGATAAGAAAAGCGAAAACCGT

## SEQ ID 3070

MDINGIRALFTWIFICFLVLYIVFNRRNKNYDDAANSIFAENQDAQDKSENR

## SEQ ID 3071

TTGTTATTTTATTTACGTTTATTTACGATATGCAATGCACGGTTACACAAATATATTCGCGCAACCGTTTAAATTTGTTGAATTTTAT

## SEQ ID 3072

LLFLPTFIYDMQMHGTYNIQAQPFNFVEFY

## SEQ ID 3073

ATGGAACAGCGAAGCCCGTCATGCTGATTGTCCGCCGTCGGGCGAGGCGAAGGACGATGTGAAGTCTCCGTCGTGCCGATGCGAGGCGGAAGTGTGAGTCCGATTGAANTCGAAA  
CCGACGAAGCAAGCTGTAAACCGCTGCCGAAATGTATGCCGTCGGGATGCCGTGTTTGGGTTCAGTCCGCCGCCGCTGTAAACCGCCGTCCTACCTTAACTTTTCAGACCGCATAAA  
GGCGCACATTTGCCGTAGGGCAAGCGCGCGTGCCTTGGCGCGTTATGCGGCGCGCGGCGGCTTTTGCACCTGAAGACCGCAACGACAGCGAGGCGGTTTTCGCCCTGCCGTTTGAAC  
AGTCTGCCGGAAGGTGCCGCGTATTGTCTGTGCGCGACACGGCGGCGGATTTTCTGATGAATGCTTGCAGGAGAAAGTTTTCGGACGGAGGTGCGAGAAGTCTATTTTCAGACGGC  
ATAAACCTTTGAACCTTTCAAAATTTCAAAACGAAATATTCGCCGCCCTATATACGTCCACAGAAGTGTGTCAGTCCGTGTTTGCACAGCTTCCGCCGAATTTTCCGATTTCTTCAA  
ATCCTTGTCTATCTTACCATCATCCGCGCATTCGCGAGGCAATGAAGCGCGAAGCGGTGTTTCGGTGCAGAACCGTCCCTACGCTGGAAGCGCGCTTCTCTATTTCCATTTCCGTT  
TCAGACGGCATGCTTTTCCGGAACCTCAAAACCA

## SEQ ID 3074

METAKPVMILVRPSGRAKDDVEVCRRAGQAEVLSPIEISTDEASLKRPLPEMYARADAVFVSPAIVETAVPYLNLSDGIKAHIAVQGGRRALARYAGAGVFPEDGNDSEAVLRFLPVN  
SLPEGARVLVVRHGGGRDFLMNALQEKGPTEVAEVYFRHKLNFQNFQNTENIAAAYITSTELVQSLFAQLPPQPSRPFKSLLYPTHFRIAEALKREGVCSVETVPTLEALSYSSISV  
SDGMVFPQTSQ

## SEQ ID 3075

GTGGCGCAACCTGAAACAAANTCATCCGAACCCGTACCGGAGATACAGGCATCAAAAGAAATGCCGTCTGAAACCTCTTCCCACGCAAGAAACGAAACAGAAAGTACACATTCCCCTG  
CTCCTTTTATCTGCAAAACAGTCCGCGAGCAACGCTTTGGCGGCTCGCGCTTGGTATTGGCGCATTTGGGTTCGCAAGTGGTTTGTGTTGTCGAAGGACAGATGCTTTGAAAAA  
CCAAGAGCTGGCATTTCAACAGAAATCGACAAGCGGCTTGGGCGAGTTCGAAACCGCGCCCTGCTCAAGACAACCTCAACCGCCAAAGTCCATACAGTCCGAACCTCGACCGTTG  
GACAGCGGTGTCAAAGCAACCGCAACAAATCTGATGACGCAAAAGCCTATCGGAGTTCACCAAGGGCGTCCGATTTGGCTGGTGAGCAACCGGAGACCACTACTCAATCTGGCGG  
CGCAACAGCTGGTGTGACCGGCAATATCCAAACGGCAGTTCGGCGTGTGGAGCATATGACAGCGGCTGCTCCGTTTGGATCAGGACAGCTTTCGCGATCAACAGCGCGTCAGCAG  
CGATTTCGGGGAACCTGAAACCCGTCCTATGTCGATATTTCCGGCAGCGCATTCGCGCTCGACCGGTTGGAACCGCGCTATCCGAGCTGCGCTGATTTTGGAGCGGCTATTTGAACCG  
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TGATTTCCTCCGAACAGGCAATTTTGTGCGTGAACCTCGGCTCTGCGCTGTTGGATGCGCGCACCGCATTTGATGACGCGCAACCGCGAAGCTATCAGGGCGGATTGAACAATGCCGA  
AGCGCGCTCAGACAGTATTTGATGCCAAGTCGCCGCCACGCAAGTCTGGCTGAAAGAACTGGCGGAATTTGAACACTGGATGTACGATGACGCGGATGACGCGTTGAAGACCAAT  
TTAAATGCCGTCGCCCTATCCGACCGTACGCGCATGACGGCGCGGAAATCAAGAAGCGGAACAGCGGCTTCCGAACCGGCAACGAAACACAGCTTCCGAACCGGCTGCCGAT  
CGGATGTGAAGGCCATAGAAGCACCGTCCCTGCTTCGGAACGCAACCGGAACAGCTGCAAAAAACAGCCGACCGGAAAGCGAGGCGGTTGCCGCTCCGCTAAAGGAGAACCGCG  
A

## SEQ ID 3076

VGEPEKSSPEVREIQASKEMPSSETSSPRKENETEVHIIAAPPFIVKQSGSNALAAALVLAALGLGASGLFVQGNVLNQLAFNQKIDKALGESENAALLKIDNLNRQSAIQSELDRL  
DSGVRKANGEQILMTQKAYRELTKGRADWLVDETETIILNLAQQVLVTGNIQTAVGVLEHIDSRISRFDAQELLPIRQAVSSDLAELKNRPVYDTSGLALRLDLETAVSLPLILDGLKLP  
GVQARNEAVSASWQNVWEKSLGTLKGLVEIRLENNDAHLISPEQATFVRENLRILRDARTALMQRNGEVYQGLNNAEAVRQYFDAQSPATQSWLKELAEKLTLDVMTADDGLKTS  
LNAVRAVYRDGTRMTAAENQAEQAASEPANEVASEPAAASDVKAIEAPSLPSEKRPBQPAKQKPAPEKAGRSPSAKGERA

## SEQ ID 3077

ATGAAAACGGTAGTCTGGATTGTTGCTCTGTTGCCGCCCGCTCGGACTGGCGCTGCGGCTTACACCGCGGACGTGTATATCGTACTCGGACAGACCATGCTCAGAATCAAC  
TGCACGCTTTGTGTTAGGTTTCGCTGATTGCGGCTCGTGGTGTGTTTCTGTTTAAATTCATCATCGGCTACTCAATATCCCGGAAATATCGGCGTTCCGTTTCGGCGCGGAAAG  
CCGCAAGGCCCGCGCTGCTTGAATTAAGCGGGTTTGGCGTATTTCGAAGGCGGTTTGAAGAGCGGAACCTCGAAGCCTCTCGAGTGTGGGCAACAAAGAGCGCGGAGACACCGGACT  
TTGGCATTTGATGCTGGGCGCGCAGCGGCGAGACAGATGGAATAATCGAGCTGCCGACCGTTATCTTGGGAAATCGCAAACTGCCGGAATAACAGCAGCTTTCCGCTATCTTCTGC  
TGGCGGAATCGGCGTTAAACCGGCGGATTACGAAGCGGCGGAAGCAATCTTCATGCGGCGCGGAGATGAATGCCAACCTTACGCGCTCTGTCGCTGCAACTTCGTTACGCTTCGA  
TCGGGCGCATGCGTTTCGAGTTCTGCAAAACCGAAACCTTTCCAAGCGGCGGCTTGGGCAAACTCGGAATGGAACGCTATCAAAATGGGCATACCGCGCGAGATGCGGATGCT  
GCCGATGCCGCGCTTTGAACACCTGCTTGAAGCGGATTCCGACAGCCTCAAAACCGGGAATTTAGCGTATCGTTTGGGAAAGTACGAACGTTTGGGACTGTATGCCGATGCGGTCA  
AATGGGTCAAACAGCATTTATCCGACAAACCGCGCGGAGCTTTTGAAGCCTTTTGTGAAGCGTGCCTTTTGGGCGAGCGGCAACAGCAGAAAGCCATCGATTTCGCGATTCTGT  
GCTGAAGAACAGCCCGGATAACGCGCTTCTGCTGATGATCTCGGCGGCTCGCTTACGCGCGCAAACTTTGGGTGAAGGCAAAAGCTACCTTGAAGCGAGTATTCGACTGGAAGCGGAT  
ATTCCGCGCGCTTTGCTGTTGGCAAGGTTTGTGACGAACCGCAGCTCGCAAAAGCGCAAGCACAGCGCAACTTGGTTTGGCAAGCGTTGCCGGGAAAAACCGCTTCCGCGGAA  
CCGCT

## SEQ ID 3078

MKTVMVIVVLPAAVGLALASGIYTGDDVYVLGQTLRLINLHAFVLGSLIAVVVYFLFKPIIGVLNIPENMRRSGSARKGRKAALALNAGLAYFEGRPEKAELASRLVGNKRGDNRT  
LALMLGAHAAGQMENTELRDYLAELIAKLPEKQSLRYLLAESALNRDYEAERANLHAAKMNANLTRLVRLQLRYAFDRGDAQLVLAKEKLSKAGALGKSEMYRQWYARQWADA

ADAAALKTCLKRI PDSLKNGELSVSVAEKYERLGLYADAVKWKQHYPHNRRPELLEAFVESVRFLGEEKQKAIDFADSWLKBPQPDNALLMYLGRLAYGRKLWGKAKGYLEASIALKPS  
IPARLVLAUKVFDETAQSOKARAQRNLVLASVAGENRPSAETR

**SEQ ID 3079**

ATGACTCTTTTAAAAACGATACCTTCTCTCCGCGCCTGTCTCAAACGCCCGTCGAATACACACCGGATTGGATGATGCGCCAGGCGGGGCGTTATCTGCCGAATACAAAGCCACGCGCA  
CGAAAGCGGGCAGCTTCTCTCGATTGTGCAAAAAACCGGATTGGCGACCGGAAGTCCACATCCAGCCTTTGGAACGCTTCGATTGTGACGCGCGGATTGTGTTTCCGACATCTTGACCGT  
TCCCGATGCAATGGGCTTGGGCTGTATTTTGCCGAAGGCGAAGCGCCGAAATTCAAACGCGCCTTGCACACGAATCGACATCGCCAAAGCTGCACGTTCCCGCATGTGAAAACTGCAA  
TAGCTTTTCGACGCGGTAACTTCCATCCGTAAAGCATTTGACGCGGCGCGTACCGCTTATCGGCTTCTCCGCGACGCCGTTACGCTCGCCTGTTATATGTTGCAAGGCGGCGGACGAAAG  
AATTCCGACCATCAAAAACATGATGTACTCGCGCCCGGATTGCTGTACAAAAATCCTCGATACCAAGGCCAAGCGCTTACCGCCTACTCTCAAGCCCAATTCGACGCGGCGCGCAGGC  
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CCTGTATCTGTGTTTGCCAAAGGCGGCGGCTGTGCTGTGAAAGCATGTGCCCAAATCGCGCGACAGCGCATTTGGGCTTGGACTGGAATCGGACGTTGCACATCGTCCGGGACAGCGCGCCGCTGTGCGCA  
ACCAAGTCTGCCCTCAAGGCACTTTCGACCGCTGCGCCCTTCTCGGTACGCCGAATCTCGTCCGCAACGAGGTCGACGATATCTCTGACCGGCTACGGACACGGCAGCGGCGCTGCTTCAA  
CTCCGACACCGGCATCAACCAACACGCGACCCCGAACACGCCAAAAATCTTAGTCGACACCGTACACGAGCTGTGCGCGCAGTATCACGCGCGG

**SEQ ID 3080**

MTLLKNDTFLRALIKQPVETPTIWMRQAGRYLPEYKATRTKAGSFLLDKNTGLATEVTIQLPERFLDAAILFSDILVTPDAMGLGLYFAEGEGPKFKRALQHESDIARLHVPMELQ  
YVDAVTIRKALDGRVPLIGFSGSPFTLACYMVEGGGSKFRTIKTMMYSRPDLLYKILDTNAQAVTAYLNAQIDAGAQAQVIFDTWGGVLSDAAFKFSLYIRIQIVAGLKRESEGRV  
PVIVFAKGGLWLESMAQIGADALGLDWTCTNIGEARRVGNQVALQGNFDPSPALFGTPESTRTEVARILTYGCHGSGSHVFNIGHGGINQHADPEAKILVDTVHELSTROYHGG

**SEQ ID 3081**

ATGATGTTACCTTACGTTTTTTCAAAGCCAGACCCAATCCTTGCAGATAGGCGACTACAGCATCCAGCTCGGATTGTGTTGCCAAAGCCTCAGGCGCTTTCGCAATTTCCCTCATCACTGTAA  
GGAGTACCTACTTTACGCAAAAGCCTTCACTGTTGGCAACGGTTGCATCGACATCGACTTTATTTGCGTGCAGGCCACGGGAATGCCGGCATATTGGACTCAGGCACGCATCACGGGGATTCA  
CGAGGTGGATGCGGTGCCAATTCGTGCGAATAGCGGCCGCCACACGTGCCAAATCAGGACCGGTACGGTTTGGAAACCCCATTTGGAACCGGATGGTTCGTAACCGCACTCTCCGGCAACAGAGTA  
ATGACCGTAACGCTCGGTTTCGCGCAGGAACGGACGAATCATTTGAGAGTGGCAGTTGTAAACAGCCCTCACGGATGTAAATATCGCGTTCGGCAACCTGCAGGGCATTTGTAAGGCTTCAAG  
CCCGCGCGCGCTGTGTTGCCGCCCTTGGTAAAGGCCAAGGGCAACCTTCAATCAACAGACCGCACTGACTACAAGCAGCGGTGAACACAAATCAGAACGCCGATTTTTTCTTCAGCCAAAT  
CTGG

**SEQ ID 3082**

MMLPYVFSQSTSLQIGDYSILQGFVCQSRFRNFLITVRSTYFTQSLHVGNGCIDFLACKPRECRHIGLRHDTIGIQOVDAVPFVGIAAAHTCQIRTGTFGTPLERMVVNRLSGNRV  
 MTVTLGFRTERTNHLRVAVVTALTDVNIASGNLQGIIVLRHARRRLCCRLGKGQGHNFNQOTDTDYKQREHQNADFFFSQLL

SEQ ID 3083

ATGTTGCGAACCTACTTGAACCAATTGACCCCTCCCGAATTAGCTGATTCTGTTTAAAAATACCGTTGATGGTTTTATGGAAAAATTGTCAAAACCGAGCCGAAAATCGCCCAAAATGTTT  
TATTGCTGGGCAATGTTCAAAGTGGCAAAACGGCAGAGTTTTGGGTGTATTAAAGTGGCTGGCTGATGATGGCGACACAAAGTTTTTTGTATCTTACTACTGACAGCGTAGATTACA  
GGATCAAAACAGTCAAAACGAGCCAAAGCCAATCTGAAAAACCTTATCTGTAATTGCTGAAGCTGACGACCGGAAGTTTTATGGAAGTAATGAAGGCAGAGAACCCCATCTTGCTCGTGATTAAA  
AAGAATGCCCGTGTTTGAACCGTGGCGTAATTTGTTTGGCACTCAAGTAGCCCTGAAAGGCTATCTCTTTGGTTATTGTTGGAGCAGTAAGCCGATCTGCCAGCCTAAATATTACTATCTG  
ATAAGCCGGCTAAAGATGCGCAGTACATTAATAAATCTGCTAAACGACATACAAAATTTCTGTGTCAAAGCTGCTTTATFCACTTGATGACACGCTCATACGCTTTTTATTATAACATCA  
AGAATCTGATTGGCAACCTGAATTTATCCACTTCTPTTGAAGCAGGCGAAAAATACATCGGCGGCAACTTTGTCTTTTCTGATCCACCAAGCTATATAGTTCTGTTTTATTGATAGCGAATTG  
GATGATATGAAGACGAGAGTGGTGAAATTTGCCGAAGGAGCAAAACAGGCATTTGCTTAGTTTTCTAATAACCTGTGCAGAAATTCGCGCTATGTGATAAGGCTAACTGTAAATTTTGCACCTAC  
ATCCAGGCTATAAAAATCAAGATCATCAAGCCTTTTCAAAGAAGATCCAAGCCTTTTTAAATGACTTAGTGCAGAGTCAATAATGGGGAAGACCTTGCAGGTAGCTTTAAAGAAAGTTA  
TTTGGATTGCAAAAAGCAAGCCCGCATATTCATATCTTTGTGATGAATATACGAAAAATTGACAGCACTTTTATGAGAATAAAACCGTTTCTACTCTTGCTCGTTAACTCCGACAGCAAAACA  
GATTTTGACTAGAAAAGAGTTTGCATATCATTTAGTGGTGTAATGTGATTGTGCTGGCTTGACGATTTTGCAGAACTCAAAACGGTATTCTTATAGTGCCTTCAACCAACCGAATCGAG  
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TATTGGGCGAGCAAAAAATTCAGGCGGCAATATTCAAGTTATTTATCCGAAAAATATCAATCCAACCTGAAAAAATGTAATTGAAATTCGATAGTATCAATCAAATTTGGGTGGTGTGAAT  
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TTCTAGATAAATTTGGGTCGTTATGTTCCAGATGACTGGAATAAGGAAAAATTTATTGTCTGGTGTAGAAGATTAAGAAACGACAAACGTCCTCAAGTTTTAAAACTATGTTTTGATCAAAACCG  
CGATAAACTTTCTGCAGCAACCGGCACAAATGCTTTTCCGAAGACGACCGTAAATTAGGAGAAAAATATCCCAATGATTTATTCCTTACGCTTTATCAAGTAGTAGGAAATAAGAGCAAAAGT  
TGGCAGGGAAGAAAGATTTTTGGTTTACCCCAATCAAGCTATACCACATAGGCTTGGGTGTACCAAAATGCAAAA

**SEQ ID 3084**

MLRTYLNQLTPPELADSVKNTVDGFMELKQTEPKIAQNVLLGNVQSGKTAQVLGVLSALADDGDKHVFLYLITDSVDLQDQTVKRAKANLKNPITVLSSEADRSFMEVMAENPILWVTK  
KNARVLKRWNLFPASQSSLGKGYPLIVTDEDAASLNTNSDKPAKDASTINKLNDIKNSCCQSLPIQLTATPQSLLLQHEESDWQPEFTHFFEAGEKYIGGNFVSPDPSPYIVRFIDSEL  
DMKDESGEITAGAKQALLSFLITCAEPALCDKAWCNFALHPSYKIQDHAQFSKKIQAFNLNDLVQAVNNGEDLAGSFKESYLDLQKTKPDIHFFDEIYEKLTALLENKQISTLVVNSQTET  
DFDLEKGFNLIIGGNVYIGRGLTIKQLTVVYSRTAKKPNADTFWQHSRIQFYDRDKSLRLRYIPFDVYVYFVQLVQANLIIGQAKNSGGNIQVYIPKINPRTKRNVLKFDSDINQIVGGVN  
YVLPFHFNEDNLSEINKLIPSTLLEIDEQSDLYQIDIEDLFLVLDKLGRVYPPDWNKCFIAGVEALKAQRPSPKTYVLITKGRKLSRATGTMLESDDRKLGKEYPNDLFLFLYQVGNKRG  
WQGDQFWLNPNIKLPHNGLYQSAK

**SEQ ID 3085**

ATGTAATACAGTGTTCCTCCAAATATCGCCAAATGCCAAAATCACTGAAAAATCTCTTAATCGCGGTTGGATGGATTTATTAAATCAGCGGATGAAGTGTGATGGCGACAGGTTATGTATCTA  
ATGACGCGAGTGGTGAGTTACATAAAATTTGGGAGCTAAACGATCATATTCAAAAATAGATTTATTGGTCGGAATGCATTATTTGGAAAGGTTTATGCCATTTACAATATGACAGCTTATG  
TAACTAAATGATTTTTCGACATGAGAAAAGAGGAGCGGTCTATGTTCCTCCCTTTGTGAAATTCACGGCAAAATGTATTCCTTTTAAAAATATCAAAAAATCAATGGATTAATGTGT  
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GCAAAAATATCCAAGAGTTGAAGACCAAGTAAATTTATTGAACATAATAGCCATTAGAAAAATGTTTGGGTGGTTTCAGAAAAATGCACCAGAACAGATTTCGGCAATTTATTTGCCAAAC  
GTCAGAATATCATTTCTCAATCCAGCTAAACCGAAGAAAAAGTAATTTGAATGTATTTTTCGGAAGAGTGCAGCAGATAAACGAGGGTTTGTCAAACCAAGCACTTGGTATGAAGTA  
GAGTTGATGTATCCAAAGACATCTTCCAGAAAGGATATCCGGTCTCGAATCTTTACAGATTATACCGATGATGGTTGGCAATTTCAATGCAAGACATCGGGGGATTACTCCAAAA  
ACTTCGCGTCAGAAAGATGATTTAAAGACATCTGGTAAATGATTTAAAGGTCTTGTGGAAAGTCAATGGCTGCTCCAAATAACCGAGAAGATTACGATGAACCCCTACGCGGATACGGTAA  
CGATGATGATGATTCGCTCAACCGGATATCTCTGATGTTTGGCTGCTCTCATTAAAGGGGAAAAAC

SEQ ID 3086

MTYFVSNLANAKITEKSLNAVMDLFLKSADEVIMATGYVSNDAVVELHKHILELNDHIQKIDLLVGMHYLEGFSPHLYQDLSLKCLNDFLRHEKRGAVYVSPFVKFHGKMYSFKYQKINGLIG  
SANTLCFWDSTERTYETMLHLNGKPAQILQADIQSTIHLKGNKIVEVERPSKPIEHNSHLENCILGVQKIAPBQIRQLFAQTSEYHPSIPAKTEEKSNLNVFFGEGRRDKRGFKVPRPWYEV  
ELIVSKDITSOBYEVLKSETVITDDGWFOCKTSGDYSKNFRSENDLKLTKGWIKGRLESHGCI ONNEKITHETLREYGNHDFELRSTNDPDMWLLSFKGKN

SEQ ID 3087

ATGCTATCTAAACAAATCTCAAATCTTAATTTCTCTAGTAACAAACCAAAAATCCTATCTCTATTTTCAGGATGTGGCGGTTTGGAATTTGGGCTTTCATCAAGCTGGTTGTGAAACTGTTT  
GGCGAACGATTTTCTCCCATTTGGGCTTGCGAAAGTTTCCGTA AAAATAATCGCGCATGTCATCGTAGAAGTGATATTGAACAAATAATCCGAATGATCCAACTATTTCCCGATTGCGACAT  
CATTTTAGCGGATTCCTTGTCAGATTTTTCATGATTTTGAAACAGCGCGGCTTAGAGGGTGAGCGCGGCAATCTTTATAAAGCTTTTACGTTTGTGTAATGCAAAAAACCGAAA

GTTTTGTGTGCTGAGAAATGTGAAAGGTTTATTTGACTGCCAACAGAAAAAGCCATCCAGCAAATATTACCGACTTTGAAAAATTGCGGTTATTACGTTACGGCGAAGCTGTATAACTTTG  
CAGAATTTGGGCTACCTCAATTTCTGTGAACGTGTGCTGATTGTGGGATACGTTTGGATACAGGATTTGATTTTCCGCATCCGGAAACCGACGCACAATGAACCTGGCGAAAAACGGCTTAA  
ACCATATGTAAACAGCAGGTTCAGGCCATATCCAAATATCCACAAAATGCCAGTAAATAAGTAATTACTGAAAATCAGCGATAAAACACGGCGTATGTTGGAAATTAATTTCTGAAGGTGGAAT  
TTTACCGATATTTCTTAAGATCATCTTTATATGTGAAAGGTATGATTACGCCAGTTTATCTGCTGATGCATCGAAACGAGCCATCAAAAACAATTTATTCGACAGGTGGCGGTGTACTT  
GGGGTATCATCTTCCCTGAACCGTGCTTTTACTAATAGAGAACGAGCAAGGCTTCAAGTTTTCCTGATGATTTTGAGTTTGTGCGGATCAACAACTGAAGTACGTCGCCAGATTGGTAA  
TGCCTGTTCTCTCTCAGGGGCGGTGTCACTTGCACAAAAAGCATTTTACCGATTTTTCAGACAACTATGAGAAAGTGAATTTGCATGAGAAATTAAGTGAAGAAAAAGAAATTTTATTCAT  
GACCGACTAAGCAAAATTCGAGGGGAAAAACA

**SEQ ID 3088**

HLKSKQISLNLSSSNPKILSLFSGCGGLDLGFHQAGCETVWANDPSHWACESPRKNIGDVIIEGDIQINPNDPTIPDCDILILGGFPQCFDSMTWKQFGLGEGERNLYKSPFLRFVNAKKPK  
VFVAENVKGLITANKKAIQOIIITDFENGCGYYVQAKLYNFAEFGVPQFEREVLIVGVRLDTGDFRHPETHNETGENGLKPYVTAGQAIISNIPQNASNNELIKTSKTRRMLELITPEGN  
FTDIPKDHPLVYKGMISHVYRRMRHNPSKTIILAGGGGTWGYHFPPEPRAFTNRERARLQSPDDFEFVGSTTEVRRQIGNAVPPQGVVELAKSILPIPSDNYEKVDLHEKLVZEKRIILFH  
DRLSKIRGGKQ

**SEQ ID 3089**

[illegible]

**SEQ ID 3090**

**LIKILVWILKVNALNATQRNATQRNATQRNATQRNATQRNATQRNATQRNSTIIFNGKVIVWDSCFVFSVIMPQNNRKPPLFVS**

**SEQ ID 3091**

ATGGCAAAAACGCTTAAACCCCTTTACCAATGACCCGAATGGCGGGCAGCTTCCCGAAATGGCAGGGCAAATGTCCGCATTGCGGCGAGTGGAAACAGCTTCAGGAAAGCTTTGCGCGC  
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CGTATTGGCGGGCGGTTTGGTCGATGGCGCGGTCACTCTGCTCGCGGGCATCCGGGCATCGGCAAAATCCACGCTGTTGTTGCAAAACCATCGCCAAAATGGCGCAAGCCGCAAGATGCTG  
TAGCTTTCCGCGCAAGAATCCGCCCAACAGATCCCTTCGCGCTCGCAACGTTTGGAACTGCACGCCGAAGGCGGTAAACCTGCTTCCCGAAATCCGACATGGAAGCGATTACGGCGGCTTGA  
AACAGCATCAGCCGCAAGTGTGCTGTTATCGATTCCCATCAAAACAGTATTCGAGCAAAATCAGCTCGCCCGCGCTGTTCCGTTGCGAGGTGCGCGGAATGTGCTGCCCAATCAGCGGTAT  
GGCGAAAACAAATGGGTATTCGCGATGACTGATCTGTCGGACAGCTTACCACGAAGCAGGACGATTCGCGCGCCGCGCGTGTGGGAAACATATAGGTCGATACCGGTGCTGTTTTCAGGGGCGACCA  
CATTCCAACTACCGCATGATACGCGCCATCAAAAACCGTTTCGGCGGGCAACAGAAATGGGCGTGTTCGCGATGACCGAAAACGGTTTGAAAGGCGTATCCAACCCGCTCCGCGCATCTTC  
TCGCGAGCTACCGCGACGACACGCCCGGTTTCGTGCGTTTGTGTACACAGGAAGGACGCGCGCGCTTTTGGTGAATTCAGGCATTGTCGATGACGCGACGCGCTTCACACCCAAACG  
CCTCAGCGTCGGATTGGAACAAAACCGCTTCGCGATGCTGCTTGC CGTGTPAAACCGCGACGCGCGCATCGCCCTGTTTCGATCAGGATGTTTTTTTAAACCGCGTCCGCGCGCTGAAAATC  
GGCAACCGCGCGCGGCTTTGGCGCTCATCTCGCGATGCTTTTCAGCTTCGCAACCGCCCTATGCTTGAAAAACCGTGGTCTTCGTTGAAATCGGCTTAAGCGGCGAAGTCCGCCCCG  
TCGCGACGCGACAGAGCGCTTAAAGAACTCCGGAAGCTTCGCGTTCAAACGCGCCATCGTCCCAAGGCCAATATGCGCGCAATGCCAAGAGGTTTCCGAACCTTGAAAATCCACGGCGT  
TTCAAGTTTGCAGGAAGCCATCGATATTTCGCGGACAGCAGGGA

**SEQ ID 3092**

MAKTLKTLVQTCGGTSPKVGKCPHCGSWNLQESFAAPEPKNARQPSWAADASTVQSLASVATAAEVPRNPFGMSELDRLVGGGLVDGAVILGGDPGIGKSTLILLQTTAKMAQSRKVL  
YVSGEESAQQVALRSORLELHAEGVNLLEAEIRMEAIQAALKHQHPEVVVIDISQTMYSQDITSAFSGVSQVRECAAOLTRMAQMGIAMLLVGHVTKDGAIGAPRVLEHVDFTVLYFEGDQ  
HSNYRMTAIRKNRFGAANELGVFAMTENGKGVSNPSAIFLASYRDDTPGSCVLVTQBSRPLLVEIQALVDDAHGFTPKRLSVGLEQNRLAMLLAVLNRRHGGIACFDQDVFLNAVGGVKI  
GEPADNLAVILAMLSFNRNPMPEKTVVFGEIGLSEGEVRPVARGOERLKEAEKLGFKRAIVPKANMPNKAKEPNLKHGVSSLOEADICRDSRE

**SEQ ID 3093**

TTGGTTTGTGGCGGATTGAAACAAGAAGGCATACCGCGACAGATAAGATTTCGGCGAAAGTTGCCCTGTGATATGGCAAAACGCATACGCCCGTCATCCCTGCGAAGGCGGGAAATCCGGAA  
TCGTCGGTTTCGGCAATGATTGGAAATCACCGG

**SEQ ID 3094**

LVCGGLKQEGIPATDKICGKVACDMAKRIRPSSLRRRESGIVRPGNDWKS

SEQ ID 3095

TTGCCTGTGATATGGCAAAACGCATACGCCCGTCATCCCTGGGAAGGCGGGAATCCGGAATCGTCCGTTTTCGGCAATGATTGGAAATCACGGTAACCCCAACCGCTTGGAATCCCGACTTCG  
GGGGAATGAGGGGCGTGCATT

**SEQ ID 3096**

LPVTWONAYARHPCEGGNPESVSAMIGNHGNPTANI PDFGGMRGVCI

SEQ ID 3097

TCTGACAAAGCCCGAGAAGGTCATGCCGACAGACCAATACGCCGAACCCATAGCGGGCGGCTAGGTGTAGATAAAGCCGGTTTGGCGTTTGGCTACTGAGCGGCAATCGCGCGAC  
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AACAGGCGATGCAAGCTGTGCGACACCATTTGCCAATGCGCGCTGGAACCTTCTTCTTCATGATGTGATGTGTCGGATGCGCGCTCGCGCGTTGACAGAAATACAGTCTTTTGAAGAAATCGCG  
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CGTGGGTGATGACGTGGAACATGCCACAGATAAGCGGACGCGCGCCAGAGCCACCGTTCATGTAGCCGAGTTGCGACAGGCTAGAATACGCAACCCACAGCTTTGATGTCTTTTGAATCAC  
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SEQ ID 3098

SEQAPEGHAEDQDYAEHSGGVGDKAGLGFAYLSEGNRADQFGGAVDDAVDNGGLADPEEVSQCARAFGEDVEIQGVVEVVFVKQNVNRTERLDFSGQVRQFVDVQKPRGNGTSRQIQ  
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## SEQ ID 3099

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CGGTACCGTCACTACTCTGTGTCGGAGAGTGGTTTACGACCATCGGTTCCAATGGGGTTCCAAACGTACCGGTCCTGATTGGCACGTGTGGGCGGCGCTATTCCGACGAATGGCAC  
CGCATCCACCTGCTGAATCCCGGTGATGTCGTGCTGAGTCCAAATATGCCGGCATTCGCGTGGCTTGACGCAATAAAGTCGATGTCGATGCAACCGTTGCCAACATGAAGGCTTTGCGTA  
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AAGG

## SEQ ID 3100

MKIQQLAERKIGVLIVFTLLVSVGLLIEVPLAFTKAATQPAFGVKPYNALQVAGRDIIYREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTPDLARVGGYSDHWH  
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## SEQ ID 3101

ATGATATGTTGCCCGTCAACACAAAAATAAAAAAAGTTCACATGCTGATTATATATGTTATTTTATTACGTTTATTACGATATGCAATGCACGGTTACACAAATATATTCGGG  
CAACCGTT

## SEQ ID 3102

MICCPSTQNKQSCNMLIYIVIFYVYLRVANARLHKYIRATV

## SEQ ID 3103

GTGCATTTGATTTCCATCCGCCATATGTCGGCGACGGGCTTATTCGCTACGGTTTGTGTATCAGTTTTCGGCGTTGCCAAAGTGTGGCCACTTCGTGCAAACTGATCGCGCTGCCG  
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CCTTGGGCGTGCAGAACGATGACTTTTCCGCGTGCATGCTCAGGCGGTTTCGGCGTCCGCTTCTGATGTCGATGACGGCAAAATGTCCATCCCTTTGCTTTTATGGCGGTTTC  
AAGGCGGCTGACGGTTTCGTCAAACGTGATTTCCGAGGTGAGGTTGCGTGTCTATAGCGGTTTCGTTTGGGTGGCGGTTTTCGGCGAGGTTGCGCGAAGCGGT

## SEQ ID 3104

VHLISIRHMSATGLFAYGFLYQFPGVQSVCHFVETDAAADDEGARIGIGGAYFAVRFGNEDAQGLQGGGGVFDHQRRTGLGRAEDDDFCRLHQAQVSACRFIMVDGKNVHFFAFYGGF  
KAADGFVKTVPFRGEGVRGHSGLVGGFAGRVCRSG

## SEQ ID 3105

ATGACCACGCACACCTCACCCTCGAAATACAGTTTTCAGGAAACCGTCAGCGCGCTTGAAACCGCCATAAAAGCAAAGGATGGACATTTTGGCGTCATCGACCATCAGGAAGCGGCAC  
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TACCGAAACGGAACGGAAGTACGACCGGCTATACCGATACGCGCGCCTCATCGTCGGCAGCGCATCAGTTTCGACGAAGTGGCAACACTTTGCAACACCGCGGAAACACTGATACAA  
AAAACCGTAGCGGAA

## SEQ ID 3106

MTHTLTSKYSFDETVSRLETAISKMDIFAVIDHQEAARRNGLTMQPAKVIVFGTPKAGTPLMVKDPALFQLPLRVLVTTETDGKVRTAYPTDTRALIVGSRISFDEVANTLANAEKLIQ  
KTVGE

## SEQ ID 3107

GTGCCGAAGCGGTTGAAATGACAGATGCGGATGCGGCGATCAGGGGAGTATGTTTCATCGTATTTCTTATCGGTTTGTATTATCGGGCTTCGGACGGGCGGCGACGCGCGCGCTGA  
TGCCGTGCCCGGTGCGGAACGCGGTATGCGGCTGAAAGCGTCTCTTTCAGACGGCATTCGGTCAATTCATCCCTTTTGTAGCAGGTCTTCA

## SEQ ID 3108

VPKRLKCRVRRRSOGVCVSYFLIGLFIGLRTGRHAPRLMPCRVPERRRMPSESLSFQTALRHFIPLSRSS

## SEQ ID 3109

TTGGCGTTGGGACATAGATGCCGCCGCTTTGGAACAGATAAAATAACTTCCGCTCCCTTAAGACGACACCGCAGGAGAACCTTATGAATATCAAAATGATTACCGCCGCACTCATTTG  
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GCACAAACGCGGTCAACATCCCGGTGACCAAAATGTCGCGCGCATATACGAAGCGCGCGCGCAAGACACGCGGTCACCTCTACTGCCGACGCGAGCGGTGCCGAAGCGCGCTT  
CAAGAGCTGAAAAAGCAGGTTATACAAATGTTGCCAATACGCGCGGTTATGAAGACCTGCTCAAAAAGGGATGAAA

## SEQ ID 3110

LALGHRRRRFGTDKITSRPLRRQPQENPMNIKQLITAALIASAAPTAQAPQKPVSAQAQHSVWIDVRSEQEFSEGLHNAVNIIPVDQIVRRIVAAPDKDTPVNLVYRSGRRRAEAL  
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## SEQ ID 3111

TTGGAACAAAAAGCGTCGAGCGGTATTGGTCTGTACCTTACCAAAGCGCCACTGCCGAGCTGAAACACGCTGCCGCGCGGTTTGGACGATGTGTGTCAGGTTTGGAAAGCAAAG  
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LEQKSVERVVVVTFKAAATEALKTRLRARLDVVLQVLESKEIAELGDDTSLDGIAYCAEHHEGDTFLPALLEQALQKESRTRLIVRLKAAIGQFDNAIYTTHTGFCQRLRLDYAFICQAP  
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EKANKDVLRRRAADYCADELARALNTEASGGRLNFKORPLQSGDI AVLVRTHNEAVMI SAALKKRQVQSVLLSRESVSFASPEAAALSALIGFWLEPRAGTLRFVLTSGIFGYDAQQLHDFN  
QNESEILLHWAESARTALDIWQYKGI FAAMQQFSQTHGIETRLSSRNNGRSLTNYFQLLELLAAEDAQRNRPAAHLKWLDRDQISLAGNGNDNRATLESSEDLVKITVTHASKGLQYPLVY  
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ATGCGGTCTGAAACCCCTTTTTCAGACGGGCATTTTCCCGTTTTACCGTCCAACCGTTTTTCATACACGGCTATGTCCGCACCCATCCGAGCATTCGACCOGC

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AGCGGCGAACACGGTTGATGTTTACCACATCTCGGCACAGCTGCATTAATCGAAGCGCAATTATAGATATGTTTCGGCGACACGGCGCAAAACCGCACTGCTGCTCCGACACCTCT  
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 ICVA5EHHGLRLYQDRGLDGFVDGTENPQCGDEFIREVALIPEGLPDAGGSYVLQKYLHDLKKWDVVPVAEQEASVGRSKETDDEFSRDVRLPDSHLGRVNLKENGVGGLKIVRRSLPFGKI  
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VKLROTORILFLYGYSKSEWERYAEAAGSGNKGKGGRHETEKREOVCKRRIHARRSGKNPPADSVL

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VL TGN ISSARKVTV SANATEKDSVFGDAVHIVLAT

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SEGLIDT 3124  
MEFLMDITQYNNYVVRQFAIMTVVWVGIVGMLVGVIVAAQLFAPALDLSNIGWPHFGLRLPHHTNAVIFAFGGCGLIGTSYYVVQRTCNTRLPGGLMPPATFFGQQAQVAVIAAVVSPFSGWT  
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SVVHFWALIPTFMWAGPHLHYTALPDWTQSLGNVLSLILFAPSWGGMINGINTLSGAWDKLRTDPIILKFLIVSLFSYGMSTFEGPMMSIKTVNALSHYTDMTVAHVHAGALGWVGFVTIG  
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**SEQ ID 3125**

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**SEQ ID 3126**

MLKFLVLGGIALVLAACGGSEGGSSAPASAISSGLIRIRINKGTVTGTEGTYAPFTYHDKDKLITGYDVEVTRAVEKLGKVKVEFKETQWDSMAGLAKGRPDVVANQVGLTSPE  
RQATFDKSEPSYSHSAGVLVAHNDNSIKSIADIKGVKTAQSLTSNYGEKAKAAGALQVVDGLAQSLTLIEQKRADATLNDLAVLDYLLKKNPNAGVKIWSAPADEKVGSGILVNKNDRA  
VAKPSTAINELKADGTLKLKLGEPFKDISVQ

**SEQ ID 3127**

ATGAGCATATCAGCGCGTGTTCGTCATAAACGGCAGAGAGGCAAGAAATTTATGAACACTGATGTCCTTTCCGAAGAAATGTTCCGCCAGTTCCTTTCACAGTCCGCTCGGCTTCAGC  
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**SEQ ID 3128**

MSI SARVSVINGREARKILLNTDVFSEELFAQFFQRAVGFQVLCRAEFHGLVIALVDNQGTGTFPIGRRGPHDFHRIRVFLQIVQNRQFIVQRRIGAFLEFNQGRILQTVHRHELRTCG  
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NRAFTVDALD

**SEQ ID 3129**

ATGACGGAACACCGCTGATATGCTCATCAGCGCGTTTGGCCCATGGTTAAAGCCGCTTTACAGTGTCTTTGCCCTTGGCGATCGCTTTCGTTATCGGCATGATTATTCGCTAG  
CCGTTCGTTTGGTAAGATCATGCTTCCGCGGTATTTTCAAAAATGCTTGTGTAAGCTGGTGAATTTTATATTTCCGTCGTTCCGCGTACGCGCTGTTGGTTACGCTTGTGATTGT  
GTTTACCGGCTGCCGTCCGTCGCGCATCTATATCAATCCGATTCGCCCGCATCATCGGCTTTTCGCTCAATGTCGCGCATAGCTTCCGAAACCATACGCGCGCGGATTTTGTCCGTG  
CCGAAGGGCAGTGGGAAGCAGGTTTCTCCATCGGTATGACCTATATGACAGCGTTCCCGCGCATCGTGCACCGCAGGCAATTCGCGCTCGCGCTTCGCGCTGAGCAACGAGTTTATCG  
GCTTGTTCAAAAACACCTCGCTTCCGCGCGGTGTAACGGTAACGGAGCTTTTCCGTGTCGACAGGAAACGCAACCGCACTTATGACTTTTTCGCTGTCTATATCGAAGCTGCATTGCT  
TTATGTGCTTCTGTAAGTCTGTTTGTATCAGCGCGCTTGGAAAAACGTTTCGACCGTTATGTGCCAAA

**SEQ ID 3130**

MTETRADMLISAFPMVKAGPTVSLPLAIAFVIGMI LAVAVALVRIMPSGGIPQKCLLKLVEFYISVVRGTPLLVQLVIVFYGLPSVGIYINPIPAAIIGPSLVNGAYASETIRAAILSV  
PKGQWEAGFSIGHTYINQTPRRIVAPQAFRVAVPLSNEFIGLPMKNTSLAAVTVTELFRVAGETANRTYDFLFPVYLEAALVYWCFCVKFLFIQARLEKRPDRYVAK

**SEQ ID 3131**

ATGGATATTGCGGATTTTAAATCATGACAACCTCTTATTTGGCGACATAACGCTCGAAACGTTTTCAAAACCGCGCTGAATCAAAAACAGCACTTTACAGAAACACCAATAAACCAATGCA  
GCTTCGATATAGACAGGCAAAAAGTCATAAGTGGCGTTTGGCGTTTCTGTGCGACACGGAAGAGCTCCGTTACCGTTACCAACCGCGCAGCGAGGTGTTTTGAAACAGCCGATAAAT  
CGTTGCTCAACCGCGGAACCGCGCAGCGGAATGCTCGCGTGCAGCATCGCGCGGAACGCTGTCATATAGGTCATACCGATGGAGAACTGCTTCCACTGCCCTTTCGCGCAGGACAA  
AATCGCGCGCTATGTTTTCGGAAGCGTATGCGCGACATTGAGCGAAAGCGGATGATGCGCGCGGAATCGGATGATATGATAGATGCGCGGAGCGGAGCGGCTGAAACCAATACACA  
AGCTGAACCAACAGCGCGGTACCGCGAACGACGGAATATATAAATTCACACGCTTCAACAAGCATTTTGGAAAAATACCGCGGAAGGATGATTCTTACCAAGCAACCGGTACGCGCA  
TAATCATGCCGATAACCGAAGAGCGATCGCCAAAGGCAAGACACTGTAAGCGCGCTTTAACCATGGGCCAAAACGCGCTGATGAGCATATCAGCGCGTGTTCGCTCATAAACGCGAG  
AGAGGCAAGGAAATTTGAACAC

**SEQ ID 3132**

MDIADFNHNSLFGDITVETFFQTRLNQKHFTETPINQCSFDIDRQKVISAVCRFLCDTEKLRYRYHGGKRGVFEQADKLVAQRNRDABCLRCDDAAERLHIGHTDGETCFPLPRHQ  
NRRAYGFSVCADIERKADDDGGNRLIDIDAGRQPVKHNHKLNQRRRTANDGNIRFHLQQAFLWENTAGRSDSYQNGYGNHADNERSDRQQRHCKAGFNHGPKRADEHISACFRHQR  
RGKEIIEH

**SEQ ID 3133**

ATGATTTAAATCCGCAATATCCATAAGACCTTTGGCGAAAAACCATTTTGGCGGCATCGATTGGATGTGGGCAAGGGCAGGTGTCGTCATCTCGGCGCTTCGCGCTCGGGTAAAA  
CAACATTTCTGCGCTGCTTAAACGCGTTGGAATGCCGGAAGACGGAACAAATCGAGTTGCAACAACCGCGCGCTTACGCAATTGATTTTCCAAAAAACAAGCAACAGATATTTGGC  
ACTGCGCGCAAGTCCGGAATGGTATTCCAAACATACAACCTCTTCCCGCATAAAACCGGTGTTGGAACAGGTGATGGAAGGGCGGTTCGCGTACAGGCGCAAGCTCGCGCCAAAGCGCGC  
GAAGAGGCTTTGAACTGCTGGAAGAAAGTGGCTTGGCGGATAAGTGGATTTGATCCCTACCAGCTTTCCGCGGTCAGCAGCAGCGTGTCCGTTACCGCTCGCGCTGCGGATTCAGC  
CTGAATTGATGCTGTTTGACGAACCCACTTCCGCGCTGGACCGCGAGTTGGTGCAAGACGTGTGGAGCCCATGAAGGAATGGCGCGGAAGGTGGACGATGCTCGGTATACCCACGA  
AATCAAGTTACGCTGGAAAGTTCACCAAGACGTCGTCGATGGAAGCGCGCGTTATCGTAGACAGGCGAGCCGAAAGAGTGTTCGACCACTCAACACGAAACGCGAGCGGAGATT  
TTAAGCCAAATCCAATCTGCCAAGATT

**SEQ ID 3134**

MLKIRNIHKTFFGEMFILRGIDLVDGKGVVILGPSGSGKTTFLRCLNALEMPEDQIEFDNARPLRIDFSKTSKHDILALRRKSGMVFQYQYNLPHKTVLENVMBGPVAVQKPAQAAR  
EZALKLEKVLGDKVDLYPYQLSGGQQRVGIARALAIQPELMLFDEPTSLDPELVQVDLMKELAREGWNVWVTHEIKFTLEVATNVVMDGGVIVQSGPKELFDLKHETRRF  
LSQIQSAKI

**SEQ ID 3135**

ATGGCAAGCATCAACCGGACATCTTCAAAGCCTACGACATCCGTGGCATCGTCGCAAAAACCTTGACCGACGATGCGCGTTATTTTCATCGCGAGGCGCATGCGCGCAAAAGCGCGGAA  
AAGGTATCGCGCGCATCGGATCGGACCGCAGCGAGCTTGAGCGCGCCCGAAGCTGATGGAGCAGATCCAACCGCGCGCTGACCGACAGCGGTATCGCGTACTCAATGTCGCGATGTTAC  
CACTCCTATGCTTACTTTCGACGCGCTCAACGAATCGCGCGCAGCGAGTGATGATTACCGCGCAGCCAAATCCGCGCGATTACAACGGTTTCAAAATGATGCTCGCGCGGACACGCTC  
GCAGGCGAAGCCATTAAGAACTTTAGCTATGTTGAGAAAGACGGTTTGTGTCGCGCGGACAAACAGGCAAGCGGTATCCGCGCAAACTCTACAAGGTTTGGGCAACGAAGTGACCGAACTTTTCGCGA  
GACACGTCAAACTCAAAGCCCGGATAAACATCGCCATCGACGCGGCAACCGCGGCGCGGCTTTCGCGGCAAACTCTACAAGGTTTGGGCAACGAAGTGACCGAACTTTTCGCGA  
AGTGGACGCGCAATTTCCCTAATCACCACCTGATCTTCCAACCGGAAACCTGCAAGATTGATTGCGCGCTGAAAAACGCGGATGCGGAAATCGGCTTGGCGTTGACGCGGATGCC  
GACCGCTTGGCGGTGTTACCAAGAGCGCAACATTTATTCGCGACCGCAACTGATGCTGTTCGCCAAGAGCTTTTGAACCGCAATCCGCGCGGAAGGTCAITTTTCGATGTCAAAT



CCACACGCCTGCTTGCCCCGTGGATTAAAGAACACGGCGGAGAACCATTAATGAAAAAACCGGCCACAGCTTCATCAAAATCCGCTATGAAAAAACCGGTGCACGTGGTTGCCGGCGAAAT  
GAGCGGACACGTTTCTTTAAAGAACGCTGGTTTCGGCTTCGACGACGGCCTGTATGCGCGCGCACGCCTCTTGGAAATCTGTCCGCCTCGGACAAATCGCTCCGAAGTGTGGACAACCTG  
CGCAAAAGCATTTCCACGCCCCGAATCAACATCTCTCCCGCGAAGCAGCAACGGGCATCAAGTTATCGAAGAACTCGCGCCCAAGCGCAATTTGAAGGCGCAACCGAAATCATACCA  
TCGACGGCTTCGGCGTTGAATTTCTCCGACGGCTTCGGTCTGATCGTGGTCTTCCAATACCAACGCCGATTTTGGTGTTCGCTTTTGAAGCGGATACGCAAGCAGCATCGACGCAATCAAAA  
CGGATTACCGCCGCTCATGAAAGCAATCGCGATTAAATCTGGCTCTTG

**SEQ ID 3136**

NASITTRDIFKAYDIRGIVGKTLTDDAAYPIGRAIAAKAAEKGARIATIGRDGRLSGPELMEHIQRGLTDSGTGVLNVGMVITPPLHYFAAVNEBCGSGVMITGSHNPDPDYNGFKMLGGDTL  
 AGEAIQELLAIVERKDFVAADKQGSVTEKDISGATHDHIIVGHVVLKRPINIAIDAGNGVGGAFAGLYKGLGNEVTLEFCEVDGNFNNHHPDPSPKPERLQDLIALKNGDARIGLAFDGA  
 DRLGVVTKDGNITYPDRQLALFAQDVLARNPGAKVIVPVKSTRLLAPWIKHGGGAIMEKTHGHSPIKSAMKRTGALVAGEMSGHVFFKERWPGFDGLYAGARLLLEILSASDNPSEVLDNL  
 PQSISTPELNLISLPGSGNHQVIEKLAAKAEFEGATEIITIDGLEVEPPDGGFLMRASNTTPIILVLRFEADTQAATERIQNRKFAVIESNPHLIWLPL

**SEQ ID 3137**

ATGACAGAATTACCGTGGATAGCCGAAGCGAGAAGGCACATCGGTTTGAAGAAATTCCTGGCGGCGAAACACAATCCGACGATTGTGCAATGGCTCAAAGAGACGGGCGGCTTCCCGCGG  
CGCGAAGTCTTTGTGACTTTTGAAGACGAAGACCGCTGGTGGCGGCTGTTTGTGCGATACTGCCCTGGGCAAAAGCGGACGCGCGGTCAATCAGGGACTGGTATCGCGCCAAAGCTCTGTCGAAT  
GTCCGGGTTTGACAGAACTCGAAGCCCTCCCATCCGATACCGGCTGACCTCGCGGTCACAACCGCGCCGGGCGGCGACAGCTGTTCTTCGTTGTGCGGCAAAAGACGCGGAAGGCAGAATCTTGGGCTTG  
GTCGGCAATCATGGCGAATATGTGATCAATCACTCCGTTGACCTTGGCGGACGATAGACGGCTACTTCTGGCCGCTCAAGCTGATTGCGCGCAAGACCGTGCCCTTCGTCGCCCGCGGAAGGCG  
GTTACCGGTTGTGCGGACGTTGCGCGCACCGCGGAACAGGCGCGGGCGGAGGCG

**SEQ ID 3138**

MTLFLPWLAERRHIGLKEIPGAHNPTTVQLKETGGFPGAASWYFEDETPWCGLFVGICLGKSGRAVTRDWYTRAKANMSGLTKLEAPAYGCTIAVKPRRGCGHVFFVVGKDAEGRILGL  
GGNOGNNMVSIIIPFDADIDGYFWPSKILGGKAVPSSPAEGRYRLSDVAATAKOGAGEA

**SEQ ID 3139**

TGCTTTGCCCTCCCTTCCTCGTCTTGAGGCGCTCTGAAACTTCGCTTTCTTCGGCAGATTGCAGCTTGCGGTTTGACGCGCTTCATTTCACACAGACGCATACGGCCCTTGATCGGCGCGTACT  
 TTAACTTGGTTCGGTTCGATCTCATACGTTTCGGATTTCGTGGTTTCGCGGTGAACCAATGCATATCGCGGCACACATGCCCAACAGCAGCAATACCGCGCCCAATTCAAACGCCAACAGGTAGT  
 CGGTATTAATACGGCTGCCCAAATCGCGGATATTGTTGTAATCGGCCGGAATGCTTTTCATCAGACCAATCGCGGCAGGTTCGGTTTCGGGTTGACAGAAATCAGGATCAGGGCAACCGC  
 CAACAACGTCACGACACACCGGCAACGAGCGCGTCCGCGCAGAAACCGCGCGCATCTTCCTCGATTTCGATATTTCAGCATCATCAGCAGCAACAGGAACAACACCATTTACGGCGCCGAGC  
 TAAACACCAACGACGCTACCGCGCAAAATCTCCGCTGCATCATCAGATCAAAATCTTCGCTCATCAGCAGAAAGGTCAGCACCAGATGCAAAAGCGGCATGGACAGGGTTTTTGGCGGTAAACG  
 TACGAAGCCGACCGGTACAAAACGATGGCGGCAAGGATATAGAACAGAAATCAGCGAAAAGTCAT

**SEQ ID 3140**

CFALPFRLEAV\*NFAAFGRFLDRFDRFHQHTHALIGAYTNLVGNIHTFRIGGFVAVQCNRGHHAQQQQYRROFKRQOVVGINTAAQIADIVVIGRNVFHQTKCGQVGFVRDQNDQGNR  
QORTDHTGNRRVVPETGAHFLDVDIQHHEDEQEHYEGADVNHORHAQKRLRHQHPNHRHAHEGQHOMQSGMDRVFGNGTNRTVONDGGKDIQNHGKSH

**SEQ ID 3141**

ATGCCCTTTAAAATGCAGCTTAACCTACATCAATAAAGTGCCACAAAAGGGAAAATTGGAAACAAAAGCAATGGCGGCCGGGTGTAAATTTATTATAACAATATGATTTATATG

**SEQ ID 3142**

MPLKCSLTYNKVPQKGKIGNKSNGGRVVIYNNMIYH

**SEQ ID 3143**

ATGCGTAGTATTGGTTGCTCTGTGGGCTTATGCTGTACTGATGTAACCATTGACCTTAACAACAAGACCGTCTGAAAGAATAATTTTTCAGACGACCTTGAAGTTTGTGCTTCAGACACAA  
TTTGTGCAATTAATCAAAACCGGATCTTAACGAAAGGAAACCCATGATTATCTCTGCACACCAACAAGGCGCATCAAAATTCGAACCTCGATTTCGACAAAGCCCCCTGTACCGCCAAAAA  
CTTCGAGCAATACGTCAAAGACGGCTCTACGACGGCGTAACTCTCCACCGCGTCATCAAGGCTTCATGATTCAAGGCGGCGGCATGGATGAAACATGAACGAAAAAGAAACCGCGAT  
CCGATTCAAAAGCAAGCGCTCAACGGCTCCGCAACGATATAATACCATCGCATGCGCGCCATCTCCGACCCCATTTCCGCGCGGCGGCATCTCTCATCAACACTGCGGCAAGCGCTT  
CTTAAACTATTCCGTTCTTAAAGAGCTGTACGGCAAAACCGTGTCCAAAGCATGGGGCATGCGGCTATTTCGGTAAAGTCGTTGACGGTTTTCAGCTGTTCGATGCATGCAAGCGTATCCAC  
CAAACGCCACGGCTACTACGACGATGTGCGACCGCAACCTGTCTATCATCTATTAAAGCGGAAGCAGTA

**SEQ ID 3144**

MRSIGCSVGLCTDVNHRPKQDRLKEYFSDLEVCRSDTICRIIQNRILTKGKPMILFTNKGDKIKELDFDKAPVTTAKNFEYQYVKGDFYDGVIFHRVIRKGFMIQGGGMDENMNEKETRD  
PIQNEASNGLPNDKYTTIAMARTSDPHSAGAOPINTADNAFLNFRSKELYGRKTVVDNGYAVFGKVVDFDVVDALESVSTRKHGYHDDVPTEVPVILIKAEAV

SEQ ID 3145

ATGAATCCCCCTGATGCAATCCCTGTTTTCCCTTCACATATCAATCCCATCTCATAAACAACCGACAAATCGTTTACAATATATTTTACACTACACCGAATTTACAAATATACTCGAAGCGG  
TTGCAGAACCGCAGCGTTTTCGCAAAACCGCTTTCGGATTGCAAGATACAAAAGAAAAACCGAATTTTGTGCTCTAAAGGACGATCTATGAACCTGCATGCAAGAACCCACCGCATCCCGA  
AAACGCTCGAGCTCTCAGTGCAGGACGCGAATACCGACTTTAAGGTTTGTCTGACCACCATTAATTTCCCGCGTGTCTTATTTCCGCGATTTACCATCTCCGCTTACAGCCCCGATGCC  
AATAAAGGATTCTGCGCTGCTGATTTTTTCGTCGCGCATTTTGTGTCACAGGCGGCTGCACATACGGTAAACCGCATTAATGTTGTCGGAFTCTGCGCGTCTGACTCGGTTTCCCGCATGG  
ACATCAAAAAGCGGATGGCTGATTTTCCAACCCGATTATCTACATTTTTTTCGCGGCTTCGCGCTTGCCACCGCCCTGCATATGCAGCGGCTGGACCGTAAAAATCGCGCTCAGCGCTGT  
CGCGCTGTGCGCGGCAATATGAAAGTGGCGGTTTTGATGTTGTTCTCGTTACTGCCCTTCTGTCATGTGGAATCAGCAACACCGCCACCGCCGCGATGATGCTGCGCTCTAGCAATGGGT  
ATGCTGAGGCCACTCTGACCGGGAAAAAGAACACAAACCTACGCTCTCCCTCTGCTCGGCATCGCCTATTTCGCGCAGCATCTGGCGGCTTGGGCACGCTCGTTCGCGCTCGCGGCCAACCTGA  
TTGCGCCGCAACCGCTTAATCTTGGACTTCTGTCGGCTGGATGAAGCTCGGCCCTGCCGATGATGCTGTGATTCTTCGCCCTTTGATGCTGCTCTGCTGCTGATCTCATCTCAAACTTAATTTGAA  
CGAACCGTGGAAATCAAAAGCGCAATCACTTCCTTGGACGCTGACCGCGTCATCGCGCTGTGATTTTCTTCGACAGCGCGCGGTGGATTTTGGGCTCCAAATTAACAAACCGGCTTC  
GGCATTTTCAATCCCGACACCGGTTATCGCCCTGAGTGCCGCCGTCGCGCTGCTGCTTTTCGCGGTGGCGCAATGGAAGGAAGTCGCCCGCAATACCGACTGGGGCGTGTGAGTCTCTTCG  
CGCGCGCATACGCTGAGCAGCGCTGTGTAAACATCCGCGCGGCTCGGAAGCCTTGGGACAGCAGGTTCGCGCCACTTTTTCGCGCGCGCCGCAATTTTATGATATCTCATGCTCGCGC  
CTTCATTAFTTTTCTGACCGGTTTACCCAGCAACCGCCCTCGCGCCCTCTGCTGTACCGATTTCCTCCGCGATCGCTATGCAGATGGGGCTGCCGAACAAGTCTTGGTATTCGTATC  
GGCATCGCGCATCTGACCGCTTACCGAGCTTGCACCGGCTTGCACCGGCTTAATCAAAACACGAGAAATGATGAATGTTCGGCATCTCTCTGAACATCTC  
TATCGCTAGTATTTGGTTGCTCTGTGGGCTTATGCTGTACTGATG

SEQ ID 3146

MNPDPASCSPYISIPSHKQNRQIVYNNITFLHRTITNILEVAEPTVSQTVSDCTIQKKNRFCLGAPMNLHAKDKTQHPENVELLSAQKPIPTDFKGLLTITISAVVCFGIYHILPSPDA  
NKGIALIIPVAALWPTAEVHIITVVALMVPILAVLIGPFDMDIKKAMADFNPITITYIPGGFALATALHMQRLDRKIAVSLLRLSRGAMKVAVLMLFIVTAFTLSMVISMTATAAMNPLANG  
MISHLDREKHTTVVFLLLGIAYCASIGGLTVGSGPPNIIAAKALNLDVPGWMKLGLPMLMLLILPMLLSLYVILKPNLNERVEIKAESIPWTLHRVIALIILFLATAAAWTPGSKITAF  
GISNPDVIALSAAVAAVVFGVAQKREMENTDGVILMLPGGGISLTLTKSGASEALMQVAATFGAPAFVILVILIAAFIIFIIFTEFTSNTASAALLVPIFGSIASQGLPEQVLVFI  
GASACAPMLPVPVPAIVFGTGLILKOREMNNGLIINLILCVLVALAYAVIL

SEQ ID 3147

TTGCGGCAGCGCGGCGGCAAAATTCCTGGCGCTGTCCAAAACTGCCAAACGTGGCTGGACGAGGAGGCGGCATGAAGCTGCCGCGCAACCGCTTCAGCTGCTTTCCGCATTGTGGTTTGGC  
GGCGGCATCTATGTGGCTGCTCTTCAAGCTGCCGACCGCGCGCGCGCTTCCCAATTTCGACAAAGCAGCACACTTGCCTGTGTTTTCGCACAAATCTTGTCTTCGGCAAAGCAT

TCAAAACCGGAAACTTCCCATCCCTACCGCAGCTGATTCGCTTCGCTCTGTTTTCGCGTCGCGCAGCGAATCGCGCAGGCATGTTTACCGCAACGCGAACCGGCAGTTTGGGCGA  
TGCTCTTGGCGACCTGACCGGGCGAGCCCTTGCCTCTTTCGCGCGCTTCTGCTGCGCCCGGACTAAATCGGTTTATTTCTCCAAACAGAGATGAATCCCCC

**SEQ ID 3148**

LPHAAANSACPKSAKRGTWRRRHEAAQPLQAPFRIVVCRRLFAALQSCRHRAAAVSTFRQSTPFCVFRNLASGQSIQNRKTSHPQLPQDCVRLIFCRRQMRAGMVRNANRQFGR  
CPCRPDGRSPCLRAFCLPPLANRFSIPKQDESP

**SEQ ID 3149**

ATGACCGAACTCAAGCAGCTTATCCAAACCAATCCATCCCGTCATCGAAGAAACCCCTCGATTTCCTGCTGTACGAATGACGATCGACGACGACCGCTCCGCCGAAGAAGTGGCACAAT  
GGCGGACATATCTGCGCAGCGCGGCAAAATCTGCGCCTGTCCAAAATCTGCCAAACGTGGCTGGACGAGGAGCGGCA

**SEQ ID 3150**

MTFLKQLIQTESIPVIEETLDFLLYECSIDDAPSAAEVAQWRDILAARGGKFLRLSKICQWILDERAA

**SEQ ID 3151**

GTGGCTGGACGAGAGGCGGCGATGAAGCTGCGCGCAACCGCTTCAGCCTGCTTTCGCCATGTGGTTTTCGCGCGGCGATCTATTGCTGCTCTTCAAAGCTGCCGACACCGCGCGCGCG  
CGTTTCCACATTTCGACAAAGCAGCACACCTTGCCTGTTTTCGCACAAAATCTTGTCTTCTGGCCAAAGCATTCAAACCGGAAACTTCCCATCCCTACCGCAGCCTGATTGCGTTCGC  
CTTCTGTTTTCGCGTGGCAGCGAATGCGCGCAGGCATGTTTACCGCAACCGCAACCGCAGTTTGGCGCATGTCTTCCGACCTGACGCGGCGACGCTTGCCTCTTTTTCGCGCGCT  
TCTGCTGCGCGCGGAC

**SEQ ID 3152**

VAGRGGGKLPFRNRFSLLSALWFAAGIYSLLFKAADTAPPPFFHFDKAAHLALFFAQILLAKAFKTKGLPIPYRSLIAFAFCFVAVGSECAQAWFTATRTGSLGDLADLTGAALALFAAR  
SACRPD

**SEQ ID 3153**

TTGGATAAGCTGCTGAGTTTCGCTCATGACTGTTTCGGATACGGAATCGGGAAATGCGCTGTGAAGGGCTTCAGACGCGATTGGATTATTTGCTGTGCGAGGAGCGGTTGCCTCTTCC  
CATTTGCGCGAAATGATTCGCGGTACGGCTGCGAGGATTTCGGCAGCGCATGCTGATTTCGCGCGGCTGTTCCGCGCTCGGTTGTTTCAAGACGTAGCCGACGACGAGGTTGCGGTTCGC  
CGGGTGGCGGATGCGAGGCGCAGGCGGTAATAGTCTGCGGTGCGGAGTTTTCGCTGAATGTCTTCAAGCGGTTGTGTCGCGCTTTCGCGCGCGGAGTTGAATTTGATCCGTCGCGA  
AGGGATGTCGAGTTCTGCTGGACGACGAGGATTCTTCGCGGTTGATTTCGTAGAACTGTGAAGCGCGGCAACCGCTGTCGCGAAGCGGTTTCATGAACGTGCGCGGTTTTCGAGCAGCGAA  
ACATCGCGCTGCGGCGAGGCGCGCGGCAACTTCGCGGAAGAATTTTTCCTTCTTTAAACGAAGCTTCCATTTCACCGCCAGTTCTGTCGAGGAACCAAAGCCCGCATTTGTCGCGG  
TCTGCTGCTATTCTTTCGCGGCTTGCCTAACGCAACCATTTTGATTGTGTT

**SEQ ID 3154**

LDKLLRFHDCSDTEIGKMPSEASDGIGLFAVQEARCLPFFAGNDVGYGLQFGDGIIVDLPAVFRARFQDVADDEVAVAGVADAQAVIVCAEFCINVFQAVVSAAAEFEFDP  
RDVEFVVDDDEPFGDFVELCKRGNRLSGTVHERGRFEQPNIAVQGGAGNFAEEFFFFFKRSLPFPQFVEEFKARIVAGLFVFFARVAQAINHFDCV

**SEQ ID 3155**

ATGTCAAACACAAATCAAATGGTTGTCGCTTGGGCAACCGCGGCAAGAATACGAACAGACCGCGCAATGCGGGCTTTTGGTTCTTCGACGAACTGGCGTGAATGGAAGGCTTCGT  
TTAAGAAGAAAAAATCTTTCGCGGAGTTGCGCGCGCGCGCTGCGCGAGCGGATGTTTGGCTGCTCAAACCGGCGAGTTTCATGAACCGTTCCGCGAGCGGCTTCCGCGCTTGC  
ACAGTTCTACAAATCAAACCGGAAAGAAATCTCGTCTGTCACGACGAACTCGACATCCCTTCGCGACGATCAAATCAAACCTGCGCGCGGCAACCGCGGACACACCGCTTGAAGAC  
ATTTCAGCAAACTCGGACGCGAGATATTACCGCTGCGCTTGGCATCGGCAACCGCGGCGAGCTTTCGCTGCGCTTGAACAAACCGGCGCGGAAACCGCGCGG  
AAATCGACGATCGCTGCGCAATCCCTGACGCGGTACCGCATATTTCGCGCAATGGGAAGAGGCAACCGCTTCTGCAACAGCAAA

**SEQ ID 3156**

MSNTIKMUVGLNPGKEYEQTRHNAGFWPLDELAWKWAASFKEKFFGEVARAALPDGDVWLKPKATFMNRSGQAVAAALQFYKIKPEETLVVHDELDPGRIKPKLGGNGGHNGLKD  
IQAKLGTADYRRLRIGLHGPGRNLVVGVLNKPSSAEHRRQIDDAVAKSLQAVPDIISGKWEATRFLHSK

**SEQ ID 3157**

ATGCTTGAATTTGAGATTGTGACGCTGTCGCGACCGACAGGTTTGAAGAACATGACGCTTGGCGAGGGAACAACCGTCCGACCGCGCGCTGCAAGCGGTTTGGACGGCATATTG  
AAAAATTAACCTGCAATTCGCGCTTTTGGCGATTTCGCGCAAGCGCTCAAGAGACGACGCGCTGCGCGACGCGGATCGAAGTGTACCGCGCGCTGTTGATCGACCCCAAGA  
AGCGCGCGCAACCGCTTCAAATCAAGAAGAA

**SEQ ID 3158**

MLIEIVGLPDRQVLKTNQLAEGTIVRTAALQSGLDGIFENLNLHSAPIGIFKAVKDDTPLRDGRIEIVYRPLIDPKERRKRVQNEE

**SEQ ID 3159**

TTGATGATTATGATTCAATATAAAATAGCCCCCTCCCTCTAGACCATGAATGGCACATCTGCTGAAATTCACACAAGATAATGATTTTCTATAGAAATAAGCCTTCGGAATTTGGGTGC  
CGGGCAGCTATCTGATTTCGGGATTTTTCGCCCATCATCTTCTATCATGATCTGCAACCGGCGCTTCCATGCGCTGCAACAAATTCGCAAAACCGCTGCGACACTGCGCGGTACG  
CGCGGAGTGGCAATCCGCTACACCGTATATGCAATTCGATTGTCGCTGCGGATTTCTTCTGACGACGAGAACCGGCTTTTTCGACGATCTGCTGCTTTTGAAGTGAAGGAACG  
GAAACGCTGCGGACCGCTTGAATTCAGCGCATTCACCCGAAATGGCGATTGCCACAACCGCTGCGGAAACAGGAGGCTTGTCTTTCAGACGCGATCTTATGACGAATTTGATTGACC  
GACCTGTCGAGATGGCTTGATTGAATTTTAGATTTCGAGGCGCAGGCAATTCGCAACGATTCCTTAAACCGCATATATCCCGATTTCGACCGGACAGGCTGTTTCGACATCAA  
AAAAATCTGCGAAGCAAGATGCGCATGTTCTCTCCCTGCCCCATTTGAGAAATATTGTTCTGCTTCCACGTGCGGACCATATTACGCGCGTTTGAACACACCGGACGACGCGCA  
CTGCTGCGCGATGCGCACGCTTCCGCGGTACGGTATGACCGATGCGCAGCATGCTTACACCAATTCGTCGAGCTTTCTCCACGAAATTTTCACGCGTGGAAAGTCAAATCCATCA  
AACTGCGCGATTTCGCCCCCTTATGACCTCGACAAGAAATAATACCGAACAATATGGGCAATTCGAAGGCAATACATCTTATACGACGATTGTTTTCGACGCGAGCGGACCATCTC  
GCCGGAATTTTATTTAAACCTGCTAGCACAAGGCAATTACGCGGTACACAACACCGCGCGGCTTTCGAGGAGACCTTGGCGGAATCGAGTTTACCGCTGGAACAAATTTTACAAACG  
GATGAAACACGCGCAACGCCATCTGCTAGCTACTACCAAAAAGGCGCACTTGCCTGATGCTGATAATACGCAACGGAAGCAACGCGACGATTCCTTGTATACGGTAATGG  
ACAAATCTTATCGGAGTGGAGGACACACACTCGGGTATTCGGAAGAACTGCAAAATCCGCTTTCGAGGAAATACCGGCTTGGATTGACGATTTTTCAGACGCGATTTCGACG  
CACCAGAGATTTCGCGCTTGCAGAAATGCTTGCACACAGGCGTGAACCTGACCTTCTCCGCGACACCGCGGCGGATATGCGGAACACATTTTCCCATTCGCGCGGACG  
GGCGATTTCGCGCGACGCTTCAAACAAACCGCGGACCATATCTGCTGACCATGCTTCAACGCGGAGAGTGGGAATTCGCGGCTGCTGCGCGCAAGACAAATCATTTGCTTTAGACG  
GTTATGCTGCAACGACTTTCGCGCAATGGGCGGATACACGCTAGGCGCAAAATCAATATCCACTTCTTCCGTGACGACATATTGCTGCAACCGCTTTCGCGGTCAGGCAACGCG  
GGCGGATACGCTTACATCATCAGATCGCAACCTGTTGGAAGCTGTTGTTGCTGCT

**SEQ ID 3160**

LIVMTHYKIASPLDHEWHLLKFTQDNDPPIEISLPWVPGSYLIRDFSRHITSIHACNCTSMPLQIAKNRWHATAVRGEWQIRYTVYAFDLVSRGSFLITERRGFFDGSCLFLKVBGT  
ETLPHRLTGIPPEWRIATTLPEGRVLFQTASYDELIDRPVEMGLIEFLDFAAGIPIHTALNGIYDPDFDRDLVSDIKKICETELAMFSSPAPFEKYLFLHVGHDITYGGLEHTDSTA  
LADRHSLLPYGHTDADDAATTLGLFSHEYFHAWNVS IKPAAFAPYDLDKENYTEQLWAFEGITSTYDDLFARSRTISPEFYINLLAQGITRVOQTRGRRLQTLAESSTAWNKFYKP  
DENSPNAIVSYQKALALCLDLIRNRSNGRSLDVTMDKLYREWDRTHSGIPEKHQIRCBETGLDLTDFPQTALYSTEDLPLAECLATTGVKLTFLPLFRQHGGSYAEHIFPIPT  
GDFGARFKQNDHIVLTHVFNSSAESALCPQDKIILALDGYACTDPAQWARYHVRKINLHFRAGILRQTVLTVQATAADTALHTIDRNLLERMLFG

## SEQ ID 3161

ATGATTTGGGGCTTTGCTGAAAAATTGAAGCCGCTGCTTATTTTGTCCGCAATCGCGTTCTTCGCGCTTCTTGGCAGCTGGACAGGGCGGGCAATACCGTTCGGGATACGGTTCGGCGG  
TGTTCGAGGTTTTCGAACGCCCTCAAGGCCGCGCGGTGGAACACGCCGCAACACGCCGCAATCGTCCGCCGCTATCAGGCGCAAAAGCGCGCGAGGAAAAAGAAAGGTTGCGCTA  
TGTGCAACCGCTTAAATCATTTGAAAAACCTGTGTACCGCAATGCTGTTTGTATGCTGACGGGTGCGGCAACTCAACCGCGCTTGACGACGGCGGT

## SEQ ID 3162

MTGALLKRWKPLLLLSAIAFFAVSNQLDRAAQYRGRYGAUVSEVSESLKAAVEHAHARKSSAAYQAQKAAREKERVRYVQTLKIIEKPVYRNACFDADGVRELNAAVDDGG

## SEQ ID 3163

GCGGTACGGCGCGCTCAGCGCTTTGCGTTTGGCGATTTCGGCTTCGTATTTGTCCGCGATTGCCAAGAGGATGGGCTTGGTCATATGCAAGTCGCTTTTTCCTCGCCGCTGTTTCAAAA  
ATATGGGTTTCCACAATCGCATCGGTGCGGCGAGGCTCTTCGCAAGAACCGCAGAGATGCACTTGGTCAGGTGATGTCGTAACGCTTGGTGGCGCGGTGCGCTTTCGCGCTTCGCG  
ATTGATGTTGATCGCCATTCGCGGACACACCGCTTCGCACAATTTACACGCGATGAGCGGTTCCTCTCCGTTCCGATAACGGCGTTCGCGGTGACAGCCGCGGAAACGACGAGTTCGCG  
CGTTTCTCTTCGCGGAAATAAATTTGTCTTTTTCGCGGCAAAAAGTTTTTGAGCGTTACGCCATGCTTTTACCAGTTTCGCAAGCAGAAAGGTTTTTACTAAGTTAGCCATATTATGT  
TCCCTCAA

## SEQ ID 3164

AVRRVSGFAFGDFGVFVADQCEDLGHMVAFLLAVVFKRMGFHNRIGRAGLFAETAEDALGQVVDVVLGAAGAVFAFRFDVDRHCRTHRLAQPTRDAFLSVRTALRVQTAETHGLR  
RFLFGKINCVFAGKRVFERAHAFDQFAKQKGFYVSHIMPPQ

## SEQ ID 3165

GTGATGCCGCTGAAAAAGTTGAAAAAACATCTTGGTCTGCACGGCGCGCAAAATGTCGAGCTGGTCGACAAGGTTGAGGATTACCCGCACTTTCTGCGCTGGTACAGCAAGACCG  
AGGTCATCGGGCGGTAGCGGCAACGAAGTGAAGGCGCGCTGTTTATGAGATTATATGCGCGTTCGCCAATCGTTGCCACGCACAACCGCAACATCCCGCGCAGGAAATCCGTATGGAAT  
GCTCGAAGGCCGCTTCAAAACCTTACGTGGAACGTGGAATTTATCGATTTCGCGCAGATATGTGCAAAATCGAATTCATTTGGAATACGATTTTCCATAGCCGTTTTCGCGCTTA  
ATTTCCCGCTCTTCAACCACTTTCCGCCACGCTGGTCAAGCGTTCGTCAAAGAGGCAGACCGCGCTTATGCT

## SEQ ID 3166

VMPVKVKNILVLHGADKMFELVDKVEDYPHFLPWYSKTEVIGRSGNELKARLFMDYMRVRSFATHNRNIPGREIRHELLBGPFTLRGTWKFIDLDDMKIEFNLEYDFSNAVLALS  
ISPVFNHLSATLVEAFVKEADRRYA

## SEQ ID 3167

GTGGGGAACACCTTTAAATCAATCCTTGTCTGGGTGCGCTTGGGTATCGGCTGATGGCTGCGTTCAACGCTTTGGACGGCAAAAAGAGCAACCGGCAAAATCGAATATTCTCAGTTCA  
TCCGACAGGTCAACAACCGCGAAGTATCCGCGCTCAACATCGAAGGATCCGTCGTCAGCGGTTACCTGATTAAAGCGGAGCGCACCGACAAAAGCACTTCTTCAACCAACGCGCCCTTGA  
TGAACACCTGATTCAAAACCTTTTGAACAAAACGTCGCGTAAAGTAACGCCGGAAGAAAACCGAGCGCGCTGACTGCGCTGTTTACAGGCTGCTGCGCGCTCTGCTGCTGATTGGC  
GCATGGTTCTACTTTATGCGTATGCGAGCGCGCGCGCGGAAAAGCGCGCATTCTCTTCGCAAAAGCGCGCGCTGCTGGAACAAAGTTCACCTTTTGGCGGATG  
TCGCGCGCTGCGACGAAGCAAAGAGAGTGCAGGAATCGTCGATTACCTCAAAGCACCAGCGCTATCAAAAGCTTCGCGCGCGCTGTTTCCGCGCGCATCTGCTGGCGGCGAGCC  
GGGAACCGGTAAACACTCTTGGCGAAAGCCATTCGAGCGAGGCGCGCTGCGCTTCTCAGCATTTCCGCTTCGATTGTTGCGAAATGTTGCTGCTGCTGCTGCAAGCGCGCTCCG  
GATATGTTTCGAGCAGGCAAGAAAACGCGCCATGCAATATCTTTATCGACGAGTTGACGCGGTAGCGCGCCCAACCGCGCGCAGGTTTGGCGCGCGCAATGATGAGCGCGAGCAACAT  
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CGGAACCGCGCATGTTGGTGATGACGAAAGACGAAAACGTCGCGCGCGCTATCATGAGTCCGACACGCGGATTTGCGGAAAGCCTGCGCTTACCGACCGCTCCACAAAGTAACCAT  
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TGCTTCAAAATCTCGATGAAAACCGGACAGATGAAAACGATGTGAAAAGCCTGATGAAATGGAAACCATAGACCGCGATCAGGTACTGGAATATTGCGGCGCAACCAACCGCAGC  
CCGCCAAGGATTACAGCCACAACCTGCGGAGAAATCGGAGCGCGGGAAGTAAACGCGCGCAGCTCCGACTCGGAAACCAAGCACTGCGCGCGCAGACACCGCTCGACAG  
AGTCCGCGCAGCGCTGAAACCAAGGCT

## SEQ ID 3168

VGNTPFSLVWVALGIGLMAAFNALDGKKEDNGQIEYSQPIRQVNNGBVSGVNIIEGVSVSYGLIKERTDKSTFTTNPALDDNLIQTLLKNVRVKVTPPEKPSALTALFYSLPVLILLIG  
AWPYFMRMQAGGGGKGAFSGFKSRARLLDKDANKVTADVAGCDEAKEVEQIEVDYLKAPNRYQSLGGRVPRGILLGASPGTGKTLAKALAGEAGVPPFSISGSDFFVEMFVGASRVR  
DMFEQAKKNAPCIIFIDEIDAVGRQAGLGGGNDEREQTLNQLLVEMDGESNQTVIVIAATHRPDVLDPALQRPGRFDRQVVPFLPDIRGREQLNVHSHKRLDESVDLLSLARGTFG  
FSGADLANLVNEAALFAGRRNKVKVDQSDPEDAKDKIYMGPERRSNVMHDEKRAYHESHAIVAESLPPTDPVHKVTIMPRGALGLTQWLPDRDRISMYKDQMLSQLSILFGGRIAE  
DIPVGRISTGASNDFERATQMARENVTTRYGMSDKMGVMVYAEENGEVFLGRSVTRSONISEKTQDIDAEIRRIIDBQYQVAYKILDENRDKMETMCKALMEWETIDRDQVLEIMAGKQPS  
PPKDYSHNLRENDAEDNAPHEAPTRKTEAPAPADTASTESGQQPENKA

## SEQ ID 3169

ATGGCTGTACGTTCCAAATCCTCAAAAGCGTGGCTGCACGAACACATCAACGACAGTACGTCATATGGCGCAAAAGAGCGGTACGCGCGCGCTGCGGCATACAACTTTTGGAAATCA  
ACGAAAAGAGCAAGATAATCAAAACCGGCGCGCTACTTGGCGACTTGGGCGAGCGCGCGGGAAGCTGGTCGAGTTGCGCGCAAGCTGACGGGTACTTCCGAGCGGTTTTCGCTTGGGA  
CATCTCGCTATGGAAGCCATAGGGGCGCTGCTCTTCACTTACGGCGGACTTCCGCGAGAACGACGCTTTTGGCGCAATTCGAAACCTTGTGGCAACCGCGCGCTGACCTTGTAAATTCG  
GATATGGCGCGCAATATGTCGGGAAACGCCGTAAAGCATCAGGCACGCGCTTTTATCTGTCGCGAAGTCTGGCTTTCGCTTCGCAACACCTGAAACCGCGCGGAGCTTTTGGTCA  
AAGTCTTTCAGGTCGAGCTATCAGGAATACATGGCAGCATGCGCGAAATTTTCGCGACTGTGCAGACGCGCAACCGGAGCGCTGCGCAATCGCTCCAGTGAGATTATTATTTGGG  
CAAAATAAACGC

## SEQ ID 3170

MAVRSSKSKAWLHEHINDQYVEMAQKDGYSRARAAYKLEINEKDIIKPGTVLADLGSAPGSWSQVAALITGTSAGVAFDILPNEAIGGVSFIOGDFRENDVLAQFETILLNRPDLIVIC  
DMAFNMSGNVSDQARSFYLCLEALDPASQHLKTGGSFLVKVFGAGYQYEMAMREIFGTQTRKPEASRNRSSEIYLLGKNKR

## SEQ ID 3171

ATGCTGCATTATCTCTTTTATTCAAAACAGTAGGAAATGGCGGATACCAAAATGAACACCAAGAAATTTTGAATTTGAAAGCGCGCGCGCACCATCTCCATCTGTTGTGATGGTTCGCTC  
AGCAGGGCTGACGCGACGAGTCATCAAGGAAACCGATGCGGCACTGACGCGCGATGAGCTGATTAAAGTGGCGGTATTCGCGGACGACCGTTCGCGAGCTATCGAAATCTGCAATACCTT  
GTGTGAGGCGTTGACGCGCAACCTGTTCCGCATATCGGGAACCTTTTGGTATTTGCGGTAAAGATATCAGGGCC

## SEQ ID 3172

MLHYFFYSNRKMDTKLNTKEILELKARAHHLHPVVMVGQQLTDAVIKSTDAALTAHELKIVRVFGDDRAERIEICNTLCEAVDAQFVRHIGKLLVLHNRKTEA

## SEQ ID 3173

GTGGTGTGTTTCTATTGTTCTTCAATGGCGCGCACGCTGCTCTCGCGCGCGCAATTCGCGGTGCGGAAACCTTTCCGGTGAACAGGATTTTGATTACCGCTCGATGCGCTCGCAA  
GTTCGCGCGGCTTCGCTATGATT

## SEQ ID 3174

VVVLLLPQMAARCPASRHPGVKPFVKTDFDYRSMPSASCGGFRMI

## SEQ ID 3175

TTGCATAAGCCCTCCAATCATCTGTCAACAATTCAAATCATACGGAAGCCGCCCACTTGCAGACGCGATCGAGCGGTAAATCAAATCCGTTTTCACCGGAAAGGGTTTCGGCACCGCG  
AAATGCCCGCCGAAGGACAGCGTCCCGCCATTGAAAGAACA

## SEQ ID 3176

LHKPSNHPVNNSTZAAATCRHRRAVIKIRPHKGRPHAEPRRTACRPLKQ

## SEQ ID 3177

ATGATTGGAGGGCTTATGCAATTTCCTACCCGAATGTCCTGGCTTCGCGTATGCGCGGTATGCGCAGGGATGATTTTCAOCCGCGCTGATGCGCGAGCATATGCTGACCGCGGATGATT  
TGATTTATCCGGTGTCTGATTGGAGGGGGCGCGCGGAGGAGGATGTCCTTCTATGCCGGCGGTGAAGCGTCAGAGTTTGGACAGGCTGCTGTTTACCGCGGAAGAGCGGTGAAGCT  
CGGTATTCGGATGTTGGCACTCTTCCCGTGGTTACGGCAAAACAAACCGGGCGTGCAGGAGGCGGTACAATCCCGAAGGACTCGTCCGCTCAACTGTCCGAGGCTTGGCGGAGAGGTTT  
TCCGAATCGGGCATTATGACGGATGTCGCGCTCGATCCTTATACGCTGCACGGTCAGGACGAGTACGAGGACGAAACCGGTACGTGATGAATGATGAAACCGTAGAAGTCTTGGTGAAAC  
AGGCTTTATGTCATGACAGAGCGGGCAGCGAGTCTGTCCTCTCCGATATGATGAGCGGCGTATCGCGCGCATCCCGGAGGCTTTGGAGGATGCCGACATATCCATACCGGATTAT  
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ATGCGCTATCAGGTTTCGGGCGAATATGCGATGTTGACGGCGCGGTGCGCAACGGCTGCTGAGCGGCGCAAGTGGTTTGGAAAGCTGCTGCGCATTCAAAGCTGCGGGTGGGACGG  
GATTTTGACCTATTACGCCATTGAGCGGCGAAAGATGCTGAAGCGT

## SEQ ID 3178

MTGGLMQFPYRNPVPSRMRMRDDPSRRLMREHMLTADDLIYPVFLGAAREEDVPSMPGVKQSLDRLLPTAEAEVKLGIPLALFPVVTANKTRAQAYNPEGLVPSTVRALRERF  
SELGIMTVALDPYTVHGDGLTDENGYVNDFTVEVLVKQALCHAEAGTVVAPSDMDGRIGAIREALDAGHTHTRIMAYSAYASAFYGPFRDAVSGSSGNLKGADKKTYQMDPANTD  
PALHEVALDIQBGADMVMVKPLPYLDVVRVDEFGVPTTAYQVSGEYAMLQAAVANGWLDGGKVVLESLLAFKRAGADGILTYAIEAARMKLR

## SEQ ID 3179

TTGGCGGCCCATCGGGGAAGTGTCCGCAATCCCCCGATTTTTCATATATCGGGCGGACGCGGCAATTTTGGCGGTTTGTGTTGCGCGAAGGGGGCGTTATACAAAATTATCAGCGCG  
ACCAA

## SEQ ID 3180

LAAASGEVSAFPPIFYISGGRGKFLFPCLREGGVIQNYQAHQ

## SEQ ID 3181

ATGTTTAAACATACACCTTCAGGGAACCTTATCAAAACAAAGCCCAAGCGCGCAATAACACGAAAGAAACAGGCGCAACCAACCTG

## SEQ ID 3182

MFNIHPSGNSYQNKSRKRGNHNRNRPNL

## SEQ ID 3183

GTGTCGGTCCGCTACGACTTCGGCGGCTGGAGGATAGCGGCAGATTATGCCGTTACAGAAAGTGAACAGCAATAAATATTCCTGTAACATAAAAGAGTTGGGAAGAAAGGATGGTACCT  
CTTCTAGCGCCGCTATCTTAAACATACAAACCCGAAAGACGAAATCAGGAAACCGTACGTTTCCACGCCGTTTCTTCTCTCGGCTGTGCAACCGTTTACGATTTCAGAGCCACAGATAA  
ATTCAAACCTTATATCGCGCTGCGGCTGCGCTACGGACACGTCAGACATCAGGTTTCAATCAATGGAAAGAAACCAACGACTGTATACCACTTACCAAGCGACGCTAGTGGCAAACTTCT  
GTTCCATCAGAAATGCCCCCAACCTGCTATCAGGAAACCCGACGACGCGCGCTTGGGCTTGGCGCGATGCGCGCGTGGGCATAGACGTCGCGCCGCTGACTTGGACGCG  
GCTACCGCTACCACTATTGGGGACGCTGGAACACCCGCTTCAAAACCCACGAAGCTCAATGGGCATGCGCTACCGCTTC

## SEQ ID 3184

VSVGYDFGGWRIADYARYRWKNDKYSVNIKELGRDGTSSSGRYLNIQTRKTENQNGTFHAYVSSLSLSTVYDFRANKPKPYIGVRVAYGHRVHVSMKEKTTTVTYPSDGSAKTS  
VPSEMPFKPAYHENRSSRLFGAMAGVGDVAPGLTLDAGTRYHYWGRLEWTRFKTHEASLGMRYRF

## SEQ ID 3185

TTGGCGGTAGAAAAGGTATGGTTGCTGCACAGTTGGACAAGCAGGCGGAGGCAATATGCTGTTTGGCCCTTAATTCCTAAAGTGCCTGTCTTCTGCGGACAGATTGGCGAAAGGAA  
TGAAGAAAAGCTATTTGGCTTTGCTCCGACCGCAACCGTCCAAAAACAAAGATGGATGATAAAGGCGCGCATGGAATAATCCAGGCGCGGATGTGGAAGCTGACGCGCAATATGGAATAT  
TGGCGTTACCGGTTTTCAGTATCCGATCAGTGAAGAAATGCGGCTGTTTCATCCTTGAGCCACATACCGGTAAGACACATCAGTTGAGGTTGTAATGAAGATCTGGGCAGCTCTATA  
TTTGGGACAGCTGTATAGAGAACAGAAATCCGAACATATGTTCTGTATGCG

## SEQ ID 3186

LGVEKVNLLHRLDKQAGGILLFALNSQSAVLAQFAERKMKSYLALSDRKPSKKQWIKGMEKSRRGWKLTRNMENIAVTRFFSIRISEKMLFILEPHTGKTHQLRVVMKSLGSSI  
FGDSLRYGTESEIMFLYA

## SEQ ID 3187

GTGTATTGTATGGCAGGCGAGTCCGCTGTAACAAACGCTGTCGGCCGCTGCTGCAAAATGCGAGATTATATCACTTGTCTTTTGGCGGCTGCAATTGATTGTTTCTATTTCGGGATGATG  
ATAAAATCCCGACTTATCCATATCTTACAAGGACAGAAACAGATGAAATTCGGACCGCTACCATCCATTCCGGCTACGATTGGGACGAAACACACCGCGGCTGATGCCGCGGATTTATCA  
AAACAGTATGTTTGGCTGACGAAATCGCGGAAATGTGCTTACCGTTATTCGCGCTGAGCAACCGGACCGCTCAGATTTTGAAGACACCGCTTGGCGGATTGGAACACCGTGCAGCA  
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ATGTTTATCAAAATGGGGGGTGAACGTTGTTTTCGGCAATTGGGCAATCCCGATAATTGGAAGCAATTGCTCAAGCGCACAAATGTCAAACCTGGTTTGGCTGAAATGGCGTCAATCC  
GCTTTTACGCTTGGTAGACATCAAAGCCCTTGCAGCGAAAGCCAAAGCAGCGAGCGCGCTGGTGGCGATCGACAACACCTTTGCCACGCGGTATCGCAACAGCCCTTGGATATGGGTTGC  
GATTTGCAATCCATTCGCTACCAATATTTGTGCGGCTTCCGAGGATTTGATGGGCAATGCTGTTGCCAAACCAAGAGCTGGCTCAGCCTTGCAGGATATGATGGTGCATACCG  
GCGGATTCAGGTCGAGCGACTGCTGGCTGTGTTGCGCGGCATCAAAACGCTTGCCTTGGCTATGAGGACACACTGCAAAACGCACTCGAAATTCGCGCGGCTTTGGAAGCCCATCC  
TGCCATGAAAAAGTGTTCATCCCGGCTGCGCTCTCAGCAACATTACGCACTGCGCCAAAGCGCAATGCCAAAGGACATCGCGCGCGTGGTTACGGTTTATCTCAAAACGACACGCGC  
GAAGCGCAACAGCGGTATTAACATGAACTGGTCAAAATGACCTCCAGCTTCCGCGCGTGGAAAGTCTGGTCAACCATTTCTATTCCCAATCCACAGCGCGCTGCCGATATG  
TGAAATGGAATGGGCATCAGGTCGAGCTCTTCCGCTTCTCCATCGGTATGGAAGACGTAGATGATTTTGAACGATATTTCGCGCGCACTCGATACAACTTG

## SEQ ID 3188

VYCHAGRCRLKRCRPPACKCEIISLAFGGICDIFYFRSDKIPTYPYL/TRQKMKP/PTRTIHSGYDCDEHNRALMPPYIYQNSMPALHEIGENVYRYSRLSNPTROILEDTVADLEHGA  
GPAFSSMAGIDAVNRTFLRPGDTIVAVADYGGAYDLLVDVYQKGNVNVFADLGNPDNLDLLKHNKLVLEMPNPLRLVLDIKALAAKAAADALVGDIMFATPYLQOPLDMGC  
DPAFHSATKYLCHSDVLMGIVVAKTKELAQPLHDMVHTGALGPTDCWVLRIGKTLALRNEAHCKNALEIARLEAHPAIEKVHFPLPSHEHYALQAQMPKIGGVTVYVYKNDTR  
EAANSVLIKMKLVKMTSSLGGVESLVNHCSQSHSGVPHNVKMEMGIRVGLLRFSIGIEDVDDIWNDSIAALDTTL

## SEQ ID 3189

TTGCAGGCGAGCGCGGACAGCGTTTTCAGACGCGATCGCTGCCATACATACACATCTCAATAATTATCTGAATATTAAGGACAAACACGCTGAAGCCATTGCGAGACGTC  
AATCCAGCAGAGATTTCGCGCAACCTCCGATCAATCAGTTCGCGATTAAAGACCTGCGCTTCCGATTACCTGAAACCGCGGAGGACACAAATCCAGGTTGCTGCGCTGACGATGAC  
GGTTTATCTGCGCGCGGACAGAAAGGACGATATGTCGCGCTTTGTCGATGATGGAGCAACATACCGAAGTCTTGGATTTCGACAAATTCATAGGCTGACTGCCGGAATGTCGCG



CTTTTGGATTCCCGCGCGGCAAAATCAGCGTTCTTTTCGTTTTTCCGCAAGAAACCGCGCGGTATCCGGTATCCGGTCTTACTGGATTATGATGTACGCTCAGGGTGAAATGA  
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GACTTCCGATGCCGAAGTCGGTATCGAGGAAGTTATCGATTATGTGGAACCGCAGCGAGCTGCCAACTCTACGGCTGCTCAAACGCCCGATGAAATACTGTACCGAAGAGCCTAC  
GAAACCCGAAATTCGTGAAGATATGGTCCGATGTCTGCTACTTCGCTGATTGCCGACAAACGCATCAAGAGTTTCGTCTCGAGAGCGAGAATTTGAGTCTATCCAAACCAATTCGG  
CTTATGCTATATCGCTACCCG

## SEQ ID 3190

LQAGGRQFRFRLPAIQYTHLNYLNIKDKQRMNAIDVQSSRLRLNLPINQVGLKDLRFPITLKTAEQTSTVARLTMTVYLPABQKQTHMSRFVAINBQHTVLDPAQLHRLTAHVLA  
LIDSRAKISVSFPFPRKKTAPVSGIRSLLDYDVSITGEMKDGAYGHSKVMIPVTSICPCSKELSYGAHNQSHVTVSLTSDAEVGIREVIVETQASCLYGLLRPDERKYVTEKAY  
ENPKFVEDMVRDVATSLIADKRIKISFVVESENFEINHSAYAIAYP

## SEQ ID 3191

ATGGTGTGGATAGACTCGAAATTCCTGCTCTCGACGACGAACTCTTGATGCGTTTGTGCGCAATCAGCGAAGTAGCGACATCGCGCACCATATCTCCACGAATTCGGGTTTCTGTAG  
GCCTTTTCGGTAACGTATTTTTCATCGGGCGGTTTGAGCAGGCGGTAGAGTTGGCAGCTFCGCGTTCGCTTCCACATAATCGATAACTTCCTCGATACCGACTTCGGCATCGGAAGTCAGGC  
TGACGGTAACGTGCGAAGCGTGATTATCGCGCCATATTGGGAAATTTCTTTGGAACACGGGCAAGCGAGGTTACGGGAATCATGACCTTCATCTGTCGGCGTATGCCCGCTTCCTCAT  
TTCACCCGTGAGGCTGACATCATATCCAG

## SEQ ID 3192

MVDRLEILALDDEFLDAFVGNQRSSDLAHHIFHEFRVFGVLPNVPFIFGAFBQAVELARLRPHIIDNFLDTDFGIGSQADGNVRLTLMRAILGNFTGRKRGVGNHDLHTVAVCPVPH  
FTREADIIQ

## SEQ ID 3193

ATGACAGTATTAAGCAAAGAGCAGGTTCTATCCGCAATTAACAAACCGCAATCTGTCGCGCATACGATGCGGCACGTAACATCAGTCCGAGGATTTTCAGTTATTTTAGAATCGGGC  
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TCATTTGGTGGTGTTTTGGCGAAGAAATGCGCGCTTCGACAGCCGTTTATGTGGAAGTCTCAACCGCGCGCGGTACCGAACCAGGATGCGGTAGAAAAATCTTTGGCGAGGTAT  
CAGGCGTTTCAAGCTGACGACATCAAGATTTTGGACGATTGCGCGCCTTGTGTTGACTGGTTCGCGCCAGACCTATATCGCGTTAGCCAACTGATGACGGTTCGGCGATGCGCGGTA  
TCGATCTTCGCGCGGTGGAAGGTTTCAACTATGCCGATATGGAACCGGATTGTCGCGGCGAGTTCGGTTTGTTCGATGCGGCAGAAATGGGCGGTTCGCGTTCGCGGACATTCGGTACCG  
GTTTCAGGAAATCGTCACGAAAGCGCGCAGGCCCTTGAAGAACCGTTATTTGGCA

## SEQ ID 3194

MPVLSKEQVLSAFKNRKSCHRYDAARKISAEDQFIFLGRISFSSVSGEPWQFVVVQNPBIRQAIKLSWGMADALDTASHLVVFLAKKNARFDSFPHLESKRRGVTEPDAVEKSLARY  
QAFQADDIKLIDSRALFDWCCRQTYIALANMNTGAAMAGIDSCPVBGFVYADMERVLSSQPLGFLDAEWSVVAATFGYRVQEIIVTKARPLEEFTVINA

## SEQ ID 3195

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CGGCTATGTACGCGCACAAGCGGAAAAAGGCTATAAATCCGCCCGGAACTGATTACCCCTGAAATTTGCTGGGAAGCGACACAGCGCGCATCAGTTTCGATCCGAAACACAAAATCGGT  
CTTCCCGCCCGCGGAGGCTCGATATCGATTACGTCGATTTGCTGTTGACCGAAGACGGCGTATCGCCAAACAGCTTATCGCGGAAACAGCGCGAGTGAAGAAATATTTGGTTC  
CGGTGCGCGCGCAATTTGGACGAAAGGAGCTTGCCTTACTGAATCAGCGATTGAGTTTGGACGGTGATAAACTCGCTCCCGCAAGTAGAATGGCAAAATGAAGACCAACTCGCGCTTCGT  
GTTGAAACAGGGTAAAGCGGCAATCCGCCGATGTGCGAACTGGTGGAGTGGCGCTGCGGCTGAAACGCATCCGATGGGCAAGGTCAAACCTCGCAGGCTGCGCGCGGCAAA  
TGGCGTTATCTCCCTCCCGCGAATCGTTT

## SEQ ID 3196

MNSKISSDHTFDTIRLSKMAQLGLCSRREADGHI BQGVTVNGKTA VLQKVPADRIELNKAHQQAARTITLLNKPVGYSQAEGYKSAALITPENWEGDTSRISFDPKHIG  
LAPAGRLDIDSVDGLVLVTDGRILAKQLIGENSGSEKEYLVVRGKLDERGLALNHLSDGDLKRLPAKVEWQNEQLRFLVKQGGKRRIRRMCEIIVGLRVVGLRIRMRKVKLRLPPGK  
NRYLAPGESF

## SEQ ID 3197

ATGAACAGCCCTTTTCAACATCGGTATCGTAACCGCGCCCAACAGCGCGGACATCCAGATACCGCACACAGCTGATTACCTTTTGAAGCAGCAGCGCTTACCGTCTATCTCGAGC  
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GACAGATGATTGAATTTGAAGTCTCTGCTCAATCAGGAATTCGTCTATACACAACGTTTGGAGCGGCTGATTGTCTCCACCCCAACCGGATCGACCGCTTATTCGCTTTCGCGCGCGCGCGC  
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GACCGCGCGCTCATTTTCGACGGAATCTCTTCATCGAGCTGCAAAACCTCGACCGCATCATCTCGCGCTACCAACATCCCTTACGCACTCTACACCGGACGAGTACCAATATTTC  
AAACCTGCGCCAAAACCTGCATCGGCGGAGCAATAGT

## SEQ ID 3198

MNSPFFNIGIVTRPNTPIQDTAHTLITFLKQHGFTVYLDVGVRECCIYTDQTDGCHIVNKTELQYCDLVAVLGDDGTFLSAAREITFPAVPIIGINQGLHFIATQIPREYHTDKLLPV  
LEGKYLAEERILIEAALIREGKTAERALALNDAVLSRGAGQMIEFEVFNQEFVYVTSRDLIVSTPTGSTAYSLAAGGPIIMQAGLHAPTLVPICPQSMTRPIALPDTSEIKLVTGG  
DARVHPDQSGIDVQNLDRILIRRYHNPLRIILHPTDYQVFKTLRQKLEHQBGLV

## SEQ ID 3199

ATGTCGCGCTCTCCCATCATCAACCGCTGATTCTGCAAGCCCGGACAGCGCTCGGAACCTACCTCTTTGACAGGCAAAACACTGACCTGAACATTGCGGGCTGAAACTGGCGG  
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CAGGCTCGAAGCGGACCTCATCTCGGATCGCGTACTGCTCTCGCGGACCTGCTGCTCGCGGACCTGCGACGAAATTTGGCAGCATTCGCGGACGAGTTCGCGGCTGCGCGGCTGCGG  
GCCACCGACATCGGACAGGCAATCAACAAATCGGCAAGCAATCGCGGCAATTCGCGGCAATTCGCGGCAATTCGCGGCAATTCGCGGCAATTCGCGGCAATTCGCGGCAATTCGCGG  
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## SEQ ID 3200

MSALLPIINRLILQSPDSRSELTSPAGKTLFLNLAGLKLGRITFDGLLSAGNGFADTEITFRNSAIRKILQGGEPGAGDIRLBDLILGLAVLSLGLSLRSASDELARIPTQAGIGSR  
ATYDIGHGKIQIGRNABQIGGFSREPESANTGNEALADCLDELISRLRDGVERLNERLDRLEIDIWD

## SEQ ID 3201

ATGCGCGCAGTCCCCCGCCCATATCTCCATCACAGGCTAGGTTACTCGGCTGCGCTGGCACAAAAGTTTACCGACACGCGAGCGCGCTCGCGCCATAAAACCGAGCTGACTT  
CGGACGACATCAACCTGCCATACCTCGACACCTTCGACCTCAACCGTACCGATGCTTTTCAGACGGCATTTGGCGGCGATCAGCGCGCAAAACCGCTGCTGCTCTGCTGCGCGC  
CTCCTTTTGGCGCATACCGCGACACCGTCAACAAATGGGCGAGCTTCCCGCGCGTGCACGTCGCAACACCTGATTTTCAACAGCAGCACAAGCGTTTACCGCGATAAAGCGCGAGAA  
TCCGAGCAACCGCGCACCGGATCCGCAAAACGAGTCCGCGCGCAAAATCTTCCCGCGCAACACACCTGCTCGCAACCGCGTTCGGAACATCGACATCTCGCGCTGGCGCGGCTTT  
ATTGCGCGAAGCGCATCCCGTACGCGCTCTGTCAAAAGCAAAACATCAAGCGCGCAACCGCGCTGCTCAATATCGTCCACCGGACATCGCGCTGCAAAACCTGTTTCAGACGGCAT

CAACCCCGCGCGGCAGCGGCTGAAAAACATTATCGAACCGCGCCACCCGACACCGCGGAATTTTATACGGAAGAGCCGCCAACTCGGCCTGCCCGCGCGGATTTCACCCGAGAC  
AGCGTGGGCAAAATCATCGTACCGTTTGGGATAACGGCTTAAGCCTG

**SEQ ID 3202**

SEQ ID 3202  
MRAVPPPHISITGLGYLGLPLAQKFYRHGSRVAIKRSLTSDIDNLPILHLPDPLNRTDAPQTALWRHDAKPVWFFLLPPSFLAHYADTVKQMAELARACNVQHLIFTSTSVYGDKARE  
CDETAAPDPQTESARQLAAEQHLLDNGVNPIDILRLGGLYCAERHPVSRILVQKQNIQGNRPVNIVRHDLAVENLFQTASNPQGRRLKNIIEPRHPTTRREFYTEAAKGLGLPAPDFSPDD  
SVGKIIRTVCDNGLSL

**SEQ ID 3203**

SEQ ID 3203

ATGCCGCTCTGAACACCAACCGCAAAGCAAAGGAAACAAATGGCGATTCTCAAACCTTGACGAACATCTCTACATCTCCCGCACTGACCAAGCGGATGCGGAACAAATCGCGCAACTTG  
GCATCAAAACCGTCATCTGAACACGCGCCGACCGCGAAGAAAGATCGCAACCGCGACTTCGCCAAATCAACAAGTGGCTGGAAACAAGCAGCGGTACCGGATTCCATCACCAACCGGTAC  
CGCACGCGCATCTCAAAAACACGATGCTGAACCTTTCGCCAACTCATCGGACAAGCGGAATATCCCATCTTGCTTATTGCGGACCGGTACGCGCTGCTCCCTCTGTGGGCTTCGCG  
CGGGCGGCAGAAAGTATGCGCGTTGACGAATCATCCGCGCGGCCAAGCGGCAAGGTGTAATCTGGAATACTCAGAGAGCGGTGGACAACGCCCGCGTC

**SEQ ID 3204**

SEQ ID 3204  
MPSEHQPGQSGNKAIALKLDHLIYSPQLTKADAEQIAQLGIKTVICNRPDREESQPDFAQIKQWLEQAGVTGFHHQPVTTARDIQKHDVETFRQLIGQAEYFLLAYCRTGRCSLLWGFR  
RAAEGMPVDEIIRRAQAAGVNLENFRERLDAEV

**SEQ ID 3205**

SEQ ID 3205

TTTCCACAAATTTCAGCGGTGAATCATCCACAGCCCAAACACAGATGTAGGCGAAGCCGATCGGAATCAGCACTTTCCAGCCCAAACGCATGATTGGTCGTAGCGGTAGCGTGGGAAG  
GTTGCACGAATCCACAGATACCACTAGCAGCACGCCGCCATTTCACGAACATCCGAATGCGGAAGGCGTACCGACANTGCCCCAGCTTTGCGGGAAACGGAGACAACACGCCGCCGAGGA  
GATCAGCGATGTGCGCGCGGCAATCAGAATCATGAAATGTATTTCGGCAAGGAAGAACACGCCGGAATGCAAAGCCGGAGTATTTCGACGTGTGTGTCGGCAACGATTTTCAGACTCGCOCTC  
TGCCACGCTCAAACCGTGC GCGGTGGTTTCGGCAACGCCGGAAATCAGATAGACGATAGAGATTTGGGAACAGCGGCAGCCAGTTCACAGAGAACAACAGAACCCGCCCGGATGCTTTTGGC  
TGCGCGGCAACGATGTGCGGAAGTTCATGCTGCCCGATACCAATCAACGCACACCGAGCGCGGCACTATGGCAATCTCGTAGGAAGAATGCTTTGCCCGGAACACGCAATGCACCTGAACGA  
ACGAAATATTTCGAGTTTGAAGCCCGAGCCCGGATATCAGCGCTTAAACCGACAGCGGGTAATCATCAGGATGTACAAAGCCCGGATATTCATTTGGTTCAGACCCCAATCTCTCGTTAA  
CGGAATCACCGCCCGAGCCCGGAAAGCGGGCGGACGACATATTCGGCGCGGATGTAGAAATAGGCTTTGTTTCGAGCTTCGGACGGGTACCTCTTTAAACAAGAGTTTGAACACGTG  
GCAATACCGCTGAAATCAGACCCCGCGCGGCTGTACGTTCCGGCGCGAGCGGAAGTCGATAAAGCCGATGACTTTACGTTCGAAATACGTCAGGTAGGCAACCGTGCAGATCAGCGGAATCA  
GGAATTCAGCATGTTTTCAGCATGACGGATACCAACAGCCTACGGTGATGCCCAAATCGCCGACAGCGAGCGTTGCGGCAAGAGGTTTGGGAACCAATCTCTGCATTAATCAA

**SEQ ID 3206**

SEQ ID 3206  
 FPGIQR\*NIHPHAQNHDVGEADRNQHFPAQTHDLVVAWVEGCTNPQIPVQHRRHFHEHPECCGRRTDNAPALRRRRQPAEEHQRQCRGNQHNHNVFGKEBQRECKAGVFDVVSGNDFRLAL  
 CHVKRCAVFGGNGGNGQIDDEWQRPVPRPREHTARDAPCLRGNDVGEVHAARYHHNAHQRGTHGNLVGNALRGSTHCTQERTIPGVGSPARDNHAVNRQGRNEQDVQKADIDIGHPFFVK  
 RNHRPRREFGRGRNRHADVE\*GFVQLRTGYLFRQEPFHVHGKRLNQTPRAGYVRADAKLHKADDFTFEIRQVGNQGQNRQNDHDFDDDGTHQAYGDAQIAQTERCGKEVLEPFLHNQ

**SEQ ID 3207**

SEQ ID 3207

GTGCGGCATCGGTGTGTGTGTCGGGATCGGTACGGCATTTTCATTTCGCGCCATTATTGGTCGCGCTGATAAATTTGTATAACGCCCCCTTCGCGCAAAACAAACGGCAAAATTTGCCGCGT  
CCGCGCGATATGTAAAAAATCGGGGGAATGCCGACACTTCCCCCGATGCGGCCGCCAACCCGGAACCGAGGTTGCGGTGCAAACTTCGCGGTGACAACCTCAATCCGCGCCCAACGCCG  
TACCAGCGCGCGGTGCCGCGCCCTGCAGTCGTTATACATACCGGCCGCTTCGAGGGCCACGGCAGCAGTCCGCGCCCGTGTTCCTTCAAGGTGCGGCAGTTTCGGGCGAGGCGCGCAC  
AAATCGCGGGCGGCTTAACCGCGGTGCTCAACGGCGGGGTGTGAGTTTCGCGCACGCCGTGAGCATCAAAACAGGCATTGCGGTACACAGGTTTTCATATTTAAAGCTTTCGACATAG  
CGCACCTTCTCTTTTCCTCGCGCGCGCCTTTTGCGCCGTGATACGCGCGCGAGCATTTGCGGGCGGTGTTCGCGCTGTTCGACCGCGCGCGCTTTCGAGGCGGTTCGGAACCTTCGACACCG  
CCGCACTGTATCCGCGACGGTATTGCGCGCGCCCTTCGCGCTGCCAGTCCGCAAGAACCGGCAAGACCGGATGTCGCGCAAAAATAGCAGCGGCTTCCAATTTTCAGCAAGCCCCAATCATTTA  
CGCTTCGCGCGCGCTGTTTTCGCCGTGCGCGCAAGCTGCGCAGACCGGTAAACCGGTTCGCGCGGGGACGAAGGCACGGCTTTCGCCCAATCAGCTTGGACGGCGCAGAGTAGCCGTCA  
ATGTTCGCGAGGGTCAACGGCATGATGGATACCATATTGCCCTGATTGCCGCCCAAGCCCAAGATCTGCCTTCGCGCTTTCGCGCAACGAAGACAGTGTCCGCGCCCGCGCGCG  
GTTTGACCGCGATCGACCGTATGCGGGGGCTTCGAGTTTCGTCGCAAAACCGGACAT

**SEQ ID 3208**

SEQ ID 3208  
VRRHLLSGSVRRHFPRPLVRLILYNAPPAQTKRQKFAASARYVKNRGECRHFPRCGRPGTDSGVANFRLTTQSAFNARTSAPCRALQSLYTPAAFRHGSTSAFVPSRCGSGQGRT  
KSAGGLTAVVNGGVEFAHVASIKTGLIAVHRFPNDPKRLHIAHPPFFLARLLRLIRGGFAGVGVFDRGGFEAFNLRHRTVTSATVLRFPQLPRNGEERDCGQNKQLRPLTQQSPNHL  
RLARALFRRGGNVGRQVTPPFGGRRRHGAANQLGRPEVAVNVRKVRDDGYHIALAAQQAQDSAFRVFADNEEHVSAAPARFDRDAAVCGGFEFRQTRH

**SEQ ID 3209**

SEQ ID 3209

TTGGCTGCCCACTCGTTTCAGCCCTGTAATCCAAAGGAGTATGCCCGTGACCCGCACTTGCAAAAAACAATACTTTACACCCGCATCATCGACGCCAGCCCTTGCGCTTTTCAACGAGGAAGGCG  
AGCGCAACATCAGCAACCAACCATATCGCGCGCATTTTGGGCATCAGTCCGGGCAATCTTTATTACCACTTCGCCAACAAAGACGAAATCATCGTCCAACCTCTTCAAAGCTTACAGCGGAAGC  
CCTGTTGGCATACCTGAATGAAGCCGFGTTGCCCTCTGATGTGGGAAGACTCTATCAACTATATGCGACGGCAATTACGATGTCTATGTGGGAATACCGCTTCTCTTTAGCGCGGTAAACACC  
CTACTTGGCGCGCAGTGC CGGAATTTGTGTGGCGGAACACAAATACCTTTACCCAAAGCCAAAGTCTCGCGCTTCTGACTCAACTCTGACCGCTGACCGGCTGAACGCTCAACGCGCGGACC  
AAACCGCTATGAACGACCTCGCGCTCAATATGTGGATGGTTGACGAAATCTGTGTCGACTTCGACAGCTCCCTGCGCGGCGGTACCAAGCTGACCGGAAGACTCCAAAGCACGCGGCGTCCG  
TCGTACTCTTAAAGCTCTCTTCGCCCTATCTTTTGGCCGAACCCGCGGGAATACGACCGCAAATCGGCAACGGCAACCCG

**SEQ ID 3210**

SEQ ID 3210  
 LAAHFQVQNPSPMPVTRIAKNTNTYTRIIDASLALFNEEGERNISTNHIAAHLGISPGNLYYHFRNKDEITVQLFKRYSEALLAYINEAVLPDVEDSINTMAGTYDVMWEYRFLPSDVNT  
 LLARSAELLGEHNTTQAKVSPLLVKLLTQNLGLNVINADQTANNDLAVNMWMTVTKYWFDPDSSLGRGRTKLTEDSKARGVRTLSSLRPYLLPEHRABYDRKIGNGNP

SEQ ID 3211

SEQ ID 3211  
TTGGCTCGCTCACCATGCGAGCCGTCGCCCTTGGTGTGGTGCTTGGAAAAATACAGTATGAGTGTGGTCAAATCACACAAGGCCGCTGTGAAAACGCAGCACACTTCAATTCAAATACAGTTA  
AAGCTCAAAACCTGCAACCCATCCGATACCGAAGCAGCACTCACCCCTACAACACTTTTGGCGCTGCACGCCCAAGCCCGGGCCCTTATCGCGCTTAAACACGCGCGAGCAATTCGCGACAT  
CGTCCGACGCGCGAGTCTGACCGCGATCTGTTTTATGGCTGGCGCGCGCAGCAACATCCTTTTGATGCAGGATTACGACGGCTTGGTCGTCCATATGAAAAACAAGGCCATACGCGAG  
ATTGCGGCTCTAGACGCGCATGGTTCTGATTGAAGCGCAGGCGGGCGAAATTTGGCAGGATTCGTGTGTCACACGCTCGCGCTGGGTTTGAGCGGTTTGGAAAAACCTGAGCGCTGATTCGCG  
GTACGGTCGCGCGCTGCCCGCTGCAGAACATCGGCGCATACGGCGTGGAGCGGAAAGATGTGATTCACAGCGTGCCTGCTCGATTGGATACGGAAACCTTTGTAACCTTTCACATGC  
CGACTCGCGCTCTCGCTACCGCGAAAGCCGTGTTCAAGCAGGAAGGCGAAAGGGCGTTATGTGATTTGTTTCGGTCGTATTGTCATTAAAAACGCATTTTGTGCCGAATCTGGGCGATCGGGCGT  
TTGGCGCGGAAGTTGCGCAATTGAGTGCAGGTAGGGAGGCAACGGCGAAAGACGTTTCCGATCGCGTATCCCGCATCCGCAACACGAAATACCGCGCATCCCGACCGGAACTTTGGCGAATGTG  
GCAGTTTCTTTAAAAACCCCGTCTGCACGCGGAAAAAGCCGCCACCCCTGTGTCAGCGCGCATCCCGATATCGCGCATATCCGACGATATCCGACCGCGAGCTTTGGCGAATGTG  
GATCGACCAATGCCGCTCTGAAGGCGTTCCAAATCGGCGGTGCGCGGTACACAGTAAACAGGCATATGGTTTTGGTAAACAAAAACAACGCCTCGGCAACGATGTCCGCGAGTTGCGCGCA  
CATCAAAATTACAGCATTTGCTTCTGCTTTCAGTATAGATTACACGCCGAACCAATTGGCTGCCCACTTCGTTACGCGT

SEQ ID 3212

SEQ ID 3212  
LPRSPQSPQPCGAWKNTVWSWSNHTRPSENAAHFNSNTVKAQTMQPIRYRTDLTPYNTFGLHAQARAFIALKHADELRLDIVRLPEFDRDVTVLWLGGSNILLMQDYDGLVVHMENKIGRE  
IARSDGMVLEIAQAGEIWHDFVLHTVALGSLGENLSLIPOTYGASPVQNTGAYGVEAKDVIVHSVRCFDLDTETFFVTLNADCRPAYRESLFPQEGKGKRYIVTSVVFALKTHFPVNLGYGD  
LAAKVAELSGAGREATAKQVSDAYSATRNKSLPDPKVLGNVGSFFKNPVVSAEKAAATLLQRHPDMFPYQPDGVSKLAAAGWLIDQCRLKGFQIGGAHVHDQALVVLNKNINASANDVRQLAQ  
HIKFTVPARFOVELHAEPNWLPTSFSL



## SEQ ID 3213

ATGCTGTGGCGCAGGTCCGCGAGGTGGGCATCGGTTTCGTGATACCGTGATGGCGGCGGTGGCGCAAGGAAGATTGGCGCGGTGGCTTTGGGCAGCAGCGGTTGGCCACGGTTT  
ATATTACCTTTATGGGCATTATGGCGGCGCTGAACCCGATGATGCGCCAGCTTTACGGCGCGGTAAAACCGGTGAAGCAGCGGAAACGGGGCGCAGGGGATTGGTTGCGGCTGATT  
GGGGATTTCGGCATGATTTTGATGTGGCGCGGATACGCCGTTCCGCACTGGCTGACTTTGAGCGATTATGTGAAGGCACAATGGCGCAGTATGCTGTTACCCAGCTTGGCGATG  
CCGCGCGCAATGTACACCGCGCAGTCAACGCTACGCTTCAGGCTGAACCGCCGCGCCCTGATTTATGTTGGTCAGCTTTGGCGCGTTTGTTGTGAACGTGCGCGTGAACATATATTTTCG  
TTTACGGCAAAATTCGGTATGCCCCCTTTGGGTGGCGCAGGTTCGCGCGTGGCGCAATGGCGGTGTTTGGTTTCAGCGCGCTGGCATTTGGAATTTATATGCCAAGGAAAAATCTTCG  
CCCCCTCGGACTGACAGCGAAATTCGGAACCCGATTTGGCGGTGTTCAACAGATTGGAAAAATCGCGCGCCCATCGGGCTGCTTATTTTTTGAAGCCAGCGCGTTTCGTTTATC  
GTGTTTTGATTGCGCCTTTTCGGCAGGATTATGTGGCGCGCAGCAGGTGCGGATCAGTTTGTCCGGGATTCCTATATGATTCCGCAAGCGTCGCGCTCGCAGGGACGGTGGCATCG  
GCTTTTCGCTTTGGCGCGCGCGCAATTTTCGCGGCGCGCTTATATTTTCAGGAGTGTCTGGTGTGCGGCTGGTGTCTGCGGATTAACCGTCTTCTTGTGATTATTCGCTTCGCGCT  
GGCAAGCATGTACACAGTATGTCGCGAGTTTAAAGCATGCTCCACCGTCTGCTGTTTCGCGCGCTGTTTCAACCGCAGACTTCAACCAATGATGCGCTCTATGCGCTGCGCGG  
TACAAAGTCAACAGGTGCGCATGTTTATCCACGCGCGCGCTTCTGGGCGTGGCGCTGCTGCGCGCTATCTGCTGCGCTACCGTTTCGATATGGCATTTACGGCTTCTGGAAGCGCAT  
TGATTGCTGCTCACCATCGCAGCGCTGCGCTTGTGTGTGCTTGGAAAAATACAGTATGAGTTGGTCAAATCACACAAGCGCTC

## SEQ ID 3214

MLLAQVAVGIGFVDTVMAGGAGKEDLAVALGSSAFATVYITPMGMAALNPMIAQLYAGCTGEAGETGRQGIWGLILGIPGMILMAAITPFRNHLFLSDYVEGTHAQYMLFTSLAM  
PAAMVHRLHAYASSLNRPRLIMLVSAFVNLVPLNYIFVYKFPMPALGAGCGVATMAVWFPFSAALAIWYIAKEKFRFPGLTAKFGRPDWAVFKQIWKIGAPIGLSYFLEASAFSI  
VFLIAPFPGEDYVAAQQVIGISLGLYMIPOSVSAGTVIRIPLSLRREP SRARYISGVSLVSGVLAIVITVLSVLFRSLASHMYNDPAVLSTASTVLLFAGLPQADFTQCIASIALRG  
YKVTKVPFIHAAAFWCGLLPGYLLAYRFDGIGYGFWTALIASLTAAVALVWLEKYSMELVKSHAV

## SEQ ID 3215

ATGTGCACCATTTATTTCTCATCACTTCCCGCTGCGGTTTTTTTTGTGTTTCAGACGGCATTTTTTATTGACTGAACACTTATGCTGCTCGACCTCGACCGCTTTTCTTTTCGGTCTTCC

## SEQ ID 3216

KCTIISHFPLPFFLPQTAPLITLHLCSTSTAFPPFS

## SEQ ID 3217

GTGATGAGAAATAATGGTGCACATTATATAGTAAAAATACCGTCCGTCAGACGGCGGATACGGGGTATATAAGTATATTAGATTGTGTGATTTTATGTTAAAGTTTGGTTTAAAG  
ACTTGACGGCATTTAGCGCGTCGGACAGGGCTGTTTCGATTCTGAATCGGAAGGAAGCATCGCGGTTT

## SEQ ID 3218

VHRRNGAHTVKNVPSIDGGYGVYKVSVCVYFMVKFGFNDLIALSRRTGAVRILNRKEASP

## SEQ ID 3219

TTGTTAATCCGCTATACCCGCTGTAAAAACGGAGAGACAGAGGACGGCAGTAAGGTTTGGCGTCTCTTTTTCAGTTTGGGTGGAATGCGGCT

## SEQ ID 3220

LLIRYTRCKNGEGORTAVRFAVLFTKLRHNA

## SEQ ID 3221

ATGAGAAATCGCCTTCTGTTTATCTGTAAACACAAAGACTGCCCGATCCGCAATCAGACGGCATCTTTGCCGCAACGCATACCGCGCTGTCAAACGGCGATGCTTCTTCCGATTC  
AGAAATCCGAACACCGCTGTCCGACGGCTCAATGCCGTCAAGTCGTTAAACCAAACTTTACCATAAAATACACACAATC

## SEQ ID 3222

MRICLLFPVWTKDCPIRNTASLPQRITPLSKRRCLPTIQNPNSPCPTAQCRQVVKTKLYHKIHTI

## SEQ ID 3223

ATGPTCCGGAAGCTGCCATGTCTGCATGAGAAATCGCCTTCTGTTTATCTGTAAACACAAAGACTGCCCGATCCGCAATCAGACGGCATCTTTGCCGCAACGCATACCGCGCTGTCA  
AAACGGCGATGCTTCTTCCGATTGAGAAATCCGAACACGCCCTGTCCGACGGCTCAATGCCGTCAAGTCGT

## SEQ ID 3224

MFRKLPLCHENLPSVLSCKHRLPDPQSDGIFAATHAAVKTAMLPSDSEBQLPSDGSMPSSR

## SEQ ID 3225

ATGCAGACATGCGAGCTTCCGGAACATATGCCGACGTACTGCCACGAACGCGCGGACGCTTGAAAGCGCGCGGAGCAGTTGTTGGCAGCTGTTCCGCTACACGGTTATGAAGTGGTAC  
AGCCTCCGCTGATGGAGTACGCACATTTCCCTGCTGACGCATATCGATCGGGGCTTTCACTGAAACCAATTTTGTAAACGGACAGGCTCAGCGGAGGAGTGGGCATACGCGCGACAT  
CAGCGCGCAGGTGGCGCTATCGATGCCATCTTTTGTCCGCAACCAAGGGAATTAACCGGTTGTGTTATGCGCGTCCGCTGTTGCACGCGCAGCGGAGCGGCTGCGGAATATGCGCGAA  
CCCTTCAGGCGAGGGCGGAAATGTACGGTTTTCGCGCATCCGTGGCGACATCGAGCTGATAGACCTTATGCTGAAAGCATGAAATTTGCCGATATGGGCAAGTGTCTGCTTTCGCTGG  
GGCATATCGGCATATTCGCGCCTTGTCCGATGCGCGCATTTGGATCGGGGAGTCGCGAGCGCTGCTTGCCTTGTATGATCAGGATAAAGATACCGGGTCCGTCGAAGCGCAGGTCAAGGC  
TTGGAAGCTGGACGCTATGTGGGCAAAAGCATTTCTGCTGCTGCCGCGCTGTACGCGCGGCGTGAAGTGTGTTCCGACCGCGCGGAGCGGTTGCCGATTTGTGCGCGTGGCGCGCG  
TTGGAAGCATTCAGCGCGGTGTGCGACCATTTCCCGATAATGAATCCATATCGACTTGTCCGAGCTGCGCGTGCACAAATACCAACAGGCTTCTGATGCGCGCTATGCGCGCGATT  
TCCACGACGCGGTGCGCGCGCGCGCGGCTTATGACGGATTTGGCGGATTTTCGCGAGGCGCGCGCGGCAACGGGATTCAGTTTCGACTTACGCGAGCTTTATCGGGCGTTTGGCGCGGCT  
CGAAGCGCAGCGCGCGCTGTTGGTGTGATGCGGAAGATGCAGAAGCGCGCGCGGCAAGCGGTGCGAGCCTTGCCTGAACAAGGCGAGTGTGCTGATGACTACGGTATCGGACACAATGTT  
TCGGAAGAGCTTCGAGCGCTGTGAAAGAGCAGCGCGGTTGGCAGGTCGTGAAACG

## SEQ ID 3226

MYTWQLPEHIADVLPTNARQLESARBQLLALFRVHYELVQPPIMEYASHLTHIDAGLSLKTILVTDRLSGRQLGIRADITPQVARIDAHLLSANQINRLCYAGFVLHAQPDGLPMRE  
PLQAGAEHYGFADIRGDIELIDMLKSMKIADMGVLLSLGHIGIPRALSDAHLDAQSAALLALMDKDTGSVEAQVKAWKLDGMWAKAFSLPLRYGREGVLSDARGRLPDLASVGG  
LDELQAVCDAPDNRIHIDLSELVDNYHTGLLYAAYAADFDAVARGGRYDLGGYFGRARPATGFSFDLRSFIRLPAVERQPAVLVDAEDAEAREAVLRBQGCQVVDYIGIN  
SEELAGRLKTKTGVWQVVKR

## SEQ ID 3227

GTGTCGATACCGTAGTCAATCAGACACACTGCCCTTGTTCACGCAAGGCTTCGACCGCTTCGCGCGCGCTTCTGCATCTTCCGATCGACCAACAGCGGGGCTGCCGTTGACGCGG  
GGCAACCGCGGATAAAGCTGCG

## SEQ ID 3228

VSDTVNHDTLPLFTQGFDRFARRFCIFRIDQHGGLPFDGGTFDKAA

## SEQ ID 3229

ATGGCTATGGCTAAAAATGTTGTAGTAATCGCGCAGTGGGCGCAGAGGTAAGGTAAATCGTTGACTGGCTGGCGGAAGAGCGCGCGCTGTCGCTTCCAAGCGCGCCACA  
ATCGCGGCCATACCTTGGTCTGCGCGGCAAAAAACCTTTTGGCGCTGATTCCGAGCGGTATCTGCACGAAGGATTGGATTGCTTCATCGGTTCGCGCGCTGTCGTTTCCCGCGAAGC  
CTGTTGGCGGAAATCGACAGTGAACCGCGCAGCGGTGAAAAACGTCGAAGCGCGCTGAAAAATCGCGCGACCTTGCCTGATCTGCTTACCATATCGCGCTCGACCAAGCGCGC  
GAAGCATCGCGCGCAAGGCAAAATCGGACGACCGCGCGCGCATCGCGCTGCTTACGAAGACAAGTGGCAGCGCGCGGCAATTCGCGCGCGCGGATTGCTGCTTCTGAAACTGC  
GTGAAAACTGGATGCGCTCTTCTGCTATTACACGTCACCTCAATACCTGCTAAGCGCGGACCGGTTAAAGCGGAAGAGCTGATGCGCGGTTATCGAAAAAGTTCGCGCGCGCATTCG  
GCGGATGATTGCGGAGCTGTCGCGCTGTTGAACGAAAAAACAACGCGGCAAACTGCTGTTTGAAGCGCGCAAGGTGCGTGTGTTGGACATCGACTACGGCATTACCCCTTCTGTT

ACCTCGTCCAATGCTCTCGCGCGCGCGCTTCGCGAGCGCGCGGCTAGGTCCTCAATGCTGGATTATGTTTGGGCATCGTCAAAGCCTATACCACGGCGTGGTTTCGGGCGCGTTCC  
CGACCGAATGTTTCGACGAAGTAGGCGCAGGTTTGGCGGAGCGCGGACACGAATTCGGTTTCGGTAACCGCGCGCGCGCGCTGCGGCTGGTTTGTATGCCCGCGCCCTGAAACGCTCCAT  
CCAAATCAACCGGCAATTCGGTATGTCATTACCAAACTCGATGTAATGGACGGCGTTGAAACCATCAATATCTGCGTGGCTACGAATTCGACGGCGCGGCAAAACCGACATCTTCGCT  
TGGGTTTCGGATGCGGTGGAAACCTGCAAAACGATTTACGAAACCATGCCCGCTGGCGCGAATCGACTGTCGCGCTGAAAGCTACGACGCTATGCTGCCAATGCCAAAGCATATTTGA  
AACGGATTGAAGAAGTCTCGCGCGCGCGGTCGCCATGCTCTCACCGGCCCGGACCGCGAAGAAACGATTTGCTGCTATCATCCGTTCCGA

**SEQ ID 3230**

MAMANNVVIGAGWDEGKGIWDLAEAGGVVRFQGGHNAGHTLVVGGKKTILRLIPSGILHEGLDCFTGSGVVVSPALLGEIDELNAAGVKNVEGRKLIAPTCLILPYHIALDQAR  
EASRGKGIKTGTRGIGPAYEDKVARRAIRAADLLHPEKLEKLDALVAYNVQLQVHNAGPVKAEDVMAVIEKVAPRIAPMLADVSRVLEKNEKNGEKLIFEGAQALLDIDVGYTFPV  
TSSNLAGAASAGAVGQMLDYVLGIVKAYTTRVSGGFPFTELFDEVGAGLAERGHEFGSVTGRARRCGWFDAAALKRSIQINGISGMCITKLJVDMDGVETINICVGYELPGGKTOLIP  
CGSDAVETCKPIYETMPGWRSTVGVKSYDALPANAKAYLKRIEEVCGAPVAIVSTGPDRETFVLEHPPA

**SEQ ID 3231**

GTGAAACGCATTTTCTGTTTTCGGTACCAATATCGCTGTTTGGTTCGTAATCAACATTTGTTTGGCGGTTTCGGCATCAACAGCGGGCGCGCGGCGAGCTGTTGGCGTATTTCG  
CCGTCGTCGGCTTCACTGGTTTCGATTATTCGCTGCTGATGTCAAATTTATCGCCAAACATCGTTCGGTTCGGAAGTTCATCGACACCGCGCACCGAAGAAGAGCTGGCTTCGAA  
CACTGTCGAAGCCCAAGCGCGCAATGGAATTCGAAACCGCAGAAGTCGCATCTACCACTCCCGCAACCCAAATGCTTTGCCACGGCGCATCGAGAAACAGCTCCCTGATCGCGCTC  
AGCACCCTGTTGCTCGACCATATGACGCGGACGAAGTGAAGCGGTTTGGCGCAGCAATGGCGCAGCTCGGCAACGGCGCATGTTACGCTGACGCTGATTCAGGCGTGGTCAATA  
CCTTTGTCGTTTCTCTGTCGCGCATTTATGCCAACCTGATTGCCGGAACCAACGACGGCAGCCAGCTCCAGGGAATTTATTTCTAGTCAGCATGTTATCCAAATCTGTTTCGGCTTCCT  
TGCCAGCTGATTGTCATGTTGTTAGCGCGCAACCGCAATACCGCGCAGCGCGCGCGGCAAACTGGTTCGGCGCACCGGAAATGATTTCCGCTGCAAAAGCTTAAAGGCAACCGG  
GTCGATTTCGCCGAAGAAATGAACGCAATGGGATCGCGGAGATACGCGGACTCCCTGCTCAGCACCCACCTTCGCTGGACAACCGAATCGCGGCTCAATCGCTT

**SEQ ID 3232**

VKRIFPLATNIAVLVIVINIVLAVLGINSRGAGSLLAYSAVVFTGSIISLLMSKPIAKQSVGAVIDTPRTEEEAWLLNTVEAQARQWNLKTFEVALIYHSPFNATFAGSRNSSLIIV  
STGLLDHMTREDEVAHLAHEMAHVNGDMVTLTIQGVVNTFVVLRSRIANLIARNNDGSGSGTFLVSMVFQILFGLASLIVMWFPSRQRYRBRADAGAALVGPAPKMSIALQRLKGNP  
VDLPEENAMGIAQDTRDLSLSTHPSLDNRIRLKL

**SEQ ID 3233**

TTGCAAGCAATGTTTTCATACCTTTGCCGAGCTGATATTCACAAGCGGCAACTTTTGGGACAATCCCAAAATTTCAAACATCACACCTTACCAAAAAGGAACATCCG

**SEQ ID 3234**

LQANVLTFAEPDIHKAATFNDPQNFKTSHPKKEEP

**SEQ ID 3235**

GTGATCCTTTTAAATGTTTATTGGAATCAAAACAGATGTTTACGATTCTACACGGCTTGGCGCAATAGTTCAAAAACCACTGCACAACTGCCATTTGCAAGCAATGTTTGCATAC  
CTTTGCCGAGCTGATATTCACAAGCGGCAACTTTTGGGACAATCCCAAAATTTCAAACATCACACCTTACCAAAAAGGAACATCCGTAAGACGCAATTTTCGTTTTCGGCTACCA  
ATATCGCTGTTTTCGTCGTAATCAACATTTTTCGGGCTTTCGGCATCAACAGCGGGCGCGCGCGGCGAGCTGTTGGCGTATTCGCGCTGTCGCGCTTCACTGGTTTCGATTATTTTC  
GCTGCTGATGTCAAATTTATTCGCAAAACATCGGTCGGTTCGGAAGTTCATCGACACGCGCGCACCGCAAGAGAAGCTTGGCTTTCGAACACTGTCGAAGCCCAAGCGCGCAATGGAAT  
CTGAAACCGCCAGAAGTCGCCATCTACCACTCCCGCAACCAATGCTTTGCCACGGGCGCATCGAGAAACAGCTCCCTGATCGCGCTCAGCACCGGTTTCTGTCGACCATATGACGCGCG  
ACGAAGTGGAAAGCCGTGTTGGCGCACGAAATGGCGCAGCTCGGCAACGGCGCATGTTACGCTGACGCTGATTCAGGCGTGGTCAATACCTTTGCTGCTGTCGTCGCGCATTTATTC  
CAACCTGATTGCCGGAACCAACGACGCGAGCTCCAGGGAATTTATTTCTAGTCAGCATGTTATCCAAATCTGTTTCGCTTCCCTGCCAGCTGATTGTCATGTTGTTTCAGCGCG  
CAACGCAATACCGCGCGCAGCGGCGCGGCAAACTGTTGGCGCACCGGAAATGATTTCGCCCTTCAAGGCT

**SEQ ID 3236**

VILLNVFIGIKQVYDSTRLAGIVQKPTAQTAICKQMFCLPLSLIFTRRLQFGTIPKISKHHTLPKRNIRETHFSVFGYQYRCFGRNQHCFGGSGHQFPGRGQPVGVFRRRLHWFDF  
AADVQIYRQTIGRGCSHRHAHRRRLASEHCRSPSAAMESENARSLHLPLRPTQCLCHGRIRKQLPDRRQHRFARPYDARRSGSRVGARNGARRRRHGYADADSRGQYLKRVFVAHYC  
QPDCKPQRQPVPGNLFPSGHGIPNPFVRLPCQPDCHVQPPTRIPIRRRGKGTGRRTENDFRPAKA

**SEQ ID 3237**

ATGAAGCAATTAATTTAGGCGCACCGGCGCGGCAAGGCACTCAGGCGCAATTCATCACCGCGCGCTTCGGCATTCGCAAAATCTCTACCGCGACATGCTCCGTGCCGCGATTAAAG  
CAGGCGACCCCTTGGGTTTGAAGCGAAAAATCATCGATGAAGCGGCTTGGTTCGCGACGACATCATATTCGGCATGGTCAAGAACGATCGCGCAAGACGACTGCAAAAACGGTTT  
CCTGTTGACGCTTTCCCGCTACATTGGCGCAAGCGGAGCGATGGTGAAGCAGGCGTGGGTTTGGACGCGGTCGTTGAAATCGACGATTCGACAGCGGTGATTCGACCGCGATGAGC  
GCGCGCGCTGCAATTTGGCTTCGCGCTACTTACCACTGTTACCTACAATCCGCTTAAACCGAAGGCAAGACGATTAACCGCGCAAGATTGATTACGCGGACGACGACAAAGAG  
AAACCGTGAAACAGCTCTTCCGCTTTACCAAGAGCAACCGAAGTTTGGTGTGATTTTACAGCAAGCTGGAAGGCGAACACGCGCGCAATACATCAAAGTTCAGCGGTACCAAGCAGT  
AGAAGCTGTGAAGCGCAAGTATTGGCGCATTTGGCAAA

**SEQ ID 3238**

MKALLLAPGAGKGTQAFITAAPGIPQISTGDMRLAAIKAGTFLGLEAKKIIDEGLVRDDIIIGMVKERIAQDDCKNGFLFDGFPRTLAQAEAMVEAGVGLDAVVEIDVSDSVIVDRMS  
GRVHLASGRYTHVYTPNPKTEGKDDVTGEDLIQRDDKEETVKRLAVYHEQTEVLVDFYSKLEGEHAPKYIKVDGTQAVEAVKAEVLGALGK

**SEQ ID 3239**

ATGTTTGAATAAAGAAAAATCAGATGCTTGTATTCGCCCTCGCGCAGAAATGGAGACGGTGCTCTGCTGCTCATTTTGTGTTTAAATCAACTATATATAACTGAT

**SEQ ID 3240**

MFENKRIKRLYSLRRNGDALSSHFQNFQIYTD

**SEQ ID 3241**

ATGAAGCAATTAATTTAGGCGCACCGGCGCGGCAAGGCACTCAGGCGCAATTCATCACCGCGCGCTTCGGCATTCGCAAAATCTCTACCGCGACATGCTCCGTGCCGCGATTAAAG  
CAGGCGACCCCTTGGGTTTGAAGCGAAAAATCATCGATGAAGCGGCTTGGTTCGCGACGACATCATATTCGGCATGGTCAAGAACGATCGCGCAAGACGACTGCAAAAACGGTTT  
CCTGTTGACGCTTTCCCGCTACATTGGCGCAAGCGGAGCGATGGTGAAGCAGGCGTGGGTTTGGACGCGGTCGTTGAAATCGACGATTCGACAGCGGTGATTCGACCGCGATGAGC  
GCGCGCGCTGCAATTTGGCTTCGCGCTACTTACCACTGTTACCTACAATCCGCTTAAACCGAAGGCAAGACGATTAACCGCGCAAGATTGATTACGCGGACGACGACAAAGAG  
AAACCGTGAAACAGCTCTTCCGCTTTACCAAGAGCAACCGAAGTTTGGTGTGATTTTACAGCAAGCTGGAAGGCGAACACGCGCGCAATACATCAAAGTTCAGCGGTACCAAGCAGT  
AGAAGCTGTGAAGCGCAAGTATTGGCGCATTTGGCAAA

**SEQ ID 3242**

MKMPYRSGQPMFHPAGRLRLTSGSGGIFIGRLFFATALHKAFCVTRTAIIACHRGRLMPLKFPQPRRSVLMCDFRGYEEPMVKRPVVVIARNRHNGKLVTVVPLSSTPEVPLADCH  
HKMSENPLPKPHIQCRKCDMTATVGLARLDYKPKGRDRCTPIISEEDFOAVKTAVAKAFKLY

**SEQ ID 3243**

AGCTCCCGCCAGTTCAATAATGCCATCAACGCAACCGCGCGGCAATTTTCGGTATGACGCGGAGATGCACACGTTTTCAGGCAACCGGCATCGGCTTTGACGCGCAACCGATACGCTT  
GCACCGTTTGTGTTGGCGACGCGGTTTGTCCGCTTCGAGGCGCAAGCTGCCAATGTGTTTCGGATTACACGCGCGGCGAGCAAGCGGCATGGCTGGTTTTCGCAACGGTTCGCGAAC  
GGCGCAGATAGAAATCAGTATGATAAATACCGACCGCGCGACGAGCAGGCGGTTTGAAGCGCTCTGAACGCGCTCCCTGCGCATGCTGCGGTTGTCCAGTTTGGACGCGAGACT  
TTCCGCAATCCAGCGGCTTTTCAGAAATCGACGCGGATCTGCTGATTCAAACCTTTTCAGGTCAAACAGGTTGCCAATACCGCGCAACACTTTCCACATCGGACGCTGAATCCCGGAAGCT  
TGTACCAAGCGGTTGAAGAGATTGCAGACGCGCTTCATATTTGATGAAGCTGCTGATTTTCGGTAAACGCGCAATCGGACGAATACGTCGACACGCTCCAGCAGCGTTTTCGCTGACAA

ACGGCGTAAACGCCATCAOGCTTTTCGGCTGTTTCAACGCGGCTACGGCTTTTGCACCGTCAACCGTATCGATTTCAGGCTCGACGTTGAGCAGCAAGACTGCGCTGTTTCGGCGTGTTC  
 CATTTCGGCAACCGCTCTCGCCGAGTTTACACCCAATACGTCGCGACCGAGCGTGTGGCGGCTTCGGCGCAAAATGCCAGCACTGCGCGGTCGGCTCCGCCAATCTTTCGGCGCGGCA  
 TAAATGCGCGGTAATCAGATGTTTTCGACTTCGCAACCAAAATCACCGCTGCTTTTCAGCGTTTTCAGGCTGCGGTAACGCGATGTTTCGCAATCGGCAGACAGGTTTTCAGAC  
 GGCCTGCCCACTCTGTCGGGATGTCGGCTTCTTGAGACAGAAAGCGCATATAACAATTTCTTCTTACTGCGCGCAATACGCTCAAGGCCATACGCTGTTTCGGCGCGCGCGCAGCGGGC  
 GGTGAGGAGCGGCTGTTTTCGCAAGTTTCGCAACGCTACCAATACGGCATCGTTGTGACGCAAAAGATTCAATCTTTTGTCCCAACCATTCGCGCACCTTTAAGGCCGTCTGAAGACGCT  
 TTGCTTGTTCGGCGCAACGGGTTGCAAGTTTAAACCAACCGGTCGCGCAAAATTTTTCGCGAGATACGCTCTTCAACCGTATTTCATCGGATTAGCCCAACCGCGACTTGTGTTT  
 GGTTCGCGCTCTTTCGGCATATCTCAATCGCGCTGCGGACATATTCACACCGGCTTTTCCAAATCCACGCTCCATCCACTCGGCAACCTGTTTGTATTTTCGGATTTCAGACGGCTTTCGTCG  
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 CCCAAAGCGTCTGTCGCGAAACGGATTTCGCGCGTTCATTCGCAAGTACGCGCTTGAAGCGGAACGGTTGCTGCTCAATGCGCGGACGGGACAAATCGATGACGTTGCCCGACA  
 GCTCGGTTCCACCGCTTTCGCGATAAAGGGCATGATTTCGAGTGTTCACACAGATTACCATCGCAATTTCTGCAAAACCGCGGATTTCCTCGGTGAAACGTACGACGCGGTACAGTG  
 GATACAGCGGCTCAATTTCTCGCGGAAACCAAGGACCCATGCTTTCGCGACGACGGAACGTTTTCCTCGGTATACGCGCTGCTGCTTTCGCGTAGCCACCGCCAAATCTTCAAC  
 TGGCATTCGCGCGCTTTCGTCGAGGTCGCAATCAAGCGGATGTTGATGAGCAGAACTCCATCAAGCTTCTTCGCGCTCTCGCGCTTTCGCGAATGCGTACGCAACATCATGCGCT  
 CGGTACCGCGCTGCGCAGGACGCGCGGTTCGCGGCTTTTCCACATCCACAGACATACGCGAGTTTCGCGCAATAGACAGCTTTTGTGTTAACAGAAATCGGAAATATAAGT  
 ACCGAGCTTTCGCGGCTTCAATACCGTTCGCGCTGCTTCACAGATACCTGTTTCGCGTTCGATTTCGATTTCGTAACAT

## SEQ ID 3244

SSRQFNNAHQRTQRFQFMQRMHVRQFTGIGFDGNRYACTVFLGDSLSVLQAQACQVRIHTRHGGMGAFQRCGTADHRI SMINTDAADTDEAV\*GRINALPCPCAAVVOFGRT  
 FRIQRVQPNRSGIVVFTFQVQVQAQHPHRT\*IAEALYHAVERLQTAFFHIDEAA\*CFGKRRNRQYVAHVQQRPADKRRKRHHAFRLPQRGYPCTVNRIDFRLDVEQDCLFRRVC  
 HFGNALARVHTQYVTRDAVGLLRQNAHQHACGRVRLRLRGINGGVIRMLHFRQNHRCFFSVFQAGNGMFRIGRQVFTACPLVGMCGFLRQKRHKQFPFTAGQYAGHTVFGGAAQAG  
 GQERLFFAQRVTDYQYGIIVSQRFNTLSQPLRTPKAV\*KTPVLLATGCKVFNTQAVGKFPQIQLFNRIHRI SPNADLVLA VFGDTFNRAADI PQRGFP IHVHPLATLFDRI PQTAFAV  
 IQAFVGTAVVGQPAFVDFVFRQHAADGMVFLYQVAAQSVVCGNGFAAVQFPSTRVEAERFAGCAGDTQIDVVARQLGFHFRADKGHDFGVFTTIHHRNPLQGTGDFPFGTETAAAGTV  
 DTAHFLGGNORTHVLDGTFPFGITAGGFVAHRQILQLAPALVAGRTIKRMVDEQELHHAFLRLSGPCRHRTHNAVRKYRGTGRQRFPGFFHILQTHAVGNGRELFPVTFERNLS  
 TELVRGPNYRRALLHRYLFAVDFDL\*H

## SEQ ID 3245

TTGATAACAGCGCTGTTGCAACCGAAAAATAATCATTCGCGCTCATTCCCGCGCAGGCGGGAATCCATTTCTGAATTTGGGCAATCGCTGTTAAATCTGATGAAGTGTGTTTATCAATG  
 GATTCGCCCTCGCGGGAA

## SEQ ID 3246

LINSVLQPKNNHSAFPRRRESISEFGQSLFKSDELSFINGFPFPAE

## SEQ ID 3247

ATGACGCTGATGACCGGTTCAAATTTATCCGAACAGTTTGTGCGGGGCTTGAGTCCGCTAGGTTCGGACATCAATGCCCGGCTACGGTT

## SEQ ID 3248

MTADVVPQIYKQFVGGSLSPRRSDINARPTV

## SEQ ID 3249

TTGAACCGGTACATCAGCGCTCATTCCCGCGCAGGCGGGAATCCATTGATAAACTCAGTTTCATCAGATTAAACAGCGATTGCCCAATTCAGAAATGGATTCCCGCTGCGCGGGAATG  
 ACGCGAA

## SEQ ID 3250

LNRYISRHSRAGGNPLIKLSSDLNSDCPNSEMSRLRGNDAB

## SEQ ID 3251

TTGAATTTACGTTGTTATAGCGGATTAAACAAAATCAGGACAAGCGCGGCGCGCAGACAGATACGATAGTACGGAACCGGTTTCGCGCGGCTTGGGCGCTTAGGGAACCGTTCCCTT  
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 CCAAACTCCGCAACAGTACCCCGTTCATCGTTGCCCTTGATTTTGCAACGAAAAAGACAGCTCGGATTTCGTCGCCAACCTTGATCCGCGCTTGTGCCAAATCAAAATCGGCAAGAG  
 CTGTTTACCGCTACGCGGCGCAGTTTTCGCGGAAAGCCTGATTCATCAGGCTTCAAACCTCTTCTTGATTGTAATAACACGATATTCGCCACACCGTTCGCGCAGGCGGTGTAAGTTCGCG  
 CGGATATGGCGGTGCGATGCTGATATGACGCGCTCGGCGCGCAGATGATGGAAGCGCGCGCGCAAGCGCTTGCGGATACGCGACGAAACCGCTCTTAATCGCGCTAACCGTGT  
 GACCGCATGCGACGAAAGCGATTTCGCGGAAATCGGTTGAACACCGCTTGAAGAACCAAGTCACTCGTTTCGCGCAAACTGGCACAAGATTCGCGCTTGGACCGCGCTGCTGTTTCGCG  
 CAGAAGCGCGCGCTTCGCGCGCAATTCGCGCGGATTTCGCTTGTGTTACACCGGCTATCCGCTTGGACGTTTCGCGGCAACAGCAGACCAACCGCGCATATGACACCGCGCGAAG  
 CCTTGGCGCGGCTTCGACTTATCTGCTGATGCGCGCGCGCTTACCGAGCGCGCATCCGCTCGCGTATTCGCGCAAGTGAACCGCTGCGCAACCTTGAAGCAAC

## SEQ ID 3252

LNLRYSGLATKIRTRRRRAADSTSTEFVRPVLGRLEPPLSRGATTYRPFVNPLYCEKDDKRLKTRNENWNLITDPTQPTQRTPTVI VALDFANEKDTLGFVRNLDPALCQIKIGKE  
 LPTATGRSLAESLIHQFKFLDLKYHDI PHTVAQACKVAADMVGMVMDHMSGRRRMEAAAEAVAGYTKPLLLIGVTVLTSMEQSLDABIGINTAPEQVIRLAKLAQSSGIDGVVCSA  
 QEAAPLRRELGRDFVLVTPGIRLDVAGNDDQRIMTPAEALAGSTYLVGMGRPVTTRAADPVAVLREVRVANLEAN

## SEQ ID 3253

ATGCCCGCAAGTTCCAACAAGAAACCTCAAATCCGTTTCGCAACAAGCAAGTCTTGTGTCGCGCAGCTGATGCTGACCGCTATTGCTTTGGCGAGCTGCCGAATTTTCGCGCG  
 AAGCACCGCTGCCGCTGCGCAAAATCGGACGAATCGACCAACGCGCGGCGCGCGCGGCAACGTTTCGCGCAACATCGCTTCGTTGGCGCGCAGGCGAGGCTGTTGTCGTAACCGCGA  
 CGACGAAGCGCGCGCGCGCTCGACGCGCTGATGTCAGGACGCGCTCGCTCTCTATCTGATGCGCGCAACAAATCGCCACACCGCTCAAATCGCGCTGCGCGCGCAACCGAGCAG  
 CTTATCCGCTTGATTGTAAGAACAATCCCAACCGCGAAGTGTGGAACAATCAAGCGGAATACCGCGAATCTTCGCGGAATACGACGCAATCAATTTTCGCGACTACGCGAAAGCG  
 GTCTGTGCTATCTCGGATATGATGATGATGCGGCAACATGTCGCGCAAAACCGCTTAATCGACGCGCAAGCGGACGATTACGAAAAATATGTCGCGCGCACTCTGATTACGCGCAACTG  
 CGCGAATTTGAAGAAGTGTGTCAGTTTGAAGAAACGAGCGGATCTGACCGAAAGCGCAAAACCTTCGCGCGCACCTCGACTTGAACCGCGTTTCTGCTGACCGCGGAGCGAAGCGG  
 ATGACCTGTTACGCAAGGCGAACCATTACAGCGCCACCGCGCGCAAGAGTTTACGAGCTGTCGCGCGCAGGCGACACCGTCATTGCGGGAATGGGCTTGGGCTGCGCGCAGGCT  
 GCACCATGCCGAAGCATGTACCTTGCCAATCTGCGCGCGGCTGCTGTCGCGCAACTCGGTACGCGCGTTGCTGCTTTCGAGATTGCTTGAAGCACTGACGCGGCA

## SEQ ID 3254

MPAKFQQTSLKSRFAQKVLVVGDMVLDYRWFQDVSRISPEAPVPVAKIGRIDQAGGAANVARNIASLGGRAGLLSVTGDDEAAALDALMVQDGVASYLMDKQIATTVKLRVVARNQ  
 LIRLDFEHPNREVLQIKRKYREILPEYDAIIPSDYKGGSLSHISDMIDWAKHVGTVLIDPKGDDYKYVGATLITPNCALKEVVGWSWKNESDLTERAQNLRHLDITAVLITRSEB  
 MFLPSEGEPIYQPTRAQEVYDVSGADFTVLGMLGLAAGCTMPEANYLANAAGVVAKLGTAVCSFABLVEALDQ

## SEQ ID 3255

ATGACCATCAATGCGCTGTAACCCCTCAAAACAAAGGAAACCGAATATGACCATCATCTGTAACAGGCGCGCGCGCTTATCGCGCAGCAACCTGTCAAAGCCCTCAACCAACCGGCA  
 TTACGACATCTGCGCGCTGATATCTGACAAAGCGGAAATTCAAAAACCTTCGCGAGTGCAGAAATCGCCATTAATCTGCAACAAACAGAAATTAATCGCGCAAGTGAAGGAAACAT  
 TTTACCTTATCAAAACATCGAGACCGCTTTTCAATCAAGCGCGGTTCGATACGATGACACGACGCGTTTGTATATGATGGAACCAACTACAGTACACGCTGGAATTGTTGGACTGG  
 TGTGACGACGAACCATCCCTTCTTTATGCTTCAAGTGCAGCGGCTTACGCGCAAGGCGAATCTTCGCGAAGAGCGGAACTCGAAAAACCGCTTAATGTGATACGCTACTCCAAAT  
 TCTGTTTGACCAAGTATTCGCGCGCGCATGAAGAAGCTCTACCGCCCAAGTCGTCGCTTCGCTACTTCAACGTTTACGCGACAACGAAACACAAAGCGCGCATGCCATCGT

CGOCTTCCACCATTTCCACCAATACCGCGAACACGGTTACGTCAACCTGTTCGGCAGCAGCGGTACGGCAACGGCGAACAAACCGCGACTTGTGTCAGCGTGAAGACGTGCGCAAA  
ATCAACCTCTACTCTCTTCGACCATTCGCAACTTTTCGGCATCTACAACTCGGCACCGCGCAGCAGCAAGTTCAACGAACCTGCGCGCGCGCGCTCAACCGCTGCGCGCGCGCGAG  
GCAAACTCGAATTGAGCTTGAAGAAGTTGGTAGAAGAAGAACTTATCCGCTATATCCCTTTCCCGACGCGCTCAAGGCAATACACAGGGCTTACCCAAAGCCGACATCAACCAANTGCG  
CGAAGCCGATATAAGAAGAAATTTTCGATGTCAAAGCAGGTGTCAACCGCTACGTCAATGGATGCTGGAATAATTTGGCT

## SEQ ID 3256

MTIQCRKPKSKQRKPNMTIIVTGAAGFIGSNIVKALNQRTDIDIVADNLTGKFKFNLABCEIAHYLDKHEFIRQVREHILPYQNIETAVFHHQACSDTMNHDGLYMMENNYQTLLDLWD  
CQDERIPFLYASSAAVYKGEIPREERELEKPLNVYGYSKFLFDQVLRREMKGLTAQVVGFRYFNVYQHEQHKGRMASVAFHFFHQYREHYVNLFGSNDGTGNGEYTRDFVSVEDVAK  
INLYVFDHPELSEGYNLGTGRSQQFNLAAAANACRAAEGKSELSLKELVEERILIRYIPFDALRGKYQGTQADITKLREAGYKEEFPVKAQVRYVKNMLENLA

## SEQ ID 3257

GTGCACTTGGCGCGCTGTGTGCATTTCCGTCATCATCGAAATCCATATATAAAGTTAAACAAATCAAANTCGCCTGATATTTTCAGACGATTTTTTTTACGGGCATTCAAAT

## SEQ ID 3258

VQLGALLHFGHHRNFTIKLNKSKSPDIFRFFYGHSH

## SEQ ID 3259

ATGCAACACCGCGCCCACTGCACCGCCAAATTTGGAAATCGCCGACGAAGTACGCGCGCGGTGGATGGCTGGGACTTTAAACAAATACGTTCTCGGCACACTTTTCTACCGCTTTATCA  
GCGAAACTTTCACCGACTATATGACGCGCGCGGACAGCAGCATTTGATTACGCGCTATGCGCGGACAGCATCATCACGCCGAAATCAAAGACGATGCGCTCAAAGCTTAATTTCAAT  
CTACCCCGCCAGCTTTTTTTCGAATATTCGCGCGGACCCATCAAAACGAAGAGCTCAACACCAAGCTGAAAGAAATCTTTACCGGATTGAAAGCTCGCGCTCGCGCTACCGCTCGGAA  
CAAGGCATCAAAGGCTTGTGTGACGACTTCGACACACAGCAGCGCGCTCGGCAGCACCGTTGCGGACAAAAACAAACGCTTGCAGCGCTCTTAAAGCGGTGGCGAACTCGATTTG  
GCAATTTTGAAGACCAACCGCATCGACCTTTTCGGTGATGCTTACGAATACCTGATTTCACACTACGCGCCAAACGAGGCAATTCGCGCGCGGAATTTTACCCCGCAAGCGCTCTCCAA  
GCTGATTCGCGCGCTGGCGGTGCACGGCAGGAGAAAGTCAACAAATCTACGACCCCGCTCGCGCTCGGCGAGCGCTGCTCTTGCAGCGGAAAAACAGATTTGACGACACATCATCGAA  
GAAGGCTTCTTCGGCGAGGAAATCAACACACCACTTCAACCTCGCCCGCATGAATATTTTCGCAACAGCTCAATTACAAACAAATTCACATCGAATTTGGCGGACACGCTGACCAAC  
CCAACTCAAAGACAGCAAAACCTTTGATGCGCTGCTTCAATCGCGCTTATTCATCGACTGGATAGGCGAGCGAGACCCACTTGTATCAACGACGCGCTTTGCCCCGCGAGCGT  
ACTCGCACCGAAATFCAAGCGGATTTGCGCTTCACTCGCGCTTATTCATCGACTGGATAGGCGAGCGAGACCCACTTGTATCAACGACGCGCTTTGCCCCGCGAGCGT  
CAGAAATTCGCCCAATATCTGGTGGAGGCAACTATGTGGAACCGTGTATGCGCTTGCGCCAATCTCTTTTACGCGCACTGCAATCGCGCTCAATATCTGTTTGTCCAAACACAAAG  
ACAATACCGACATCCAAATTCATCGACGCAAGCGCTTCTTTAAAGAAAGAACCAACCAACAGCTTAAACCGAAGAACATTCGCGAAATCGTCAAACTTTCGCGGACAAAGCGGATGT  
GCCGATATTCGCCCAAAACCGCGCCGCAAAACCGTCAAGACAAACGCTTCAACCTCGCGCTCAGCAGCTATGTGCAAGCGGAGAACACCGCGAGGTTCATCGACATCAGACGCTCAAC  
GCCGAATCAGCGAAACCGTCCGCAAAATCGAACGCTCGCGCTGAAATTCGCAAGTGTTCGACAGATTTGAANCC

## SEQ ID 3260

MQQRAQLHRQIWKIADVEVRGAVDGFQYVLGTLFYRFSIENFTDVMQAGDSSIDYAMPDSIITPEIKDDAVKVKGYFIYPGQLFCHIAEAHQNEELNWKLEIFTAIESSASYPSE  
QGIKGLFDDFTTSSRLGSTVADKNKRLAAVLKGVARELDFGNFEDHRIIDLFGDAYEYLI.SNYANAGKSGGEFTTPQSVSKLIARLAVHGGQKVNKIYDPACGSGSLILQAKQFDEHIE  
BQFPQGEINHTTYNLARMNFMFLHNVNKFKHIELGDTLTNPKLKDSPFPAVSNPPYSIDWIGSDPTLINDRPAFAPAGVIAFKSKADPAFILLHALNVLSGRGAATVSPFGIFVYRGA  
QKIRQYLVENGVETVIALAPNLFYGTICIAVNLVLVSKHNDTIDIQFIDASGFKKETNNVLTTEEHLAEIVKLFADKADVPVHIAQNAAQQTVDKNGYNLAVSSVVEADTREVIDIQIN  
AEISSETVAKIERLRREIDEVIAEIEF

## SEQ ID 3261

TTGATAAATAATTTTTATGGAGATCGTCTGAAAAATGGGCTTCAGACGGCTTTTGTAGTTTCATTGACAATCAATACTGTTTAAAAACGTTTACTGCCACTTTCGCGCTCAITCCCGCACAG  
GCGGAAATCCATTTTTGAATTTTCGGCACTGCTTTTCAAAATATCGGCTCTG

## SEQ ID 3262

LINNPLWRSEKWSADGILLSFIDNQYCLKRLPPCRHSRTGPNPFEPFRQLLFKYRVL

## SEQ ID 3263

ATGGGACGCGCGCAGCGGCGACAGCGGATGACAAGCGCTCCGTGCTGTGATGGGCGCGGAATGCGCCCTTGTGCTATCTGCAACCGCTTACAAATCCCAATCATCCCTTCAA

## SEQ ID 3264

MGSRARATGDDKPSVRVMGRMRPLSYLTPTNPQSSIQ

## SEQ ID 3265

ATGACAACGAAATAACGCTTTTGAACACGCCAAACACATCGACGAAACAGGCAATGAATATGTCGCGCGCACCTTGCAGCAAACTCTTGAATATTCGGAATTCGCGCAATTTCCAAAC  
GGGCAATGATAAAGCCATAACCGCTTTCGAAACATCAGGAAATGACAAAAATCATCTTTTGTGAAACCAAAATGATAGCCCTTGGGAAAGGCGGCGAGCGGCAAGTGGCGGATTA  
CGGCTTTCCCGCTAGCTGCTACCTGATTGTGCAAAACGCGGATCCGTCCAAAGCGGTGATTCGCCGAGGCGAAACCTACTTTGCGCTGCAAGCCGCGCGCAAGAGCTGCAAGACGAG  
GCAGCATTCAGGATTTGGGCGAAGACAAACACGCGTCTGCTTTCGAGGAGCTGCGGCAACACATACCGACTTGCAGCGGCAAGGATGCAAGGCTTGAAGAAAAGCCAGAGATTCAGACCATGAACGCCAGCA  
ACGCGCTTCCAAACACCGCTATCGGGGCTATACGAGGAGCTGGAACAGCGGATACACAGCGCGCAAAAGGCTTGAAGAAAAGCCAGAGATTCAGACCATGAACGCCAGCA  
ACCGGCTGCCAATCTGTTTCGCGCCACGCAACCGGAGAAAACCTACGCGCGCAAAACATCCAAGGCAAAACACAGGCAAAACCGGCTGCAATTCGAAGTCGGAACAAAAGTGGCCAAAC  
ATTGAAGAACTGGCGGCGCATGCTTGAACACGCGCTACCCGAGAAAAGCATCAACAGCTTGAAGAACGAGAACAGAAAAGGCTTGCAGCAACCGAACAGCATCAACACGCAAA  
AA

## SEQ ID 3266

MTTENNAPENAKHIDETGNEYWSARTLQQILEYSEWRNFQRAIDKAITACETSGNDKNHVFETNMKIALGKGQREVADYRLSRYACYLIVQNGDPSKSVIAAGQTYFAVQARRQELQDE  
AARSLGEDKQRLRLRLREHNTDLAAAADAGVEKPEYAVFQNHGYRGLYGLDKQGIHSRKLKKSQRIIDHMANSEPAANLFRATQTEELRRKNIQKRTQANRVHFEVQKVRQT  
IEELGGIMPENQVPEKSIKQLENEBQKRLAATBQHONGKX

## SEQ ID 3267

GTGAGCCGAAACCCCGCGCAACCGCCCACTCCCGCGCAGCGGGAAGGAAACGGAAACAAACCATGGATATGCAAGCAAGCGAAAAATTTGAT

## SEQ ID 3268

VSRNPPRNPTSRSGKETENNHGAKQSEKID

## SEQ ID 3269

ATGCAAGCAAGACCGGAAAAATTTGATTGAGATGATTAGACGCGCACCGGTGGAGTGAAGCCATTGGGGGAGGTTTTAGTTTCGTACAAAGGAATAAGATAACTGCTGGACAAATGAAG  
AAATGCATAAGATAATGCGCGTTAAAGATTTTTCAGGAGGAAAACTTTTCATAGTTGACTTTGATGATGATTCCTGATAAGGATATCCATAGAGAGCTTCTATTTATTCGTTAAATC  
AAGAGGTATTTAGTAATTCGAATATTACGATAAACCAATTTTCGATAAAATGAAATGTTGCTTATCATTCAGTTAATAAACATATTTATATAAATATGTTTATTTCTTAAAAACA  
CAAGAAAATTTTTCGTAATATCGGATCAAAATGCAATGCCAATAAGCAACACAGATACAGATAAATATAAATCCCATCCCATCATTTGGAACCCCAAAAAATTTGAAAAA  
TACTTGACAAATTCACCGAGCTGGAAGCTACGCTGGAAGCTACGCTGGAAGCGGAATTAGCCCTCGCGCAACGCCAATAACCGGTATTACCGGACTTACTTTTAGATTTCGACAAATCAAT  
CGGGGGGATAGC

## SEQ ID 3270

MQSKARKLLEMIQTAPVWVKPLGEVLVTRKTKITAGQMKEMHKDAPLKIFAGGKTFALVDFDDVPDKDIHREPSIIVKSRGIIIEFYDYKPFPSHKNEHMSYHSVKNHITIKYVYVFLKT  
QENYFRNIGSKMQPIATPDTDNKYKIPISLETQKIVKILDKPTELEATLEATLEALALRRRQYRYRDLLDFDNQIGGS



## SEQ ID 3271

TTGACAAATCAAAATCGGGGGGATAGCTGATGCTATCAATGCCGTCTGAAAAATGTGGTTTGGAGAGAGCTTGGGGAGGTTGCCGAATATTCAAAAAACCGTATTGTTTCGGATAAACTGA  
ACGAACATAATACCTTTGGCGTGGATAATCTCTTACAAAATAGAGAAAGTAAAGTTATCCGGTTATGTTCCAGCGAAGGAAAAATGACAGAAATATATTTGCAATGACATTTTGTATTGG  
AAATATTTCGTCGGTATTGAAAAAATCTGGCAGGCAGATGACGCGGCGGAAACAAACGGTGTATGTTTGGTTATCCGGGTAAACAGATGAAAAGGTTAATCCAAAATATCTGTATCAGGTA  
TTGGCCGATGATAAATTTTTTGTCTTTAATATGAGCACGCCAAAGGTGCAAAAATCCGCGTGGCAGCAAGCAGCGATTATGCAATATAAAATCCCATCCCCCGCTCCCGAACAGG  
AAAAATTCGTCCCATCTTAGGCAAAATCGATACCTGACCCACTCGCTCAGCGAAGGCTGCCGCAAGAAATCGCCCTGCCCGCAACAAATACGAATATTACCGCAACAGCTGCTTGC  
CTTCCCCAAGGCTGCC

## SEQ ID 3272

LPIKSGIADGYQCRILKNVWMTLGEVAEYSKNRICSDKLEHNYVGVNLLQNRREGKLSGYVPSGKMTETIVNDILIGNIRPYLKKIHWQADCTGGTNGDVLVIRVTEKVNPKYLYQV  
LADDFAFPMFKHAGAKMGRSKAALIMQYKIPPLPEQEKIVAILKGFDTLTHSVSEGLPHEILARRKQYEVYREQLLAFPKAA

## SEQ ID 3273

TAACATCATTTATTATATTTTAAATGACTTAAATAACTCTTTAACAGCAGCTCATTTGCTTTCATCTGTAGGCTCAAACTTTTACACCAATTAATTAATTTACATCGCCATGCAATATC  
CTACTGCATCGCAA

## SEQ ID 3274

\*LIYYIFK\*LK\*LFHSTLIVFICRLKLPDPNYIYIAMQYPTASQ

## SEQ ID 3275

ATGGCAATTGTTTCGATGAATTCACGCGAGGATTCCTCGATGTCGACATCAACGTTACGCGTGGTGGAGCTGATGCTGGTGTGCTGATGTTGTTATGATTACTATGCCGGTCTGA  
CGCATTCATCCCTTTGGAAGTCCGACCGCGTCCGAGCAGGCAAAACAGCAGGCAAAACAGCCTAAAGACCCCTGCCGCTGACGATTGATGCGAACCGCGCTATTATGTCGGCGGGA  
TTCTGCAAGCAAATGGAATCGGGGAAGTGGAAAGCGCTCTGAAAGCGCGCAAGGAGCAGAAATGAAACGCTGATTGTTGGCGATTGCCGAGCAAGCGGCTGGAATACGATTATGTAAC  
AAAGCTTTAGAGCGCGCGCTCAGGCGAGGAATACCAAAATCGGTTTGTAAACGAAACCAAGCGCAA

## SEQ ID 3276

MAPGSMNSDDSPMDINVTPLDVNLVLLIVPMITMPVLTHSIPLELPTASEQANKQDKPKDLRLTIDANGYVVGDSASKEVEGESRLKAAEQENNVIVAIAADKAVENDYVH  
KALEAARQAGITKIGFVETRAQ

## SEQ ID 3277

ATGAACCTCGAAACCAAAACCCATCGCGCAAGCGGCAATTTCACTGCTGCGACCAATATGAAAAATTCGAACAGTCGGGACGTACCAATCGGAAACCGGTTGGAAGCGGAGTTAATCG  
CCGATTTCGAGAAATCAGGGGTACGAATACCGCAAGGATTGACAGCCAAAGCAGGCTGCTGGAACCACTGCGCGCCAGTTGACGCGGCTGAACGATGTTGGCGTTTTCAGACCGCGAATG  
GGCGCGGTTTTTGACGGAATATCTGACAGCGCGGCTGAAACATTAACGATAAAACCGCAAAATCCACGACGACCATATTACGATTTCGCTTTTATGACGCGCGCTGAAACCAATT  
TATCTGCTGACAGAAAGAAACCTTGGCGCAACCATGTCAGCTTATCAACCATTTGAGCAGACGGGACGATGCAAAACCGTTATGACGTTACGCTGTTGTTAAACCGCGCTGCCGCTGG  
TCCGATTGAAATTTGAAAGCGCGGTTGGCGGTCGCGAGGCAATTCAGTACGCTGACCGCTTACAGCAAGAGAGCTTCAACAGCGGAAATTCGCTGTTCAAAATTCCTGCAAAATCTTCGT  
GATTTCACGCGCAGGACGCGCTATTTCGCAACACCAAGCGCGCAAAACAGCTTCGATTCAGATGAATTTGGCGCGGTCGGAATCATCGATTAAAGATTGAAAGAC  
TTTACCGCCACGTTCTGCAAAAGCGTATTGCTGAGCGTTTGTCTGATTTACAGCGGTTGCTGATGCGAATGATACGCTGCTGATTATGCGCGCGTACCAGATTGCCCGCGCGCAACGCA  
TTTTTGGAAAAATTAACAGCTCGCGCGAGCGGAAGATTGAGCGGGCGGAAAGCGCGGCTATGTTTGGCATACACGCGCAGCGCAAAACGCTGACCGCGCTTAAAGCGCGCGGCTGT  
GGCGAGGAATCGCGGTTTATCGACAAGGTTTCTTCGTGGTGGACAGGAAGATTGGACTATCAGACGATGAAGGAATACCAACGTTTTCGCGCGAGCGGTAACCGGCTCGGAAAGT  
ACGGCGCGGCTTGAACCGCAATTTGGAAAGACGCGCAACAAATCATCTGTTACCACTCCAAAGCTGAACAACTGATGAAAAGTGAAGATAATTCGCGGTTTATCAGCGCGAGGTTG  
TATTTATTTTCAGCAATGCCACGCTCGCAATTCGCGCAAGCGCAAAACCACTGAAAGAAATTTAAAAATTCCTGCCAGTTGCGCTTTACCGCGACCGGATTTTTCCGAAACCGC  
TTTGGCGCGGAAACACCGCGCGGCTGTTTGGCGGAGCTGCAATCTTATGCTATACGATGCCATCCCGGATGAAAAAGTATTGAAATTCAAAGTGGATTACACAGATGACGCGCG  
CAGTTCAAAGCGCTGGAAGCGGAACAGGACGAGAAGGAAGTGAAGTCCCGCGCAAAACCGCGCTGCTGCAACCGCAACGATTCGCGGAATCAGCGAATATATCTGAGCGCGGTTCA  
GGCAGAAACCGCACCGCTTGAATGCGGGCGCAAGGCTTCAACGCGATGTTTGGCGTACGAGCGGATGCGCGCAAGTGTATTACGAAAGGTTCAAAACCAACAGGCGAGCGGCT  
GCACCGGTTGAAACAGCCACCATTTTTCCTTTGCGCGCAACGAAGAGCAAAACCGCGTGGTGAATTTGTTGACGAGACCTTTGAACCGGAAGCGATGGACAGCGCGGCAAGAAATTT  
TGCAGGCTGCCATCAACGATTACACGCTGTTTCAAAACCAATTTCCGCGAGCGCAAGAGCTTTCAGAACTACTACCGCGATTGCGCAAAACCGGTAACCGGGAAGTGGAGCT  
TGCTGATTGTTGCGCATGTTTTGACGGGTTTACGCGACCGAGCTGAATACGCTGTTGCTGATAAAACCTGCGCTATCAGCGCTGATGAGCGGTTTTCTCGCACCAACCGCAT  
TTACGATGCTACCAAAACCTTCGGCAACATTGCTGCTTCGCGCATTTGAGCAGGCAACCATTTGATGCGATCAGCTCTTCGCGCAACAAACCAAAATGTAGTCTGGAAGAAAGC  
TACGAAGAAATACATGAACGCGTATACCGACAGCGCAGACCGCGCAAGCAGCGCGGTTATCTGGAATGTAGCAAAAGAAATTCACGAGCGTTTCCTCGATCCGCAAAATTCGAACCGGAA  
AAGCAAAAGAAATTTGCCAACTCTTCGCGGAATACCTCGCGGCGGAAATGTATTGCAAGTACGATGAATTTGCGCGCTGCGCGAATTCGAGAAATGTGAGCGCGCGGCAAGAA  
TCGATGAAGCGCTTCAGGAAAAATACCTGACGCGAGCAAGACGTGCGAGGAATGCGGAGTGGCGCTGAAAGGCGGTCGAGCACTACCGCTTCGCGCTATACAGCATC  
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AACGAACCGCGCGCAACCGCTATTTGACCGGCTGCTCAACCGGCTATGCGCAGGAAACGCTAGCGAACTGACCGAAACCTCGCGGAAATGAGTCCGCTCAACCGCGCAATATCTGA  
CGAAGAAACAAAGCGCTTCTCAAAATTCGCGCGGTTTGTGGAGAAGTTTTCGCGGAATAGGCGCGGATATT

## SEQ ID 3278

MNLETKPIAETPNFIVLDQYKEIEQSGSYQSENRLAEALADLQNGYEYRKDLNSQSRLEENLRAQLQRLNDVAFSDGEMARFLTEYLDRPAENITDKRKIHDDHYDFAFDGRLKHI  
YLLDKKLNARNHVQLINQFETGTHANRYDVTVLVNLPLVQIELKRGVAVREAFNQVHRYSKESPSNGSLFKFLQIFVLSNGTDRYFANTTKRKNSPFTNMAASDNHPIDKLD  
FTATFLQKSVLLSVLHYSVFDANDTLINRPYQIAAERILWKINSSAQAKNSGSPESGTVVHNTTSGSKTLTGFKARLATESAFIDKVFVVDKDLDTQTHKEYQRFSPDSVNGSES  
TAGLKRNLKEDGKNIIVTTIQKLNLMKSEDLNLPVYHQVVFIFDECHRSQPGEAQKLNKKRFFKFCQFGTGTPIFENALGAETTAGVFGRELHYSVITDAIRDEKVLKFPVDYNDVRP  
QPKAVEABQDEKLSAENRQALHPERIRETTYILSRFRQKTHRLNAGGKGFNAMPVAVSVDAAKCYEAFKTTQAGSLHPLKATATIPFAANEQNAVGEIVDETFRPEANDSSAKRF  
LQAANDYNACPKTNFGTDSKAPQNTYRDLAKRVKNREVDLLIVVGMPLTGFDAPTLNTLPVDKLNRLYHGLMQAFSRTNRIYDATRTPGNIVCPRLEQATIDAITLPDKNKNVLEKS  
YEEYNGYTTDSGEARRGYLDVAKELHERFPDPDKIETEKDKDPAKLFGEYLRAENVLQNYDEFAALRELQNVDADEDAKPAQEKYYLSEDEVDQEMRKVPMPSEARVQDYSAYNDI  
RDWLRQKAGEQREQSKIDWDVVEVDLLKSQRLNDYILQLVFEHKKIKGKAEVBETIRIRASIGHRAKBLIVDFINDTDLKVPDVPALLETFTYTAQEVMRHEAAGLIAEGL  
NETAAKRYLGLSKRGYASENGPELTETLPKMSPLNPQYLTKQSVFQKLAIFVEKFAIGADI

## SEQ ID 3279

TTGTCGAGGAGATTAATATGCTTGCCCTGAATTGGAACAGATTTCGAGCAGCTTACC CGGAGGCGGCTAAGGCTCATTATGAATTTATCAGCCTCGAGCATCTGCTTTTGGTACTCA  
TCGAAGAAGATGCCCGCGTCCGCAACGCTTTAAACTCTGCGGTGCGGATTAAAGCGGTGTCGCAACAGCTCGCGCCAGCGTTGCCGAAACACCCCTGATTCCCGACCACTTTT  
AGCACGCGTGGAAACCGCGCCACGCTCGGCTTCCACCGGTCATCCAGCGCGGATGTCGATACCAATTCGCGCAGGCAAGGCTTGGCCGAGCGTTTGGGAGCTTTGGTGGCGCTGATG  
AGCGAAACCGGACAGCCAGCGGCTTTATTTTGGGTTTGAATCTGTTACGCGTTTGAAGTTTGGCGTGTATTGCCACGCGCTCTCCGATGAAGATGAAGACGATGCGCACTATTTT  
CAGACGCGCATGGACGACGATAATGAGAACCGCAACAAACCGGCAAAACCTTTATCGCGGTACACCGTCAACCTCAACCGCGAAGTCAAAGCGCGCGCATGACACCTTTGATTGGTGG  
CAACACGAAATGGACGCGCTGTCGAAATCTGTGCGCGCGCGCAAAACCAATTCGCTTTTGGTGGCGGCAAGCAGCGTGGGCAAAACCGCGCTGGCGGAGCTTTGGCACATCAAAATC  
GTCAACGACGACATTCGCGAGCGCTCAAGAGCGCGAAGTGTACGCGCTGATATGGGTTGCTTTTGGCGGCGCAAAATACCGCGGCGACTTTGAAGCGCGGCTCAAATCCGCTTGA

AACAGCTCGAAAAATCCCGCAGCCATTTCATTCATCGACGAAATCCACCATCATCGGCGCGGGCAGCACCGCGCGGCACGATGGACGCGTCCAACTGCTCAAACCCCGATTGCC  
GAAAGGTTCAATTCGCGTGTATCGGCGCAACCACTTACGACGAATACCGTACTATTTTGACAAAGACCAAGCCCTTAAGCCGCGCTTCAGAAATCGACGTTGGTGAACCCCGATTGCC  
GAAACCGTTCAATTCGCGGCTTGAACCGGATGTCGAGGCTTCCACCAAGTCCGCTACACCGAAGCGCACTCGAAGCGCGCGCGAAGTCTCGCGCCGCTACATCAACGAGCGCT  
TCCTGCCGCAAAAGCCATCGACGTAATGGACGAAGCAGGCGCGGCGCAACGATTCCTGCCAAATCCAAACAGAAAAAGTCATCGGCAAGCGCAATCGAAACCGTCATCGGCAAAAGT  
CGCGCGGATTCGCAAAAGACCCGTGTCGACGACGACAAAGTGTTCGCAATTCCTCGGCGCGGATTTGAACAAATATGTTTACGGGCGAGGAGACGCGCATCGACGCGCTGGTTTCGCG  
GTCAAAATGTCGCGGCTTGGGCTTGGGCTGCGGACAAACGATAGGACGCTTCTCTCTCGGCGCGTACCGCGCTCGGCAAAACCGAAGTCCGCAACAGCTTGGCTACTCAATGGGCG  
TACCGTGCACCGTTTGTATATGTCGGAATACATGGAACCGCACGCGTATCGGACTCATCGGCGCGCACCGGCTACGCTGGCTTTGAACAGGCGGCTTTTGACCGAAGCGCTCAA  
CAAGCAGCTCATTCGCTGTTGCTCTTGGACGAAATCGAAAAAGCCATCCAGATATTTTCAACGCTCTCTGCAAGTCATGACGCGAGGCAACCTGACGATAACACAGGTAAGAGCGC  
GATTTCCGCAACGTCATCTGATCATGACCAACGACGCGCAGAAAGCCCTCAGCGGACCGCAGCTAGGCTTTACCGCAACGCGGAGCGCGGACGAAATCGAGGCAATCAACAAAC  
TCTTCACGCGCGAGTTCGCAACCGCTTGGACGCGATCATCCGCTTTCACCTTTGCAACCTTTACCGCAACGCGGAGCGCGGACGAAATCGAGGCAATCAACAAAC  
CAAAAGTTCGAAGCGAATTCACACCGGATTCGCTAAATATTTGCGAGAAAAAGGTTTCGACCGCAATGGGCGCGCGCGGATGACCGCGCTGATTCAGGAAAAATTCGCAAAACCG  
CTCGCGACGAACTCTCTGTCGCAAACTCGCGGACGCGCGCTTTGTCGCGATAGACTGGGATGCGCGGAAAGAAAGCGGTATTGAAGTTTGAAGAAAGCAAGGTCAAATAAAACCG  
CCTCCGA

## SEQ ID 3280

LSRRFNLAFLEQLQOLYREARKHYEFISLEHLLVLTEEDAAPVNLKLCGADLKAVSEBQLAASVAENTPLIPDHLLDTVETRTPLGFORVIRAMVHTQSAGKGLAEPLDVLVAILM  
SETDSHAVYFLGLQSVTRFEVLRCIAHSGFDEDDGNYPDGMDDNENRTKPGKNPLSAYTVNLNAEVRAGRIDPLIGRKHEMERLVQILCRRKNPLVGEAGVGKTALADGLAQI  
VNDIFDALKEAEVYALDMSLLAGTKYRGDFEARVKSVLKQLEKIPIHALFIDEIHTTIGAGSTGGGTMDASNLKPKALAGSLRCIGATTYDEYRTIFDKHALSRRFQKIDVVEPTVA  
VNDIQLRGLKPMFPAFHQVRYTQGALEAAELASRYINERPLDKAIDVMEAGAAQRIPLPKSKQRKVIKAQIETVIAKVARIPKFTVSHDDKQVFLGRDLNMMVYQEDAI DALVSA  
VKMSRSLGLPLDKPIGSLPSGPTGVGKTEVAKQLAYSMGVPLQRFDMSEYMERHVRSLIGAPPGYVGFQGGGLTEAVNKQPHCVLLDEIEKAHPIDFNVLQVMDAGRLTDNNGKSA  
DFRNVLIMTINAGAESLSRPSLGTAKRERGDEMQAINKLFTPEFRNLDAIIPFAPLSEPIIVKVDKFLQLQLEHRLLDKKVEAEFTPALRKYLAEKGFDPQHGAPMHRILQEKIRP  
LADELLPGKLDGPFVRIDWAAREAVLKFKKSKVKIKTASA

## SEQ ID 3281

TTGTTAAGACAAAACGTCAGCTATGTTTCAAAAAAGTGGGAAAATAGCGGAAAGTACCGAAAATACACAAAAANTCCGCTGTAACCGCGCTTTCAATGGGACACGCTATGACCGCGC  
AACACCAATCCGACACGCTTTTGACCGCGCTGAACACCTCGCGCGGAAACGTTACCGCGGATTTTATTTGAACGACGATTACACCAAGTGAATTTGCTGTTGAAATCCTGACCGAAAT  
CTTTATGCTCGCGGAGGAAACAGGCGGTAGCGGTAATGCTCTCGGTTTCATCAGGAAGCAAGGCGCTGCGGCACTTACACCGCGGATATCGCCAAACCAACAGCAACAGTTCATGCAAG  
CGGCAAAAGCGGAGGACATCCGCTGCAATGTAITGTCAGGAGAGTT

## SEQ ID 3282

LLRQNVKLCFQKSGKIGESTENTKMPSERFQMGHMTAQHSDTLHLRLNLTLPKRYGVFLNDDYTTREFFVEILTETPMLQGBQAVAVMLSVHBEKGLCGTYYTRDIAQTKQQQVMQ  
RAKAEHPLQCTVEEI

## SEQ ID 3283

TTGCTGATTTTGTAAATTTTAAATATAGGAAGTTTCTAATGGCAACCGGTATCGTAAATGGTTTAAACGAGCTAAAGGTTTGGTTTCATCTCTGACGAAAGCGCGGAGAGATTGT  
TCGCACATTTCTACGATCAATATGGAAGGTTTCAAAACCCGTAAAGAGGCCAACCGGCTCTTTTCGACGTAACCAACCGCGCTTAAAGGCAACAGCGCGCAACATTCAGGACGCT

## SEQ ID 3284

LLILLIFKYRKLMAATGIVKWFNDKGFPTTPDEGGEDLFAHPSAINMEGFKTLKEBQVRSFDTTGPKGKQAANIQA

## SEQ ID 3285

TTGCACATTTTTCATCAGCACTGATTTTCCCTTATCCGTCAAAATACTAAGCCACTTCCCAACACAGGCTACACAAAGTTCAGGATAAGCGCGCGGAGTTGGGAGCTTTTCCGCC  
ATCGGCAAAACGGCAGACAAAAACGGCGGACATTCGCTGTCGCGCGCTTTCAATATACATTTGACCGTACATCAGGAATTAAGCTGCTGAATGTTGCGCGCTGTTTCCCTT

## SEQ ID 3286

LHIFFIISTDFPLSVKILSHLPTTGYTQVQDKAGDWGLFRHRQNGRQKRRDIACPAVKYTFDRTSGLKLPFCNRPVCL

## SEQ ID 3287

ATGCGCTCTGAAGACGAAGCGCGCGCTTTTGGCCCGTGGCTGCCGCTTTGCCGTTTATGCGGCAACCGCTTTTACCGCGGACATTCGACATTTTTCATCAGCAC

## SEQ ID 3288

MPSEDEGGAFPCVPARLPFYAAPPTGDLAHFFHQH

## SEQ ID 3289

CTGCATCGCAACTACACCCGCTGCTTTCGCTGCGCAAAATAAAATCAAAATATGCGAATAAAGTTTGTATAAATTTCTCTTAACCTCGTATTATCAACGATGAATAAAACCA  
ATCCTCTGACCTTCATGATCAAAATATGCAACAAATTAAGCGGTTTCCATATCTTTCAAAAGAGCTAGAAATTTAGAAAATTTCCGACAAATCTGATTAAGAGCGGATTGAGTGTG  
TACTCTTACCTTTGTTGCTGACCGGTATAGAAATAAAATTTTAGCTTCCACCATTACCACTCCCCAC

## SEQ ID 3290

LHRNHPVSLTCQNKITIMRIKFV\*ISPVLFIITR\*IKTNPLTFMIKYCNKI\*AVSISFKKD\*KFRKPTNLIKRIECLTLTFVGCTV\*NKNPSFHHYHPH

## SEQ ID 3291

GTGCGGCATAAAACGGCAACCGGCGAGGACGCGGCAAAACGCGCGCTTCTGCTTCAGACGCGCATCGGCGAGGCGTTACGCTTCCGGCAACCGTCATCCCGCAATCAGAAATCGAAACG  
ATTTTGTGTTGACGAAACCGCGCAAGCGTCATCCGCCACGCGGAGATGTCGCGGTACATATCTGCAAGCGCTCCGGCAACGTAATCTCGTGGACGCGGTTAGGCAATCAGCGCTTTTCCA  
CCCAAAACCGCGCGCGCGCGGAATAGTCGCGGTAATGTTGTCGACCGCTTCCATCAATTCGTTTACGAGCAATCCCGTGCCCATTTCTTTCAGAGGTCGAGTTGCGTTTCTG  
CGTATGTTTCAATACAGGTTGTCGCGCGCGCGCGGCTTGCCTGCTGTCATTCGAGTTTTCGCGCGCGCTGTAACGCGGAGGAAATAGCTTCGACAAATCGCGGCTTTTGAATCAGGAAG  
CGCGCGCGGTCGCAACCTTTCGCGCATCAAAATAGCTGCTCGGAAAGAGCGGCGGATGTCGCGTTCTTCGCGCAGGTTGAGGAAATCGGCGAGGACTTTTTCGCGATGCTGTCGATCA  
GGAACCTGCTTTGCGGCTAGAGCGCGCGCGGAGAGTGTGCGGACGAGGTGTCGATCAGCGGCTGTCGATCAGCGGCTGATCGAAGAGGAGCGGCTAGCTGCTGCGGATGCTGCGGCT  
GCCGAGTCGCGCAAGTGTGCGCGCGCGCGGCTTGAACGATGTTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCT  
GCAACGACGCTGCGAGGAAATGCTGCTGCTGCTGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCT  
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TTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCT  
TTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCT

## SEQ ID 3292

VRHKTANGQARKTRRLRLQLTASAGRSASGNRHRPNQRTDFVGRTPQSVIRHADIVAVHILQASNGNLDVGVGNHVPKTRRAARIVAGNVRLTSHQFGYQQSRAHFFQVGLRFPV  
RMVQIQVVRAGVARGLHSEFARAATAEIAFDNAVNLNHEARRGGNTFRILAAERAGDVRFPAQVEIIGQDFPADAVDQETALAVRAAGECADEVSDQPARNGGIEEDGVAACRDA  
AESQSAAGGGLTDGFAGVHIRMAAGGIVPVVALHSVPVGGNDAGNAVVRALPVGKCTVGVAVNVVLVSGLHRRAPGVFDAVRVQRCLFALFCQADGGFRIQIPVVKVGADVLRHQL  
GVGKSGATVPGVAGDVGGADGVAQGLFGEVGGAGAAFAFADVNGVQRFVLELDFDFAQAHADALSERFAEVGFGGRARCFQVERAAAEVEEFGSGVGVQHNLSWSVVA



**SEQ ID 3293**

ATGCTGTTCAACCAACCGCTTCGGAATCTCTGCACTCTGTCGCCGCCGACGCTCGACTTTGGCAAAAGCAGCGGGCGGACGCCGCCGAAGCCGAGCTTCAGCGAATCGCTCGGACAAGCG  
TCAGGCTGCGCTTTGGCGGAAATCGAACAAATCGAGTTCCAGCAGGACAATCGCTGGACATTACCGTTTACGTCGGCAAAACGCAAGGCCGCCGCCGACCCGCGACTTCTCCGAACAGC  
CCTGCGCGACACGCTCCGCCGCCGCCGACATGCCCGCCACACGCGCGAAGACGGTTGCGCCCGACTTGGCGAACCCCGAGTTTGATGGCGCAACACATCGCGCGACCCCGACCTTTACAC  
GATATGGGATTTTGATACGGAAGCGCGCGCTCGCGTTGCGAAAAAATGCGAACAGCGACGCTTGGACACGGACAGCCGCATCGAAAACCTCGAAGGCCGCCGGTGCACAAACCGGACACTACC  
AATACGCTTTACGGCAACACCCACCGTTTTGCGCGACACCGGCAAGACGCAACACAGCATTTCTCTGACGCTCGTTGCCGCCGACGAAAACGGAATGCAGCGCGACTACTGGTACGATT  
CGCTTCCGCCCATCCGGATATGGACAGCCCCGAAACCATCGGTCAAACGCCGCCGCCGCACTTTGCGCGCAGCTCGGCAGCCGACGATCCCGACAGGCAGTACCCCGTCTCTGCGAT  
ACCAACGCTTTCCGGCGGGCTGATCGGACACCTCGTGGCACACTCTCCGGCGCGCGCTTACCCGCAAAAGCAGCTCTCGTGCAGCAGCATCGGCAAAAAAGTCTGCCCGATTTCTCTCA  
ACCTGCGCGAAGAACGCAATCCCCCGCTTTCTCCGACGACGCTATTTTGATGGCGAAGGTTGTGCCACGCGCGCGCTCTGATGTTCAAACGAGTTCTGCGAAGGCTATTTCCCTGG  
CAGTTACAGCGCGCAAACTCGGATTCGGAATCGACACCGGCACGCGCGCGCGCGCGCACCACTGTATTTGAACCATGACGACGAACGCAATCCGACCTGCTGAAAGAAATTTGCCACGGGA  
TCGTCGGTATACCGAAATTGATGGGACAGGGTGCGAACACCAATTACCGCGCACTATTTCGCGCGCGCGCGCGGGTTTTTGGGTGAAAAACGCGCGTATTGCTTACCCGCTCCACGAGATTACG  
TTGCCGACGCTTGCAGGATATGTAACCGGCACATCGTCGGCGTGGCGGATGACGCTTTGCGCGGTTCTGTCAACAAAATCGGTTTCGATTCTGATTGCGGGGATGACGGTTGCCCGGAAGC

**SEQ ID 3294**

HLFNHTASELLDLCRTLDLAKAAGATAARADFSLSLQGSVSVRLGRIEQIEFQDDKSLDITVYVGKRGAGTADFSEQALDRTVRAAADTARHTAEDGCAGLADPELMAQHGIDPDLYH  
EWDLDTEAAVGLAKQCEQALDTSRIENSEGAIVQYGHYQYVYVGNTHGPAHRQSTHHSISCSVVAADENGMRDQYWDTSACRHPMDSPETIGQTAARRTLRLGSRSTPGSTPVLFD  
TTVSGGLIGHLVGLTSGGALYRQSSFLDISGKVKLPDFLALREEPHLPFRSSSYFDAEGVATAPRFVIONGIVEGYFLGSYSARKLGMQTGNAGGAENLYLANHTHEQSDLLKEKGTG  
LLVTELMGOGANTITGDYSRGAAGFVWENGVIAPVHEITTVAGRLQDHYRDIQVADDALEARRSSNKIGSTLIAGETVAGS

**SEQ ID 3295**

TTGCAAGGCGGTGCGGTGCAAAAAGCCGTCTGAACGCGGCGGCATTCTGTAAAAATACGCTATTGGAAAAAATTCGAGAATCAAGATGTTTGAACAAGAAGACAGTGGATCAGCAAAACCC  
AAATGAAAAGCAGATGAACCGTATTGAGGATTGGGTATGGAACCTGACACGCGCTCTCAAACGACACGCTGAAAAAAAATTCGTTTGGATGAAGATTTGTACGAGGCGCGTCTACCTATAAA  
AAAAATTACGCTCAAACGCGCGCTCAAACCTGCGCGCAATTATCGGACGCTGATGCGCGATACCGGATCCCGCGCCCATCGAGGCGCTTCCTCTCCAAGATGCGCGCGCAGCATGCGCGG  
CACACGCGCTTTTTCGACGCGTGAACACGCGCGCTGACGGTTATTGGCAGCTACGACGCGCGCTGACACGATGTTATGTTCGGAATTTTCCAAACGCGCGCGCGGACGCGTGAAGACGCTG  
TCTGCGACACCAAAAAGAACAGGAACAGGACAAACGCGCGAAAATTCTCCGCGCCCTGTTTCAAGAATTGAAAACCGTGATGGAACCGGGGCGGGAAATTT

**SEQ ID 3296**

LQGVRCCKPSERGGILLKYAIGKNSRIKMFEQEDEWISKYQMKQHNLGLDLMELTRLNDTLKIGLDEDLVEAVVTYKXITSNGALKRQAQPTIGRLNRDTPDAPTEAFLAKLRGDDAA  
 HNAFLORVEQARVRLLADEGALTOFMSDFPNAGAGRLTLVVRNTKKEQEQDKPPKNFRALFORLEVTVMENGGAKI

**SEQ ID 3297**

TTGTGTCACACCCGGCCCTTCAAAGGCCGCTCAGCTTCGCCGAATCTTCGGGATGTGACGGCGAACCAGTATTTCCCGCCCATCATCACAGGCTGCCCTTTTCCAATTTGGGCATTGTCTTCGG  
CAACCACACCGAAGGCGCGGATTTGGTCTTTGTCAACGCTTTTGGGGTGATTTGTTTGGCTGACCGGGTGTGTCATCCCCGCAACATCATCGTACAGCGGTTCAGTATCAAGGTGTCCGCG  
CAAAACGGCGCGCGTGTGTTTACGGAACAACATTTTATCTTCCAATCTAAATAACGGCGGATGCCGTCTGAAAAATATGCCATAAATTTCCGCGCCCCCGTTTCCATCACGGTTTTCATTC  
TTGAAACAGGGCGCGGAAGTTTTCGGCGGTTTGCTGTCTCTGTTCTTTTGGTGTTCGGCAGAGCTCTCAGCCTGCCCGCGCGCGGCTTTGGAAAAATCGGACAATAAACCTGGCT  
AGCGCGCCCTCGTCTGCCAACACCGTACACGGCTGTTCACACGGTTGCAAAAGGCCGTTGTGCGCGCATCGTCCGCGGCAGCTTGGCAAGAAACGCCCTCAGATGGCGCGGAGATCGG  
TATCGCGCATCAGACGTCCGATAAATGCGCGCTGACGTTTGACGCGCGCGTTTATAGGTAACGACGGCTCTGACAAATCTTCATCAAACCGATTTTTCACGCGT  
GTCGTT

**SEQ ID 3298**

LSNPAFKRPVPSAESSGLTANQYFPPIITRLPFSNWLSSATTPFKARIWSLSTCLRVIVWLITGLFIPTRNLTIVQPFSSIKVAAKTAAVVLRRNNILSSNLNNGCRLKIKLINFAPVVFHGGQF  
LKGQAEVFRFRFVLFLFFFGVADERPQPARAGVWKIGHKLQRALVCQOPYTRLPHALQKGVVRRIVAAQLGKERLDGRGIGLAHQTSDKLRLFFERAVGRNFFIGNDGLVQIFIQTDFQR  
VV

**SEQ ID 3299**

TTGGAAGATAAAATGTTGTTCCGTAACACACCGCCGCCGTTTGGCGGCAACCTTGATACTGAACGGCTGTACGATGATGTTGCGGGGGATGAACAACCCGGTCAGCCAAACAATCAACC  
GCAAAACACGTTTGACAAAGACCAAATCCGCCCTTCGGTGTGGTTGCCGAAGACAAATGCCCAATTTGGAAGAAGGGCAGCTGGTGATGATGGCGGGGAATACTGGTTCGCCGTCAATCCGA  
AGATTTCGGCGAAGCTGACGGGCTTTTGAAGCGCGGTGTGACAAGCCCTTCCAATAGTTGAGGATACCCCGAGCTATGCCCGCCACCAGCCCTCGCCGTGCAAAATTCGAAGCGCCCGC  
AGCCAGAAATTCAGTACCGGAGGTTCTTGCGCTGATGATACCGGCAGACCTGACGACATCGCCAAGCTGAAACAGCTGTGATGTTAAAGCGGCTCAAACTGCAAAATCGGACCATTTACA  
CGCGCTCGCTATCGCCAAAGGCAAACTACTGCGCACGCGCAAAAGCTGACGCGCATATCATTTGTAGACAAGTGTCCGCCGATATTTATTAATACGGTTACTGAAAAAATACGCA  
CAAAATTCAGTTTGGAAAAATCTCTPATATACGCCGCCCTTTGGATGATTGGATCGCGCGCGCGGGTGTGGTCTTGCCATGGCTTGATTGACGCCCGGAATTCCTCAGACAAA

SEQ ID 3300

LEDKMLFRKTTAAVLAATLLILNGCTMILRGMNPNVSQTTIRKHVDKQIRAFGVVAEDNALEKGSVLMMGGKYHFAVNPEDSAKLTGLLKAGLDKPPQIVEDTPSYARHQALPVKFEAPG  
SONPSTGGCLCRYDTGRPDIDAKLKOLEFAVKVLDNRITTYTRCVSAGKGYIATPOKLNADYHFEQSPVADIIYTTVTTEKHTDKSKLFGNLIYTPPLLLDAAAANVLVLPMAIAAANSSDK

**SEQ ID 3301**

ATGTGTCAGTCAAATCCAAACCCGCCCGTCAATACCGACGTTTTCATCATTTTGTCTGCCGCCGGCCGGAATCCTTTAATCGCCCGGCTTGTGCTCGCGGGTGTGCAAAAGTCTGCGG  
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SEQ ID 3302

MSVLIQTRFVNVTVFNHLLAAGADPLIARLCASRGVQSPAELDDKLASLLPQYSI/TNCEAAAGRLADAVERKEKILTVADYDADGATACAVGLDGLAAMGAKVDFLVPPNRFEXGYGLTPEL  
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RILVSOGLKMRMSCKMRPGIRALFEVARDWRKAOPFDWGFALGPRINAGRLDDMSVGIACLLARDDEAOELARLANNINRIERREIQSMRLDALNAPFETLPSCQTTLVAYRDDFHQ

VVGIVASRLKDRFYRPTIVFAPADNGEVRGSGRSIPNLHLRDLALDLVSKRHPDLILKPGGHAMAAGLSLEHNTIPAFQAFEEAVREHVCEDDLSTQYITIDGSLPACDITILEQAQNLACHV  
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## SEQ ID 3303

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## SEQ ID 3304

VFRLEQAVRPHKMPKTSIKRRRNYAVRITPPSRQRVITDCLKNQTLILLWSLKFDAPYILEP

## SEQ ID 3305

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## SEQ ID 3306

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GNRVIVHIGLHNVRQYGGGRTAGNNGFEPTAAHTARHFQDPGKRRARHFIVARTLDMAGNTK\*FGTACIRNPTIGKRLSAVTDNKRDDGGERFIVDGGRFVPAERGGERRFEARLA  
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## SEQ ID 3307

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## SEQ ID 3308

LRQLGCLIGPFSVGIIMNLKLVFESGDPVLIGVFLMLIMSTVTWCLVLRICKLYARKGNAAVKRHRMDTSLNDAVEKVRVADAPLSKLAQEAQSYNRYRNEASELAQALPLNEYL  
VIQIRNSMAQIMRRFDYGMALASIGATAPFIFLGTWVGTYHALINIGSQGMSIAAVAGPIGEALVATAAGLFAVPAVLNPLNRTKILITQDLAMADHLVRLINQKDS

## SEQ ID 3309

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AGGCATTACGCAAGCGTCCGCGCAAG

## SEQ ID 3310

VYVHTPLIKKPTGGLSGHLRMCCFHEQSTNLKRPPTSSWSKRGFTFVELKQNTISVSPKSNVQTILGAEPWFLGDVAETILQIQNARQLPLKQDGIQKSSVATKKGQELLFINE  
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## SEQ ID 3311

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## SEQ ID 3312

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## SEQ ID 3313

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## SEQ ID 3314

MPSETPSTTRQVRGPHCRFRARRAGNRRHGNAPVQTVCAVRLCGFTAACTSKFHASWRKSVAVRPNRVRFRASY

## SEQ ID 3315

ATGCCCAAAATACATTTTTCATCAATTTTCTTGTGCTTGAACCTGCCACCCGACATCTTTTTCGGGCGCAGGGTCAGACTTTATTTGCAGGGATGAAGCCCTTACAAATC  
AGAATAATACA

## SEQ ID 3316

HPKIHFFINPSSLLEPCPPHPFSGRGGTFLFAGHKPLTNQNT

## SEQ ID 3317

ATGAAAAATGTATTTTGGGCATTTTGACCGCGTGTGCCCATGCCGTGCAATTTGCCGACAGAATCAGCGATTGGAAGCAGCTCTGGCGCAGTTGGAACACCGTGTGCGCGTATTTGAA  
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## SEQ ID 3318

MKRCILGILTACAAMPAPADRIDLEARLAQLEHRVAVLESGNTVKIDLFSGNSMTYVCSVTTPQKTFEASDRNEGVARQKVRQACNRETSAFPCGDEAIRCRKFD

## SEQ ID 3319

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## SEQ ID 3320

MHTVHLHLETFDNPQLQRLCGSFDNLSLAKALDIHSRRFEHFTFNGAFHAGKRALKLLETAQTRDINDSIIRLAAVETQTEDAGHQEKNHEHAYFPTRKRSIGGRTPRONGYIR  
ALLDHDIVFGLGPAGTKTYLAVAAVDANEKHQVERIILVRPAVEAGEKLGFLPGDITQKVDPLYRPLYDALYDLHGFDRTVKLIEKGLIELAPLAYHRGRTLNGAYIILDEAQTTPPEQ  
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## SEQ ID 3321

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CGCGGGAATGACGGCATTTTCAGTATTTTCAGTAGGGCGGATCT

## SEQ ID 3322

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## SEQ ID 3323

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ACATTCGCGCGCGCGGAATCCATCGTTTCAGACGCGCAACGATACCTCGTTTCCGTGACGATGCGCATGTCTTAGCCCTCTCAAATAATATGAACACCATGCCGATTTTTCGCGGAA  
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## SEQ ID 3324

LAQCPQLRLNIGSGSQEBQLKQQAADLGIAHAVTFLGALQPEAILDLMRNSDAFILASRTETFGVYIEALSQGLPVIAIHCGGASTVSDGNYLVSVDADVLLALKIYEHADFSAE  
QLRTDCLATPGEIDAVIGRLIAVFRQARNTARKRPKNRLK

## SEQ ID 3325

ATGTCGAACCGTTGCACGCTCTGTCATCCCTTATGGTATCCAGATCCGAACAGGATGTGGAGGGAATTTTTCCAAAATCAAGCACAGACCTCCAACGCAAGGCATCAAAACCG  
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TTCTTCCCGCTTTTCGTTTATCGACATCGACCGCATCCGCTGGGTGCGCGCGGTT

## SEQ ID 3326

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## SEQ ID 3327

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GCATTCCTACGTTTAAACGAACACAGCAGCACCATCAGCGCGGTCTGATCCGTCACCACTATGGCAGCGGATGAAAAAGCAGCGCGCGCGCTCCGACGTTCTGCGGTGAGCGG  
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## SEQ ID 3328

VRAGLKAPKHYIRENGLPDLIHAHCNVAIGILAQKISEKYGIPVLTESSTITRGLIRHQWQPHKAAAPASARLAVSRHPAHLVQHKYGCENQYLPNIPGGIFKQTFE

## SEQ ID 3329

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CAGTTT

## SEQ ID 3330

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QF

## SEQ ID 3331

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## SEQ ID 3332

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NVTPEPEWEGYVTLFESNTTLPKAIYAGEGVAQLFFESDEVCEISYKDRNGKYMGTGVTLLPKA

## SEQ ID 3333

CTCCAACCTCCGCCAGTTTCTTCTCAATCGCCTCTTCGGTCATAAAGCTGCACATGCTGTGGTTGTGACACGATAACGGGGCATCGCGCAGCGCCCATGCATTGCGCTTCGACAAAG  
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## SEQ ID 3334

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FGLGDTQRAHDGDTALVGGIFRQLNVDLF\*GFCG\*H

## SEQ ID 3335

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AT

## SEQ ID 3336

MDKERILTPAVVFSVALLHLAIVALLWQAHKLPVIESGNVIEFVDLDFGGGGGAPGAGAPAAPEPQAPDPKPKPVEPPKPVLPVTKKADADIQPKPKPKPEPKPEPEAKPAP  
KPAEKPAEKPSKPAHSGNASAKAGSBQNGEGKGTGKGDGTGRBGSSEKSGGAKGHEGEGAGGSGGGTGVGSSKGNPLRANGSIPRPAYPALSMENDBQMVVLSVLVSPGCHVESV  
KVVSSGFSRLDNAARKAAQNGHFQANAWTEFKVPVFKELN

## SEQ ID 3337

ATGATTTTAAATCGAGTAAATGTATCTACGATTATTTTCAACAGGGGGAAGATGAACCAACCAACCAATCCAAAAAGCTACGAATCTAAGCGCGTTTAAAGCAGCGTTTCAATT  
ACACTGAAAAAGAGCTAATTTATTTGGAATTTTCCAATAATTTAGACTTCTCCAATGGGTAAAGAAAAAGCTGAAACATGAACCTGAATTAGAAAACTGAAAAA

## SEQ ID 3338

MILNRVKCIYDYFQQGGRMNPTKQSKSYESKRVLKHVSFNTKEANLLEFSNNLDFSKWVKEKLKHELEKLEK

## SEQ ID 3339

ATGCTTAAACATCTCGCATTCTACTGCCCCCATGATGTTCGCCCTCCCGGCCAGACCGCGCTCTAAGCCCCATACAGGAACCGGCTGCACCTACGAAGCGGGATCGGAAAGAGCG  
GGCTTCTTCAGGCAAGGCATATGCGGTTCGCCGGATGGCGCGGTATACCGGTTCAATCAAAAACCGCAATTCGACGGGCAAGCGGTTTATACGGTTGCCCGCGCGCGGAGGATTT  
TCTCGAGCCGTTCAATTCGCAAGTACCAAAATCCGCAATATGCGATTGTCGGGACGTTCAAAACAGGCTTGGCACACGGCAGGTTCCCGCCTCGCAAAACGGCGAAACCCCTTTTAT  
TATGAAATGCGAACACGCGCATGAT

## SEQ ID 3340

MLKHLAFLPAMPFALPAQTAVLSPYQETGCTYEGGIGKDLPSGKGIWRCRDGRYTSFKNKGFDQGVYTVAAAGREVLFEPNSDSTKFRNMALSGTFKQGLAHGRFAASQNGETLFPY  
YEMRTRED

## SEQ ID 3341

ATGTGTTCAAGCAGATTAGTTTTTATCCGCTCAACAAAGAAAGCTGCTGAGGCGGACGTACTTGGCGCAAACTTCTGAAGCTGAATTTACCAATTGCCAAGGTTTGGAGCTGTTCA  
CGAAGGCTTTACCGCACCGGTTTCTTTTTCGCCGAACCTGTTTCCCTGCGCACTTACCTTTCGCGCTGCGCCTGAAAAAGAGGAAAAAGTCTGCTGCCGCGCTCATCCGCGATF  
TTTGAAGAGAAGGTAGCGGAAATCCAAACAAATGAAGCCCGCAATGTCGGTCGCAAGAAAAACAAGAGCTTAAAGAGCAAAATACAGACGACCTGCTGCCCGGAGCGTTTACCCGCGC  
AGCGGTACAGAGCGGTGTTTAAACCCCGCCAGGCTACCTGCTGCTCAATAACCGGCTTCCGCCAAAGCGGAAACATCTGACCAAGCTGCGGCAAGCTTTGGGAGGTTTGGAAAGCT  
CGTGGCAATACCAACAAATCGCCTCTTCCCTGATGACCGGCTGGCTGTTGCAAGGCGATTCGCAAGGCGGTTTGAATTAGACAGCGATTGCGAAGCTCAAAGGTACGGCGGATATTGT  
TCCGCTGCTCAAAGTATCCAAACAGACTTAACCGCCGACGAAGTGTTTCAACAGCTCAAAAACCGTAAACCGTTACCCGCTCGGTTTGTGTTGGCGGCAAAATCGCCTTTATCCTC  
ACTCAAGCTTCACTCAAGCGCATCAATACCTCGACGATTGTCAGGAAGAAGCGCAAGCAACGGCAGCATGCGCGCGGCTTGCCTTCGCTCGCAATCTCGATGGCGGAATCCG  
TCAGCACCATTGGAAGAGCTGTTTCTTATTTGGCGGCTGGCAAGAT

## SEQ ID 3342

MWFRQISFYPLNKEKLPEADVLADKLAEARFTHCGLDWFSEGTAPVVSFPELVFPADFLRLVALKKEEKVLPAGVIRDILEEKVAEIQNNEARNVGRKEKQELKEQITDILLPAPRTS  
SRTRAVFNRHGYLLVNNAASAKAENILTKLREALGGLASLPNTKQSPSSLMTGWLLQGHCEGGFELSDCELKGTGDIVFVVKVSKQDLTADEVVQHVKNKGTVTRLGLVWRQIAPIL  
TQDFTLKRIQYLDVLQBEAESNGDDAAGLAFASQILMAESVTMLERLVSYLGGWQD

## SEQ ID 3343

GTGTTCACTTACCGAACCGCACTTGACACAGAAAGCCCAATCATGAAACCAACCATCGCGCTTATCGGCGCGCCCAACGTCGGCAAACTACCTTGTTCACCGTTTGAAGCGCACCA  
AAGACCGCTCGTGCATGACCTGCGGGTCTGACCCGCGACCGCCATTACGGACACGGCAAGTCGGCAGCAAACTTATTTGTTCATGATACCGGGGTTTCGAGCGGTTGTGGACAG  
CGGCAATTTGCAAGCAATGCGCAAAACCACTTCAGGCTGTCGATGAAGCGGATGCGGTTGTGTTTTCGTTGAGCGCGCTACCGGTTTAAACACCGCAAGCAAGATTATTGCCGACCGT  
TTGCGCCAAAGTCCGCGTCCGTTTATTTGGCGGTGAATAAAGCGGAGGCGCGGACAGGCGGTACTTCCGCGCGGAGTTTACGAGCTGSCATTGGCGAGCGCGCAGTTTATTTCCGCGC  
CGCACGCGACGCGGTGATTACCTGATTGAAGAAATTTAGAAATCTTCCCGAGCCTGAAGCGCAAGAACCGGATGCAAAACATCCCGTTTTCGCTTATCGGTGCTCCGCAAGCTCGG  
CAAACTACGCTGTTTAAAGCCATTCTCGCGCAAAACCGGTCATCGCTTCGATATGCGAGGACCAACCGCGCAGCATCCACATCGATTTCGAGCGCGAAGGCAACCGTTTACCATC  
ATCGATACCGCAGCGGTGCGCGCTCGCGGCAAGTGGATGAAGCGGTGGAAGGTTCTCCGTTATCAAGCCATGACGGCGGTTGAAGCGGCAAGCTGCTGTTTGTGATTGGACCGC  
AACAGGACATTGCCGACCAAGATGCGACGATTGCGGTTTTCGTTTGAAGCGGACCGGCTGAGTGTGCTTCAACAAATGGGACGCGCATAGCGAAGAGCGCGCGCAACAGTGAA  
ACGCGACATTTCGCCCAACTGTATTCTCGATTTCGCAAGTTCACCTTTATTTCCGCGTTGAAGAGCGCGGTATAGACGTTTGTGTTGAAGCAATTCAAGCTGCTTACACCGCGCG  
ATGATTAAAGATGCCGACCGCAAAATCACGCGGTATTGCAACCGCGTCAAGCGCAACAGCGCGCGGTGCGGCTTGGTCCGCGTCCGAAATGCGTTATGCCCAACAGGCGCGATGA  
ATCCGCGGTGATTGTGGTTACGGCAATTCGCTGACCGGATTTCGCAAGCTATACGCGCTATCTGACCCAGACCTTCGCGCAAGGCTTCAACCTGCAAGGCAACCGGTTGCGGATTCA



ATACATACTGTTTCGGAACCCCGTATGAAATTCGGGAAGACAAACCGAAGAAAAACCGCTCGCGCGTCAGCCTGAGCAACCGTATTGAGAAACCGAAGGCCGAAGAGAGAAAAAC  
CGCTTCAAGAAGAAACCAAGTCAGTGTGAAAAACAATTACGAAA

SEQ ID 3344

SEQ ID 3344  
VFSSTERHLTKQDPIMKPTIALIGRPNVGKSTLFNRLTRTKDALVHDLPLGLTRDRHYHGKVGSKPYFVIDTGGFEPVVDSGIIHEMAKQTLQAVDEADAVFLVDGRTGLTPQDKIADR  
LRQSPRPVYLVANVNGEGGDRAVLAAEFYELAGEPHVISAHGSDVYVYLIEELLENPEPEAEADAKHPVFAVIGRPNVGKSTLVNAILGSKRVIAFDMAGTTRDSIHIIDFEREGKPFPTI  
IDTAGVRRRGKVDEAVEKPSVITAKMQAVEAANVAVLVLDAAQQDIADQDATIAGFALEAGRALVAVNVKWDGISERREQVKRDISRKLFLDFAKPHFISALKERGIDGLFESTIQAAYNNA  
MTKNPTFKITRVLQTAVERQQPPRAGLVFPRKRYAHQGGNNPPVTVHGNLSLHIDSDSYSTRVLTQFFRKAFLNQGTFPLRIQYNVSENPYENAEADKPKKFLRPLRSLNRIEKREGGRKEKN  
RPFKKKTKQVSVKLTQFSK

**SEQ ID 3345**

SEQ ID 3345  
ATGCGAGCCCTCTCGAAGAAACAACAGAGTTAGACAACCTTTAAATATTTTTGGAAAAACCAAGCGGCAAAATGGCTGTTTGGCCCTGCTGATTTTGGCGGCACTGGCTACTTGGGATACACGG  
TTTACCAAAAACCGTGGCGGCTTCCCAAAATCAGGAAGCGCGCGCGTCTGGCAAAACATCTGTGAAAAAGGCGCAAAACAAAGCCCGCAAGCGGAAATCAATGCGGAATCTCCAAACTCCA  
ACAAAGCTACCCCATTCATTTTCGCGCGCCCAAGCCACCGCTGATGGCGCGCGCAACCGAATTGACGCGCAGCGTTACGATGTTTGGCCGAAGGCTTTGAAATGGGTGTTGTGCCAACCA  
AAAGACAGCCTGATTACGCGTGTGGCGGCGCAGCGTCTGGGCGTTGTGTGTTGCAACAAAAAATACGATGCTCCGCGTTCGCGCACTAGCAAGCCGCTTGGCGGAGCTTTCGCCCC  
TCTGTATGGAACTAAAGGCGATGTTATGCGCGCACAGGAAAAAGCCAGGAAGCTTAAAAAAGCTACGACAGGCTTTGAAAAAATGCCTCAAGATTCTGTGGTGGCGAATTGCTTCA  
AATGAACTCGATTCTGTGAAA

**SEQ ID 3346**

SEQ ID 3346  
MAAHLEEQQELDNFKFYFKWTGKWLPAALLIALAALGYLGYTVVYNRAASQNGEAAAVLANIVEKAQNKAPOSEINAELSKLQSYPHSISAAQAATLHAAATEFDAQRYDVAEGHLKWLVSQ  
FVSLIQALAAORIGVLLLOOKKYDAALAAALDTTVEADPAFLIMETKGDVVAQOEKSORALKNYGQALEKMPQDSVSGRELLQMKLDSLK

SEQ ID 3347

SEQ ID 3347

ATGAACGACGCTTCTGCCGTGTCGGGGCAAAAGATTTCAAACTCAGCGCTGTGTTTGGCAGCGGTTTGAGGATACGGTAAACCGTTGGACGCGAGCTTACGGTTATCAGCAAAATCCGTACGC  
CGATTGTCGACGCTCAACCGGTTTGTGTTGTCGCGTCATCGCGAGGAACCGATGTAGTCGCGCAAGGAAATGTACACCTTCTCCGATTCAACGATTCCTTTAGTGTGAGCGCTGCGTCCCGA  
AGGTACGCGCCTCTGTGTCGCGTCGGTGGTGCAGAACACAACCTTCTGTACAACAGCCCCAAAGCTGTGGTATATGGGGCCGATGTTCGCCCGCGAGCGTCCGCAAAAAGGACGCTACCGC  
CAATTTTCATCAGTCCGTATCGAGGCTTTGGGTTTGAAGGGCCGATATTGATGCGGAAATCATCGCAATGTCGCGGACTTGTGGGAAAAAATTGGGTATTCCGGAATACCTGACTTTGG  
AAATCAACAGCTTGGGCAACCGTGAGGAACGCGCGGCACACCGTGCGCATTGGTTGAATATCTGACCCGCTATGAAGCGCAACTGGACGAAGACAGCAAAACCGCGTCTGAAAACCAATCC  
TTTGC CGCTTTTGGATACGAAAAACCTGTATTGTCAGGAATATCGCAATGCCCGCCGCGGTTTGGTAGATTACTTGGGCGAGGCTTCGCAAAACCACTATGCAACGCTTCAAGGCGATGTG  
GACGCTTTGGGTATTCAATATATTTGAAAATTCGCGCTTGGTTCGCGGTTTGGATTATTACAATCAGACGGCTTTTGTAGTGGACGACCGACAGCAAACTCGGCGCGCAGGCGACTGTGTGCGCG  
CGCGACGTTTACGACGCTTTGATTGAAGAACTCGCGCGCAAGCTTCGCGCTCCATCGGCTTTGCGATGGGCTTGAACGCGCTGCTGCTTTTGTGAGCGCAATACGAGCTTCGCTGGAAGTGAA  
CGCCGCGCTGATGTCTATGCAATGCACCAAGGCGAAGGGCGGCACTTGCAGATGTGATGAATAACGACAGCTTCAAGCGCAAGGTTTCAATGTGAATACAGCATTCCGGCTATCAAGC  
CTGAAGGCGCAATGAAAAAGCCGACACAGCGCGCGCGCTTTGCGCTGATTGTGTCGCGCAAGACGAACTGGCGGACGCTACCGTTACGCTCAAGACATGAACGGCGCACACGCTCAGC  
AAACCGTTTCCGCCACCGAATTGACAGATACTTTCAACAATGGAAGAAGCGA

SEQ ID 3348

SEQ ID 3348

MNDDLFPVGQDKDFLTAVPFQAPEDTVNRWTRAYGYQQIRTPIVEQTGLFVRSIGEEBTVVGKEMTYTFSDNSLSLSLRPEGTASCLRAVVEHNLLYNSPQKLWYMGPMFRFRERPQKGRYR  
 QFHQVGI EALGPEPGPDIDAEI IAMSADLWEKLGIREYLTLEINSLNGREERAARAAALVEYLTRYEAQLDEDSKRRLKTNPLRLVLDTKNPDLQEI CNAAPRLVDYLGEASQNHYARFKAML  
 DGLGIQIYIENSRLVRGLDYYNQTFVFWTTDKLGAQATVCGGGRYDGLIEELGGKPAPSIGFAMGIBERLLL VSEYGSLEVNAAPOVYAMHOGEGADLVQMKYAQALRAQGFNVIOHSGYQS  
 LKAONKKADNSGARFALIVAODELADGTVTTLKDMNGAHGQQTVSATDLTDTLQWKNMA

**SEQ ID 3349**

SEQ ID 3349  
GTGAGGATGGAGATGCTTTGCGGGCGGTAAAAATGCCGTCTGAACACAGTTTTCAGACGGCATTTGACTTACTCTGCGCGCCCTTGCTGATTGTGTCGACTGCAAACTCCGTCTGCCGCT  
TGGGA

**SEQ ID 3350**

SEQ ID 3350  
VRMEHVCGRVKMPSETVFRRLTYSARPCLICPTANSVCRIG

**SEQ ID 3351**

SEQ ID 3351  
TTGCGCGCTTCGTGCTGTACGCCGTTTCGGGCTGCACACCACATCTGTCTCAAAGGAAAAACATGTTTCAAATTTTGACTTGGCGGTGTTTCTGCTTGTCTGCTGCCCGTGTGCTCGCCA  
TTACCGTCAGGAGAGTGGCGCGCGGCTATACGCGCGCTACTTGGGAGACAAACATGCCGAACAATACGGCAGGCTGACACTGAACCCCCCTGCCCATATCGAATTGTGTCGGCACAAATCAT  
CGTACCGCTGCTTACTTTGATGTTACAGCCCTTCTGTTCGGCTGGGCGCGTCCGATTCTCATGATTGCGCAACTTCCGCAACCCCGCGGCTTGCAATGCGGTGCAATTGCGCGGTTCGGC  
CCGCTGTGGAATCTGGCGATGGCTGTTCGTGTTGGGCGTGTGTTTGGTGCTAACTCCGATATGCCGCGGGCGGTATACAGTCCGCGCTGGCTGCAAAATGGCAAACTACGGTATTCTGATCAATG  
CGAATTTTGTTCGGCTCAACATCATCCCATCTGCTGCTTGGACGGCGCGATTTCATCGACAACCTTTCCTGCGCGCGGAATATTCCGAACAAATCGAAOCTTCCGAAATCGAAGCGTGC  
GATTATCTCTGCTGTATCTGACGACCGGGTTTGGGTGCGTTTATTGCCACCGATTGTGCGCGCTGGTGATTGCGTTTGTGCAGATGTTGCTC

**SEQ ID 3352**

SEQ ID 3352  
LPLLVSRSRGLHTTSVQRKTFMFQNDLGVFLAVLPVLLAITVREVARGYTARYWGDNTAEQYGRLLTNPLPHIDLVGTTIIVELLTMTPTPLFGNARPIPIDSRNFPNRLAWRCIAASG  
PI.SMLAMAVLIGVVVLTPYAGGAYCMPLAQMANYGILINALPALNIIPILPDGGIFIDTFLPAKYSQAPRKLEPYGTWIIILLMLTGVLGAPITAPIVRLVIAFVQEFV

SEQ ID 3353

SEQ ID 3353  
TTGAATTATATTATATAAAAAAGGTGCAAAATAAGGTGCAAAATAAAATTAGTTTTCCCAATGGGTTAAAGAACAAATCCGAAAAGAGTTCT

SEQ ID 3354

SEQ ID 3354  
LNITYKKGANKVQIKLVFPNGLNKKSEKSS

SEQ ID 3355

SEQ ID 3355  
TTGAGATTCCTGTTTACCAATGGCTGACAAACGCTTCCAAATCGGTATCTTGGGCTTATGCACATCTCTGTGCGGGTGCAGCATCATCAGGCCGATGATTTTATCTTATCTCGCAA  
CCGAAGAGCTCCCGAACATATGGGCTGTGACCCACATCCCGTAATCAGACATATTGGAATCCTGAGCCGTGTGCCGCGAGTTGCAGGCGCATACGCCGCACAACCCGCGTCAGCATCT  
GCTCCCATTCGGGTTTCGGCTTAGGCACATCGCGGTTTCGGCACAAACGTTACCCCGATGACCATCCGCGGCATATTTCGCCACTTTTTCGCCCTTTTTCATCGCATCTGTCGCCGAATTCAG  
TTCGGCAACCGGTTTCCTTCAACATCTCGCGAAACGTTGCAATCCTACCTCGCCTTCGACATCGGTAAACCGGAAGGGGCGCTGCTGCGTATCGGAAACTTGGGTTGCCCGCTGCAAT  
ATTTCGCTCAACTCCGCGCATCGGGGGCGGGTGCTTCAGCTTTTTCGAAGATCGGCGGTTCGTCAA

SEQ ID 3356

SEQ ID 3356  
LRFPLPMADKRFPQIGILGLMHFLCRADHHQPDFFILILATESLPQQWAVDPHPRNPDIVESLSRCRQLRIRRTTRRQHLLPFRFLRIATHAVHKRYPDDHRRHIAHFRLFHRIVAEIQ  
FNNRLLOHIAKTLOSYLALNHGKTEGAHVAVIGNLGCRILOYLFQLRRIGGGVLQFGRSAVRQ

SEQ ID 3357

SEQ ID 3357  
ATGAATTACCTTTTCGGGCAATGGTGTCTGATTAGCTGGGCACACTTTTAACACCTGAACATTTAGTGGGTGATCTTAACATTGATACTCTGAGAGTATTAGAGCAAAAAGCGTGAGATA  
TTATTTTGGCAACAGGACGCAATCATACCGATATGTCATCCATTCTTGGAAAAATCGGTGCGGAACGTGGGTATTGATTACATCAAAACGGTGCTCGTGACGGGATTACAGGGTAATTT  
GCTTTATAGCAATAGTTTGCCTGAAGAATTAGTCTCGAGCTTTACAAAACATCATATGTGGGAAATCTTATTTACAGACACCAAGATTTTGTGCCATCAA

## SEQ ID 3358

MNLPFRANVSDLGSTLLTPEHLVGLDITDLRVLBQKGVDIILATGRNHTDMSSILGKI GAERAVMITSNGARVRDLQGNLLYSNLSPEELVLELYKTSYVGNLIQTFRFCRHQ

## SEQ ID 3359

ATGCCGCTCGAAACATGTTTCAGACGGCATTTTACCCGCCGCCGCAACCATCTCCATCTCACAAGCCCTTAAAAATCCGCTATAATCGCCGCCAATTTGATTTACGACCCCCCTTTTGA  
AATGGCACA AAAAATCCAATCCGTC AAGGCA

## SEQ ID 3360

MPSEXCFFRRHFYPPANHLHPKPLKIRYNRPQDFSTPFLKWHKSNPSEA

## SEQ ID 3361

TTGTGCACTATCCGATTAATAAGCAACAAAAAGCTGCTTGGAATTTTCAGGCAGCCTTTTCAGGAGGATTTTGATGGAACAAAAAGCGGCTTTGCCGCTTCCCTGCTCCTCGCCGCCG  
CCCTGCCGCTTTGTGCACATTTCTTTCCCTTTGCGGAAGAAAAACCCATAGCCTACGCCGAAAGTCAAAATACAAAGCTGGAAGCGCGCGGATTTCAATATTTGTAAGCAGGATTTGGA  
TTTTTCCTGCGGGCGGCTTCGGTGGCGACGCTTTTGAACAATTTTACGGGCAACGCTGACGGAAGAAGAGTGTGGA AAAAATCGGTAAGGAACAGATGCGCGCGCTGTTTGAGGAT  
ATGCGGCGCATATGCGCGATTTGGGTTTGAGGCGAAGGGCTATGCCCTGTCTTTGAGCAGAGCTCGCGCAGTTGAAAATCCCGTCATCGTGTATCTGAAATACCGCAAGGATGATCATTT  
TCTCGTATTTCGCGCATAGCGCGCAATACGGTTTGTCTTGGCGACCGCTCGCGCGGTGATGTTTCGATGAGCAGAGCGCAGTTTTCGAGGCTTGGCAAAACCGTGAGGGAATTTGGC  
AGGCAAAATTTTGGCGGTCTGCGGCAAAAAGCGGAGGCGATTTCAAATAAATGTTTTTCACACATCATCCCAAGCGGCAGACGGAGTTTGAGTGGCAAAATCAGGCAAGGCGCGCA  
GAG

## SEQ ID 3362

LSHYPIKQTKRLLGNFRQFFRILMBQKRRFAASLLLAALPLCAHSFPFAENPLAYGKVKIQSWKARRDFNIVKQDLDFSCGAASVATLLNNFYGTLTTEEVLKLGKBMRASFE  
MRRIMPLDGFAGKGYALSFEQLAQLKIPVIVYLKRRKDDHFSVLRIGGNTVLLADPSPHVSMRAQFLEAWQTRGNLAGKILAVVPKKAELSNKLFTHHPKQTEFAVGQIRQGRA  
E

## SEQ ID 3363

ATGATGAAGAACAAATATATTTTAATAAAGCAGCAATCGGCATAACCGCCATATCCATATTTATCTCTGACTCAAGGAAGCATCGGCAAACTGAAGAACCATCATATTTCTGATGT  
TCATGTTTCTCAACTCGCTTTGGTTTGAAGAAAATAAACAGTTATGCTGCCGTTACGGCAATGATGCGGCCACTTTATATTTGTGCGCATATCCGAT

## SEQ ID 3364

MMKNKYILIKAAIGITAISIFYLLTQSGIKTEPSYFLMFMLNSLWFEENKTVMAAVTAMIAAHFIFVALSD

## SEQ ID 3365

ATGCCGTACCGGTTAAATTTAATCCACTATATATTTATCCGATATATCAACATCTCTCTATCTTATTCGAAITTTATGTTGAAACTTGCATTA AAAACCATACAAGATGATGAAGAAC  
AAATATATTTTAATAAAGCAGCAATCGGCATAACCGCCATATCCATATTTATCTCTGACTCAAGGAAGCATCGGCAAAAC

## SEQ ID 3366

MPYRPFNPLIYIPIYQHSILFRIILLKLALKTIQDDEEQIYFNKSSNRHNRHILSSDSRKHQON

## SEQ ID 3367

TTGTTTTTTGATGAATTAATAATGAATATATGTTAAACGTTACAACGGAAGCCTTAGCCTCCCGATTGCAGTATTTCAATTCGAAGATGGATGCCGCA

## SEQ ID 3368

LFFDEIKIMYMNVTTEALASRLQYFNSKMDAA

## SEQ ID 3369

TTGGAATTGAATATGCAATCGGAGGCTAAGGCTTCCGTTGTAACGTTTACCATATATTTCAATATTTAATTTTCATCAAAAACAAATTCAGATTATACATACCGCCCAATCGTTTC  
TTGATTTGTTTGTAT

## SEQ ID 3370

LELKYCNREKASVVFTTIYPIILISSKNKIQDVTYRQSFDCPV

## SEQ ID 3371

ATGAAGATTTATTTTATTTTCATGTTCTGTTGTTTATTATCTATTTCTTATTTGATTGCGAAGCAATTCGAAAAACAATCAATAAGATTAAA

## SEQ ID 3372

MKDLFLFSCSVCLLFYFLILLIAETIGKTINKIK

## SEQ ID 3373

TTGCAANTCCAGCAATTTGAATATTGTCAATGTTCCGTCGCAAAAGGAATCTTTATGATGTTGTTGTTACTGGGTTTCAGCTTGGCTTTT

## SEQ ID 3374

LQIQQFEYCHCSVKESLLMCCVLGFSLAF

## SEQ ID 3375

TTGGAAGTGAGAGGAGGTAAGGTAGTGTTCCTGTTATTTCTTTTCGACATTTGGGCTGTATTTTACGATGGAATAAGAGATATTCCTAAAAATAAAATCAAAAAAATTTTGGCAAGATCCT  
TATATATTATAGGAATAATAAATGAATAATCAGCTATGTTAATTAATAAATAATATAGGTTCTGTTTCGGATGGAGGTGGAATAAATATGTTGCAATATATTTATCAATCTTTT  
TTGACAGTATTTGATGTTATGTTCTTGTGAAAAGATTATCTAAAAAGCCAAGC

## SEQ ID 3376

LEVRRGKVFAVIFPSTLGCILAWIRDIPKIKSKILARSLYIIGIINVLISYVLKNIILSVSDGGGKIYVAIYLSNLFPTVLMYVLVKRLSKKPS

## SEQ ID 3377

TTGTTTCTTATCTTACATCTTCTGCTTGTCAATCAAAATAAGACAGAGCATATACAAAACTGACCGACATCTGAAAAATACCTATCCCTTTCCATGCAATCTCCGACCAATTCGAC  
CAATAGATCAGACTGAGAAACAACAAAGCCACAGTATAAATCAACGTAAAAAATATAGCGTAAAGCGCAATAAAGGGAACCTTTATCTACGGTTGTTTTTATAATATATTCAGCAACTT  
GATTTCCGAATATACC

## SEQ ID 3378

LFLILTSSCLVNIKTEDYTKDRHTENTYPLPCNLRTIDPIDQTEKQSHSINQRKKYSVKRNKGNFYLTVVFFYNIFSNLISEYT

## SEQ ID 3379

ATGGATGATCTAATACTATATTTTATCAGGTATATTCGGAATCAAGTTGCTGAATATATATAAAAAACAACCGTGAGATAAAAGTTCCCTTTATTGCGCTTTAGCGTATATTTTATA  
CGTTGATTTTACTGTGGCTTTGTTGTTCTCAGTCTGATCTATTTGGGTCAATGGTGGGAGATTCATGGAGGGGATAGGTATTTTCAGTATGTCGGTCAGTTTTTGTATAGTCTTCTG  
TCTTTATTGATTGACAAGCCAGGAAGATTAAGGATAAGAAACAA

## SEQ ID 3380

MDLLIYFLSGIFGNQVAZYIILKNREIKVPIIALYALPFTLIYTVALLFLSLIYVWNGAEIAWKIGIFMSVSFCIVFLYLIDKAGRCKDKKQ

## SEQ ID 3381

TTGTTAATCCACTATAGTTTAAACAACCTTATTTTGTATTTATCCCAAGTATAAACCTGACATCGTATTTAAAAAGCCGATCTACGCC

## SEQ ID 3382

LLIHYSLNFIIDFIPISINLTIVPKSRIYA





ACTTCTGCCGAAAGCCACGGCAATGTCGCGGTATGGCCTTCCAAAGCAGCCCCAAAGAGCAAAACATAGACAAACTCAAAAAACGTGCCGACAACTGAGCAACGCATACGGATTGGAC  
TTCACCCGCATGCTCCGCGGCTGAAAGCGTCAACCCCAACACGGCAAGCATTTCCACCTT

**SEQ ID 3396**

MARHPYRRLRPAKSGFFVEVGI SEBGNIRSLHLSGSDTVQSSMNLDRPSELVLSYRRAMGWLFAERLPQHTTQIGLGGGSFARWTDFTLPDTRQTAVIDINPQVIAIARNLFELFFEGGKPE  
IIEADGA EYIKVFRHNTDILVDGDFGEQIILDTLVEBPFFRDCRNALSSDGIFVTNWNWSGDKRYQRFIERLLSVFBGRVLELPAESHGNVAVMAFQSSPKBEQNDIKLKRADKLSNAYGLD  
PFRMLAGLKA SFPNNGKHFHL

**SEQ ID 3397**

ATGCAAAACAGCCGACTGTTTACACAATCGGCGTGTCAATCTGGTGCCGCAACCAAGAGTCGAACCTCGGACCCCTGATTACAAGTCAGGTGCTTACCAACTGAGCTATACCGGCA  
AAGAAGCCGAATTATGACGGCACTTCACACTTTGGCAAGAAATTTGTTGACCCCTCATAAAAATACAC

**SEQ ID 3398**

MQNSPTVLHNRVAKSGAGTKSRTRDPLITSQVLYQLSYTKEGELCRQLHTLARNLFDPLIKIH

**SEQ ID 3399**

ATGATTACTGTGACACACTGCAAAAAATGAAGCGCGCCGGGAGAAAAATCGTTATGCTGACCGCTTACGAATCCAGTTTTCGCGCGCTGATGGACGATGCCGCGTGGAGTGTCTGTTGG  
TCGGGGATTCTTTGGGAATGGCGGTTACGGGCGACAGTCGACGCTGCCGCTGACGCTGCGGATATGCTGCTATCACACCGAANTGTGTAGCACCGGTCGAAAAAATGCGATGATTGTCTAG  
CGATTTCGCGCTTTGGTGATATCAGCAGAGTAAGAGCAGCGCTTTGCCCGCCCGCGAAGTGTGCTGCTGCGCGGCGCATATGCTCAAACTCGAAGCGCGCGTGTGGATGGCGGAAACG  
ACTGAATTTCTGCAAAATGCGCGGAATTCGCGTGTGTGCCACATCGGTCTGACCCCGCAATCCGTTGCTTTCGCGGATATAAGTTACGGGCGCGCGCGCAAGCGCGAGCGCTGTC  
TTAACGATGCCAAGCGCATGATGAAGCCGAGCTGCCGTCTACTGATGGAATGCGTGCCGCGGAAGTGGCAAAAAAGTAACTGAAACTGTTTCTGTGCCACATCGGCATCGGGC  
GGGCGCGGATTGCGACGCTCAGGTTTGGTGATGCACGATATGCTCGGTATTTCCCGGCAAAACCGCGAAATTCGTCAAAACTTTATGCGCGGCAAAAGCAGCATCCAGGCTGCGGTT  
CGGCGTATGTTGCGGAAGTCAAAAGCCAAACCTTCCCTGCTGCGGAACATATTTTGCAGAT

**SEQ ID 3400**

MTVTNTLQRMKAAGEKIVMLTAYESSFAALMDAGVDVLLVGDLSLGMVQGRSTLPVSLRDMCYHTCVRGAKNAMIVSDLPGAYQOSKEQAFAAAAELMAAGAHMVKLEGGVWMAET  
TEFLQMRGIPVCAHIGLTPQSVFAPGGYKVGQGRGKAQALLNDAKHADEAGAVLMCEVPAELAKKVTETVSCPTIGIGAGADCDQGVLMHDMGIFPGTKAKFVKNFMRGQSSQAAV  
RAYVAEVKATTPAAEHIPAD

**SEQ ID 3401**

ATGPTCCGACGAGGGAAGGTTTGGCTTTGACTTCGCGCAACATACGCCGCAACCGACGCTGGATGCTGCTTTGCCCGCGCATAAAGTTTTGACGAATTTTCGCCGTTTTGCCCGGAAAA  
ATACCGAGCATATCGTGATCACAAAAACCTGACCGTCGCAATCCGCGCCGCGCCGATGCGGATGGTCGAGCAGGAAACAGTTTCAGTTACCTTTTTTGCCAGTTTCGCCCGGACGCAAT  
CCATCAGTACGACGCGAGCTCCGCTTCATCATGCGCTTTGGCATCGTTAAGCAACCGCTTGGCGCTTTCGCCCGCGCGCTGAACCTTTATATCCGCGAGGCAAAACACGATTCGCGGGT  
CAGACCGATGTGGGACAGACCGGAATTCGCGCATTTGCAAGAAATTCAGTCGTTTCCGCCATCCACACGCGCGCTTCGAGTTTGACCATATGCGCGCGGCGAGCCATCAGTTTCGCGCGG  
GCGGCAACCGCTGCTCTTACTCTGTGATATGACCAAAACGGCAAAATCGCTGCAATCATCGCATTTTTTGCACCGCGCTGTACACATTCGCTGTGATAGCACATATCGCGCAGGCTGA  
CGGCGAGCTGACATGTCGCCCTTGAACCGCATTCGCAAGAAATCCCGGACCAACAGCAGCATCCACCGCGCATCGTCCATCAGCGCGGCAAAACTGGATTCGTAAGCGGTGAGCATAAC  
GATTTTTCTCGCGCGCGCTTCATTTTTTGCACTGTGTTACAGTAATCATCAGATATTTGTTATCCCGCGCTTTTCAGACGCGCTTTTCAGTT

**SEQ ID 3402**

MFRSEGFDFGPNIRPNRSLDAALPAHKVFDEFRRFARENTHEIVHQNLTVAIRARPDAGRTGNSFSYLFQCFRRHAFHQYDSSGFI MRLGIVKRLRLAAAPLNFISAEGKHGLRG  
QTDVGTDRNSAHLQKFSRFRHPHAAFEFDHMRAGSHQFGGGGKRLLLTLLICTKQRIADNHRIPCTACTYFGVIAHLAQADRQRRLSPLNRHSQRIPDQHIHAGIVHGRKGTGFSVQHN  
DPLAGRLHFLQCVHNSHQILPRPPTAFSV

**SEQ ID 3403**

TTGCAGATTGAACAAGGCTGCTGCGCATGCCCTGTGAAAGCGTTTCAGACGGCATTTGTTTTGCGCGTGCGCGCGCTATAATCGCGCGTTTTGTCGGGACGAAAGCCGAGGATA  
AGGATTACCGTAATGCAATCATACATACCAATCGAGAACTCGCGCATGCGG

**SEQ ID 3404**

LQIEGGLLPMPSESRRFRHFLPCAARIIGAFCRAGSPKDKYRNANHTYHSRTAHVA

**SEQ ID 3405**

TTGGCCACCGTACTTCTCTACGAGCATACGCGGTGTGATTTCGCGCGGCTCAATGGTAACAGGTGTGTAATACGCGTTTTGCTCTCTGTCATAACGCATTTCCACATAGCCGAA  
ATCGGGAAGCTTTTCGGAACGAGATTCGACAAAGCCGTAATCGGTGAGGATCGCGCGCAAGTCGGGATGTTGTTGAACATGATGCCGTACAAATCGAAGGCTTCGCGCTGTTACCAAT  
CCGCGCTGTGTAATATCGGCTACGATTGACTACAGGAAGTCTGCTGTGAAACCCAGACGCGTACGCGGATGCGTTGATTGTTTAAACGGAAGCAACTGACTGACACCGCAAA  
GCGTTTGCCCTGCCATGCTTCGTTTTGTAAGTGTGTAATCGACCGCCGACAAAGTCAACAGAGGCTGCAAAATGCAAAATCTTATGCTGCTGCAATGCGGTGACTGAAATATAGTGC  
TCGGGACAGACTCGACGGTAATCTGCCCAAGCTGAAATGACTTTGCTGCTGATGCCAAGCAGCGGACGAGCTCTGTAAGTTTGAATGCTTGCCAT

**SEQ ID 3406**

LATVLLATDDTRCDFARLNGNRLVNHAFLFLVITHFIAGNREVFARMSDKAVIGQDAQVGVNVEHDAVQIEGFALVPIRAVVNIGYGFYREVVV\*NPDAADALIVPNGQLTDWKG  
AFALPCFVFSVIDAAQVNQKLEMQIFMVQCGHD\*NIVLGQTLGDLNLAQS\*NDFACLIAKHADDGLV\*VLNACH

**SEQ ID 3407**

TTGGTGATACGCTGCTGGCGCAGATCATGCGAGCAGCAGACCGCATGCGGAGCAGTCCCAAAGACCGGACGGGAGGCAATCCGAAACGATGCCGTCCGCGGCTGCAAACTTTGGAAG  
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AACGTTTCCGAAAGCGCACTGCTCAGTTTATGAGCGGCAATCCGATGATCAAAATGCGAGGATCAGCTTCGCAACCGAAGAGGAGGCGCTCAGGCGCAGCAGCTCTGCTCAAA  
GGGCTGTCTTTGAAGGGCTGATGAAGCGTTATCCGAACGAGCAGGCGTTTCAGCGTTTCATTATGCGCAGCAGCTTCCGAGCGCTGCGCTTCGCAAGTTTCCCGGTATGAACCGTG  
CGGAGCTTACCCGCAATCCGCTCAAAATGGGCGAACGCTATTACTGTTCAAACTCGGCGCGCTCGGAAAAACCCGACGCGCAGCTTTGAGTGTGTCAGAAACGATTTGGAACAAAG  
TTTTGAGGACGAAAAAGCCGCTTGAATTCGATGCCCTTTTGAAGAAAAAGGTTGTCACCG

**SEQ ID 3408**

LVDTLVAQIMQADRHAESQRPDQAIRNDAVRLQTLVLKNRLKEGLDKDKVDQNRFKIAEASFYAEYVRFLESETVSESALRQFYERQIRMIKLQVVSFATEEEARQAQQLLLK  
GLSFEGLMKRYPNDEQAPDGFIMAQQLPEPLASQFAGMNRGDVTRNPVKLGRYLYFLKGAVKNFDAQPFELVRNQLQGLRQERARKLIDALLEENGVPK

**SEQ ID 3409**

GTGCAATTTGTGCCACCATGGGCAATCGATGAAGGCACTTGGCTTGTTCGCGAAGCCGAAAAACGCGCGGCAACGTTGTTGTGACGATATTCGTCACCGCTTGCATTCGGTC  
AGGCGGAGGATTCGACAAATATCCGCTACTTTGCAACAGGATCGGCAAACTTGCCTCGGAAGGCGTTGCGGTTGTTTTCGCGCGGATGAGAAAGAACTCTATCCGAACGTTGGAACA  
GCGTTTCAACGCTCGAACCCTCCATTTGCAAAACGAATTTGTCGCGCAATTTCCGCGCGGCAATTTTCGCGCGCTGGCGAGCGGTGTTCAAGCTGTTCAATATCGTTTTCGCGATGTT  
GCTGTTTCGCGAAAAAGATTACAGCAGCTTGGCGGTGATTAAGGTTTGACCGAGGATTTGAATTTTCGATATCGAAATTTGTCCTGATACGCGCGGCGGCGGAGCGTTTGGCAG  
TCTCCAGCGCAACCGGTACTTGAGCGTTTGGGAAACCGCGCGGAGCAGCGGCTGTACCGCGAGCTGACAGGCTTTGCGGAAATCGCTGCGGAAATCCGCGCGGCGGATACGCTCGAAATGGCGCGGCGGAGATAAGAACTGGTGGTCTTGGCGCGC  
GCGCGCTGCGGAGCAGCGCTGATTGACAAATGGAAGTGGCGCTGCT

## SEQ ID 3410

VAFVPTMGNLHEGLALVREARKRADNVVVSIFVNRLOFGQGEDFDKYPRTLOQDADKLAAGVAVVFAPDEKELYPNVQRYNVEPPHLONELCKFRPGHFRGVATVVSKLFNIVLPDV  
ACFGKDYQQLAVIKGLTEDLNFDEIVPVDGRAADGLALSSNRNRYLSVGERAEAPRLYRELQAVAESLKQAGLDYAGLERQADHLTAAGHLVDYVEIRRADTLEMARAGDKKLVLVLA  
ARLGTTRLIDNVEVGLP

## SEQ ID 3411

ATGTATGATTTCATTACGGTAATCCTTATCCTTCGGGGTTCCTGCCCCGACAAACCGCCGATTATACGCCGCCGACGGCAAAACAAAATGCGGTC

## SEQ ID 3412

MYDLHYGNPYPGFLPDKTRRLYAPRTAKQNAV

## SEQ ID 3413

TTGTCCGCGCATCGCATAAGGCAACCGCAATCTCAAAACACAGCCCTGCCCTTCGGGGGGGTTTGCAAACTACAAACCGTTGGCTTG

## SEQ ID 3414

LSGIAYRQTDALSKHSPAFGRVLQTYKPFGL

## SEQ ID 3415

GTGAAACGGGCGGTAAACATAATCATCTTATCCGACATCCGTCGAACCTTCAGACGGCATATTGAGTATCTAGACAAGCGTCACCTTATCACAAGCCAAACGGTTTG

## SEQ ID 3416

VKRAGNIILYPTSVTRFRRHIEYLDKASLYHKPMGL

## SEQ ID 3417

ATGATTATGTTACCGCCCTTTCACTATTTTATCTGTCCTCGCAGCAGCCTGCTTGGCGGACAGCGTATGCTGCCGGCGCGCGGATGTGGAGCTGCCGAAGGAAGTCGAAAGGTTT  
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AGGGCAGCGCGGAACCGGCTCTGGCAACCTATATGCTGATGTTGGAACGCACAAATCCCCGAAGTCCCGAACCGCCTTGGAAATGGCGGTGCTGCTGAACCGGTTTGAACAGCGGAA  
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CCACTT

## SEQ ID 3418

MTMLPARFTTSLVLAALLAGQAYAGAADVLPKEVGKVLKRRYSSEEIKNERARLAUVGERVNRVFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFQAE  
NIYQWRQIEPTIPGEAQKRWLRNVLRREGNQLDGLLEVLQASDDVQKRRIPLLIVQAAVQGGVQKASKAVRRAALKYEHLPQAAVADAVFGVQAREKEKAIETALQRLAKLDTKYCP  
PL

## SEQ ID 3419

TTGCCCCCACTTTAATGACGTTGCGTCTGACTGCACGCAATATCCGAAATACTCGACGGCTTTTTCGAGCAGACAGACACCCAAACCTTTTCGGCGCTTGGCAGGAATGGAATTA  
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AGGTGCGTCCGTTATCGACGGCTACGCGGAAAGGCATACGCGAGGGGACGGGGGAACAGCGGGGCGAGCGGCAATGACCGCGCGGATGATATATGCGGACCGCAGGGATTACCCAAA  
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ACGATACCGCGCTTAACGACAGCATAGGCTGGCGTATTAACGAAAGCGACCGGGAAGCGCGCTGCCGTATCTGCGGTATCTGTTGAAAACGACCCCGAGCCGGAAGTTGCCGCCA  
TTTGGCGGAAGTGTGTTGGCGATTGGCGAACCGCATCAGCGGTTGACGTATGACGACAGCGCGCACACTTAGGGGAGACAAGAAAATATGCGCGGAGACGCTCAACCGCTACGGAATC  
GCTTGGCGGACCTTCCCGAAAACCCCGGAA

## SEQ ID 3420

LPPTLMFLRLTARKYPEILDGFFEQTDQNLNAVWQEMEIMNLVSLRKPDDAYARINVLLEHNPNANLYIQAAITLAANRKBGASVIDGYAEKAYGRGTGEQGRAAMTAAMTYADRDRYAK  
VRQMLKRVSAPEYLPFDKGVLAAGAAELDGGRAALRQIGFRVKLPEQGRYPTADNLSTQIMLALSKLPDKREALIGLNNILAKLSAAGSTPEPLAALAQRSITYEPGKRKMIADLETA  
LKLTPDNAQIMNIGYSLSDSKRLDEGFALLQATYQINPDITAVNDSIGWYILKGAESALPYLRYSFENDFEPEVAHLGEVLWALGERDQAVDVWQAAHLRGDKKIWTRETLKRYGI  
ALPEPSRKPRK

## SEQ ID 3421

GTGCGAAGTCCGTCGCTTTGCCCGAATGCCCGCGCTCCCGGCAACCTTATGCGGCTGTAAGAGTATGGCGCTGCATTATTTCCGGGGTTTTCGGGAAGGCTCGGGCAAGGCGATTCCG

## SEQ ID 3422

VRTACRLPECPGFPANLMPSERMGLHYFRGFBGSGRAIP

## SEQ ID 3423

TTGTTTCGGCGGGCGCGGTGTTAAGGTAGCGGTATCGACAGTTGACGAGGAATATTTGATGAACTGTATATTTACGACCATTTGCCGCTTTTTCGCTGCGTGGCGGATGGCTGCCG  
GGCTGTTTGGTCTGACGTTGAAGAAGTCTGCTGCAAAACGACGACGAGGCAACCGCGATCGGTATGATCGGTGCGAAACAGTGCCTGCTGCAAAAGAGACGCTTGGTTTATGGG  
CGAGAGTTTGGACATTGTGTGCCATTTCGACCGGAGAAAGCGCTCTGAAAGACGAAAGTCCGCCCGGAGATACAGGCGTGGCTGGACAAAGGTAGGCGGATACAAACAAATTTGTTTACGCCA  
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## SEQ ID 3424

LFRAAPGVKAGIDRLTRNLMKLYTYDHCPCVRARMAAGLFGADVVEVVLANDDEATPIGMIGAKQVPVLQKEDGSPMGESLDIVCHFDRGLKDEVRPEIQAWLKDVGGINNKLVPQ  
RLIKLGLPEFVTPFAVKYPTDKKEKISIGSFANLNKTAQYLERINADLQLEENLMDGTSINGIGIHEDILVFPVLRNLTVVRGIAPFRKTHDYILGMESEKSGVPLTFDRAL

## SEQ ID 3425

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TATGTCAACGACGCGCGAGGTGAAGTGCCTTCTTTGACGAAATGAAGGACAGATTGCCGCAACCTTCAGGCGGAACGGATTGACCGTGCCTGCGTGTGGTGAAGCA  
ACATCAAACTGCAAAA

## SEQ ID 3426

NRKALIFSVALLACSGSIFAQTLATVNGKIDSSVIDAQAFAFRAENRAEDTPQLRSLLENEVNTVVAQEVKRLKLDRAEFKDALAKLRAEAKSGDDKPKSPFTVWQAVKYGLNGE  
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## SEQ ID 3427

TTGACGGCAGCGCCGACCCGTCGGCGCGGAGGATGACACCCGTTAAGGAACTCTGATGAAACACACCGTATCCGCATCGGTATCTGCTTTTGACCGCTTGGCGCAATTACCTCAAA  
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CGTGGAAACCATCAATATCAACACCCCTTTGGGCACTACGCTCGGACAGTTGTGTCAAGACAGGACCGCGCATTCGAGTGGACGGCAAGGAAATGTCTATCAGGACAGAGGTACGGAA  
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## SEQ ID 3428

LHGTPHPSAGRMTPVKETLMKHTVSASVILLITACAQLPQNNENLWQPSHISFPAEGRLLAVKAEKGSYANFDWYQPPVETINLMTPLGSTLGLQCQDRDGLAVDGKGNVYQABGTZ  
DLSRQLVGFKLPIQYHLWABEGRRVAGAPYRISDGLBQYGTWITGRADSGGQVRLQLNNGNLNIRLVFTIEIGMPSETETPERCAARTR

## SEQ ID 3429

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## SEQ ID 3430

MNIADGRQAPPAPAKINLDRITGRREDGYHNI ESIFCLIDLQDTVYLKPRDDGKILHNPVGGIPQEADLSTRAASLLQKYARNLAGVEIWLKKIPTGAGLGGSSDAATVLLVLRNW  
QCGLTQWQLIDLGAALGADVPFPIFGKNAFASGIGKLI GMDIFKQWYVIVKPPHVSTAKIPTYBGLTRDSASSIMPTFQNLQPPFRNDMQUVVFKEYPEVWKAYSLSKYGSAMTSGSA  
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## SEQ ID 3431

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## SEQ ID 3432

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DIGGVVRAVARAKSLNADLAIIDKRRPKANVAEVMNIIGDIQKRTCLIVDMIDTANTLCKAAVALKERGAERVILAYASHAVFSGEAVSRISSEIDQVVTDTITLSEAAKNCDRIQVT  
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## SEQ ID 3433

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AGGCTCTGACCTTACCGGTACAGAATACGGGATTTGGCTTTCGCGACGACGCGCGGCTTCGACCAAGTGCCTTGTGCTTCAGCAACAGAGGCTTGAATTTCAATAGTCATGTTAAAT  
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## SEQ ID 3434

VQNVAGNHFTIQTIESRDIGRQKHFNSRVQRYATALQFNGLRIFSVNNVQGNADAYKILGFHSLEVDVLFDAERVHLEIADNVFQFAVQRQFNQSRMERFFQCVKGTGVYIYNGN  
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## SEQ ID 3435

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## SEQ ID 3436

WYIEIQASVREAQGTGASRRLRREGQIPGILYEGGEFVAIAVDHKTFFVYALEKESFHTALIKLSINGETKDVIVRDFQMHPFRREVQHIDFQAVKADQLVIRIVPLHIWNAENSQAVKIQ  
GGRVSLNFAVEVLALPANIAPFLDLDAEIVVAGDILHLSIDIKLPEGVESVSLKRNENLAVATVTKKRR

## SEQ ID 3437

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## SEQ ID 3438

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## SEQ ID 3439

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ATAACGCTTCATCAGCCCTTCAAAAGACAGCCCTTTGAGCAGGAGCTGCTGCGCTGACCGGCTCTCTTCCGTTGCGAAGCTGACCTGCTGCAATTTGATCATCGGATTTGCGCTCA  
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## SEQ ID 3440

MTARISRPYLVNQRLRLQTSVSEMPRLPDTVPFQKIDFQAGFFLPQTLFQVLSQDLERLKVGVFPDRAEFQVIAQFQDRIAGNVATVHTKGLRSQRLKLLRHNETVERLLVVR  
ITLHPKRPQFQELRLRL/RLIFGCEADLLQFHDHDLPLIKLTQCAFGNFRFTQKTDVLLGKRRPFDKAVLDILILITLQFQCPVQNFQSLQPADGIVSDCLPVRSLGLLRMPVCL  
LHDLRHQRIHQSRVDFGFCGRKTCQHSNNGSGFLFPHGICPARRQNAQNMVLPYPVFRFLPFRFVCLTQRTDGTVPNFRFLKVGANLSFHFVRRRHFLAAVVDIINAVELAVFQR  
RCRKFAPFQVNLCLIKRNTLFIQFQRHISVRRAAGPFAVVERVLQNGIKTFRILQIGNRFRIFLPLVQDQFALQDLFLRAFIKTDIVVNGFYFLGNRLFGDMQCVCLAVQALFVRLP  
NGFBSRFLVVARLFRFTQFGRKIFLKRPFVFAFHFLCDHGVDFHVFQQLAQLRVRPVTAVFTBCGNLRIDGTVDFLTVNGCQRLGKQAAGTKQRNGSQDFCFHNLISLAFKLY  
SGRLHSVRREMLIVRGRPDARVNHAA

## SEQ ID 3441

CTCGTACGCGCGATGCTGGAAGTGGCTTGATTTTTTGTGGAGCTGAATCAGGCGCTAAATCAGAGCTTCGCGAGTCGCGCGACAACCGGCACATAAAGCTCCACCGGCAGGACACG  
TCGCGACCGCGCACACCGAATAAGAAATAGTGATANTAGCCCGCGCTTGGCACAGCAACCATAGACAATACCAGCGCGCTCGCGAGCTGCTGTCACGCGAGCGAGGCTGCGG  
CCATTTTATTTGTCAGCTGCTGCTGCCAATCATCAGTTCGCGCTGACGTCGCGAGCGGCAAGATGCTACCGAAGCGCTCAAGGTCATACCGGCAATACCGCATATTTCCAC  
GGCGCAGCAGGCAATCTGGAAGTAAACCGGCCAATGAACCGGCACATGAACCGGTCATGTTTCAACACCGTATCCGCGCTGCTGATGAAACCTTTTTTCAAAACGCTTCTATTTCCATTTCCA  
GCGACCTTTTTTCCAT

## SEQ ID 3442

LVTRDGSALDFLELQAVNQSPRSRTTRHINVRHDTVGTAHNGIRIVIAAAVGTTRHQYPARLGEVHVHATQGRHFIGQRTCHNQGVLWGRTEENDTETVKVITRHTRMHFFH  
GAAGQSESNRPQ\*GTGHVHQHRIAGGDETFQNAFYSHSSAPFFH

## SEQ ID 3443

ATGAACACGCGCCCTCTCTTATTCCGATTACCTCATCCGCATCTGACGGCATCTGCTATGATGTAGCGGTGCAAAACGCTTTGGAACCGGCAGCAGCGCTTTCTGTACGTTTGAAGAA  
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GGCAATCAGCACAAGCGGTGGCTTTCGCGACAGGCTTTCGCGCTGCGGTTCATGCTATGCTGCGCGAGACTACGCGCAAAATTAAGTGGATCGGTTTAAAGCGGTGCGCGCGAG  
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CCAATAATGAGATTGCCAAATCCATATCCGCTATATGCTGCGAGGCGGACGCAAGTAGGCGCAGGCGCTGCTGCTGATTTTGAAGTTTCGCGAGCGCTCCGCGCGCTTGGCGCGCTT  
TTTGAACCATATGACGCGCGGTGGAACATACCTCTTCCATTAACGCAACACGCTGCGGATTAACGCGCGGATTTTGGTGGTATCGAGCTGCCCGCGCAGGATGCCCGCGCATTTGAC  
GGTTTCTTGAAGGCTGCGGATACAGTATACAGGAGAACGAAATGCCGCGTACAAGCTGTTCTTCTGCC

## SEQ ID 3444

HNPLPYSYDLIRILTASVYDVAVETPPLPARSLSVRLKNILLKREDLPVPSFKIRGAYNKMSKLPKDALACGVIAASAGNHAQGVALSQRLGCRATIVMPETTPKIKVDKVRSGGE  
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GNGTFRILCKELLDIITVDTDAVCGAVKIDFDDTRSITEPAGALALAGLKAYIAREGAENQTLTAVTSGANMNFHRLRVHVSERSELGEGNEGIPAVTIPEERGSLFQVNIIGNRNIETFN  
YRYGGDEKAHIFVGLQAAGPDLAVIGSRLEAGLPVNDLTNNEIAKIHIRYVNGRTDKVGHRLVSEFFPERPGALARFINHMGQGNITLPHYRNGADYGRILVGLVDVPPHDAAFD  
GFLESIGVSYHEETQNAAYKFLA

## SEQ ID 3445

ATGAGTATTACCATTTCAAACTTAAACAAAAACGCTTCGCGCAATTTTTCACGCGCTGAAACCAATCAACCTCAACGTCCCGCGCGGCAACTCGTTTCCCTGCTCGGTCCCTCCGCGCGG  
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CCAACACTACGCGCTCTTCCGCCACATGATGTGTTTGAACGCTGCGCTTTCGCTTTCGCGATTTGCGCAAGCGCGCAAGCGCGCTTCAAGGACAAATCCGCGCAAGTTCGAAGATTTG  
CTCAAACTCGTACAACCTTCCCACTTCGCCAAATCTATCCGCAACACTTCCGCGCGGCAACGCGCGGCAATCGCGCTGCGCGCTTGGCGTGAACCGAAATCTGCTGCTTTTGG  
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AFEGRIEQLIWHYNGFAWKLDQYQKWQEQATGYIRPHEWQIAAEHETPMIRARIEKIHAVGALTHVLVKHGKQDVHITLAGSDAARYPIAECKKLNLIIPKQYVVFQSNELIKEYSI

SEQ ID 3447

ATGTGTGCTGATTCGCCCGCGCTGGGCTTTCTGCTGCTGATGCTGGTCTGTCGCCGCTCGTTCGCCGTGTTTTACGAAGCCTTAAAGGCGGTTGGGAATTGTACCTGAAATCCTTTAAGCGATC  
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GTTGCTGACCAACCTTGCTCGAATTTCGCGTTCTCGGTATCGCCGCTGGTTGCGCGGTTTGATGTGCTGTATTTGTTGTTGGCGCGCACACGCGGTTGGGCAGCCGGCTGGAAGCGCAAGGCATA  
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TGGTACTCGCGCAAGCGGTTGGCAGATGTTTGGCGCGTTACCTTGCCCAACATCAAAATGGACGCTGCTCATGCCGATCATCTCATCAACGCGCTGCGATGGCGGAGTTCCGGCGCGT  
CAGCGTGGTATCGGCACATACGCGGGCGAAACCAACATATCCCGCTTTTGGTCTGCGAATCTTCTACAACGAATACAACCTTACC GGCGCATCTCCCTCTCCGGCGTATTGGCACTTTTA  
GCACTGGCGACGCTTGGCGTGCAGAACATCATCACAAATTA

SEQ ID 3448  
 MLLIAAALGFLLEMLVVPLVAVFYEALKGWGDLYLKSLSDEPEANSAVKLTLTALITVVPVNAVIGVAMAWLITRFDFLKGQLLTTLTLLDLFFSVSPVAVGLMFVLLFGAHTALGSRLEAQGI  
 QIIFAIPGIVLTALFVTFPPFAAREILIPLMQTQGDSEEQAALVLGASGWMFWRVTLFNKIKWTLTYGIILTNRAMGREGAVSVVSGHIRGETNTIPLLVEIFYNEYNTGAFSLSGVLLALL  
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SEQ ID 3449

ATGCCCTGTCCTCTCTGCTGGTGTTCCTCCGCTTTGCGATGATGGCGCGCGAAATCGCGTGGGGCGGCTTTTCGGAACACGATTGCCGAGCCGACAGCTGCTGGCGGCGCGTCCGGCTGAGTTTCGCG  
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CGCGCTGGTTGTCTGTCAGCTGCCCTTTATCTGTCGCGCGCTGACGCGCGTATTGGAGGAATTTGTCGGCGCAATGATAGGAAGAGCGCGCGGACTTTTCGCGCGCAAAACGCTTTCACAACTTC  
GCCGCTGCTGCTGCCGGAATCAGCCCGGCACCTCTTGAACGCGCGCGGCATGATGTTTCGCGCGGCGCAACGGGGAATGACGCTGCGGCTGTTTATTCGCGCGGACGATCTCCGATGATTTC  
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SEQ ID 3450  
VFVASGGFAVCDGGGNRLGRLSEHDCRAERAGGGAAEFADVVLCDADQCVVFGTLVANVLVRYEFGPKDLANALVDLPALFALTAVTGIALAALYAPNGWIGRFFPEPLGIKIAFTPVGWI  
ALVVSLTFFITRAVQPVLEEISGEYEEAAATLGANRFTTFRVLLPEITPALLTGAGMFPARATGEYGSVIFLAGSIPMISEILPLIITGKLEQFDVQGASAVALLVSVFVILPALNVL  
QWALGRRSGAKG

SEQ ID 3451

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SEQ ID 3452

MTAISPISQTSATQLRELREWFDSYCAALPDNDKNLIGTAWSLAQEHYPADAATTPYGEPILPDHFLGAAQMVDELDLLPDVAATLLADIGRYVPDNNLVSERCNSTVAELVKGVDVQKLT  
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DILRTELKKNYINHFVAGRPKHITSYKKMVKKLSFDGLFDIRAVRILVDTPCEYTTGLIVHSLWQPIGFEFDYIANKPGNGYKSLHTVIVGPEDKGVEVQIQTITMDHQFNEFGVAAH  
WRYKEGGKGDAYSAYEKIAMLRLQLDWRNMAESGKEDIAAATPKTELFNDITYVLTPHGKVLSLPTGATPIDFAYALHSSIGDRCRGAKEVQIVPSTPLENGQVEIITAKBHPSPVNNL  
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LAKCKPAPPDDIAGFVTRERGISVHRKTCPSFRHLAEHAPEKVLDAQWAAQLQEGQVFAVDIEIRAQDRSGLLRDVSALARHKLNVTAVQTQSRDLASMRFTLEVQKVNDLPRVLGLG  
DVKGVLSVTL

SEQ ID 3453  
TTCCTCATCCAGGCGACCTTTTTTCCATTGCTAAACAAAGCCTACCGTCAGGACGACGATATAACACCGCATAGACCAAAGCGGTACGCGCCAAATCTTTGAACACGACTGCCACGGC  
AGCATAAACGCACCACTCCAAATCGAAGAGGATGAACAGGATGTCCAGCAGGTAAATAGGCGACGTCGAACCTTCATCTCTGCGTTTTCAAAGGATTCAAAACCGCATTTGTGAAGCGCGCTCTT  
TTTCGGCATAGTGGGCTTTTCGGGCCCAAATCTGCTGCCGAGCAGGATAAACAGTACGCGGGCCGCGAGGCCGACGAGGATAAAGACAAGACGGGAAATAAGCGGACAACATGGTTACACC  
CAAAATCCGTTAACA

SEQ ID 3454  
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 QIR\*Q



## SEQ ID 3455

ATGCCGGCTGTCGATTTGATCCGCGAAGCGCTGCAGACGCTCGATCCTCTGGTGTGGAAATCGCGCATGAGAGCCATCTGCACAAAGGACACGCGGCAATACCGCGCGGACATTATG  
CCGTTTGGTGGTTCAGCGGCGCTTTTGAAGTTTAAAGCGCTGAAACCGTCAGAAAACGGTCAATCGCTGCTCAAGATTATTTTCAGCGCGCATGATTACGCGCTCGGCATCCGGGC  
GGCTACCCCTGACGAGTATTTCCATACGCGGAC

## SEQ ID 3456

MPAVDLIRERLQYLDPLVLEIGDESHLHKGHAGNTGGGHYAVLVVSGRFEGLSLNRQKTVKSLKDLFSGGMIALGIRAATPDEYFHTAD

## SEQ ID 3457

ATGCCCGCTGAAAAACGAAAAATGGAAGTTTGGTGCAAGACGAATTTGTTATAAGCGGTGGCAGTTTTCAGCGCGCGCATGTTT

## SEQ ID 3458

MPPEKRRKKVCKDEFVIKRLAVFQAGAMF

## SEQ ID 3459

ATGCAGATTTTATCTTTTCAGCGGACATTCGCGAACGTATGCTGGAAGGTACGGAAGCGAGTCGGTCAACGAAAAACGACAATTTGTCGCTACGGACAACGGCTATTGGATTGCGTGGC  
ATGAAGCGCTGGCGGCACTGCTTGGCGCCGATACGCCCGCGGCACTTCCCTGTTTGGTGGTGAAGGGCGGAAAGCCTTGAAGAGTTGTCGCGATGGTGAACGCGCGGAGTTTACGA  
AGTGAAGAGTTTACGCGCATGACGACGCTGGCTCGAAGCGGCTAAAGATTGCGGACACCAACGCGACGCTTGGCGCTGCGGACAT

## SEQ ID 3460

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## SEQ ID 3461

ATGCCCTTAATGTCCGACGGCGCAAGCGTCGCCGTGGTGTCCGCAATCTTTAGCCGCTTCGAGCCACGCGTCTCATGCGCTCAAACTCTTCCACTTCGTCAAACTCGCGCGTTCACAC  
ATCGCGCACAACTCTTCAAGCTTTCCGCCCTTCCACCCAAAAACAGGGAATGCCCGCGCGGTATCGGCGCAAGCAGTGGCGCACGCTTATGCGACGCAATCAATAAGCGTTGT  
CCGTACGCAAAATTTGCGTTTTCGTTGACCGACTCGCTTCCGTACCTTCCAGCATAGCTTCGCAATGTCCGCTGAAAAA

## SEQ ID 3462

MPMSAGASVAVVSAIFSRFEPRVVIKLVFVKLAAPHRAQLFKAFRPFPHKTGNARRRIGRKQCRHAFHPRNPVAVVTDKLCVFDRLAFRTFQHTFRNVLKR

## SEQ ID 3463

TTGACGGAACCAATCATATAAGGAACACTTATGACAGATTTATCTTTTCAGCGGACATTCGCGAACGTATGCTGGAAGGTACGGAAGCGAGTCGGTCAACGAAAAACGACAATTTGT  
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TGCCTGATGGTGAAGCGCGGAGTTTGAAGAGTTTGAAGAGTTTGAAGAGTTTGAAGAGTTTGAAGAGTTTGAAGAGTTTGAAGAGTTTGAAGAGTTTGAAGAGTTTGAAGAGTTT  
AAAGGATGCGCAGCTTGGCGCAAGGGTGAAGGCTTGGCGCTTTT

## SEQ ID 3464

LITENHHIKELCRFYLFRTLRNVKVKASRSTKTHNSVRTTAIGLRGMKAWRHCLRPIRRRAFPVFWGKRKALKSCARWNAASLTWKSLTAMITRGSRLKLIADTTATLAPADI  
KGMAGLPQGVQGFVAF

## SEQ ID 3465

TTGAATAAAATTTATCTTGTATTATAATAAGGACGATCAATATTTTGGGACTGCAACAAACGCAAGCATTGATTTGCGTTTGTGCAAACTTATTTATAGCAGTTTGGCGCGCG  
ACTTAATGGGAATTGTTTATAGACA

## SEQ ID 3466

LNKNYLGIIIRQHLPWDCNKRKALICVCKLIILAGCGADLIGIVRA

## SEQ ID 3467

ATGACAAATGATTTAAGCATTTAAGCGTGTTTTATCATAGACTGTATTTTACCGCTCTCTATTAAACATGAAAAAGCCTTGATTGCCAAAGGGCGGAAACATACGAAAAACCA  
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ATTTGTGATATTATCATTTGATTATTAAGCAGTTTGGGAGATTTGGACGGTTTAAATCTATATTTTGCCTAAATCATCAAAATTAATCGTGTGTTTAAACATTCGCGCACCGCAAT  
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AACAGCGATGGCAACACTTTT

## SEQ ID 3468

MTMLSLSLFFIIRLLFLAVSIRHEKALIAKAKQYKTNSTVLAAVHTLYYLACFVWVWLSDTAFNGISLIGTLVHASFVLSLIIKQLGEIWTVKIYILFNEQINENLFTKTRHPH  
YFLNITPELIGIALLCQAWYVLLIGLPTIYLLVFKRIRQEQANATLF

## SEQ ID 3469

GTGTTCAACCAACGCGGCTCAAACTTGAACCAACCTTCTACTGGCTGGGTTTACGCCAAAGGCCAAGGCAAACTTCCGCGCACTGGCGCGCCCATCGATGCCGAATGGGCGAGT  
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TCCGCTGACCACTGAAACACGCGCTCTTGACTTGGGACGCTGGGAAACGCGCTACTACATCGACTACCGCAACAGCGCGCCCACTACCTGGAAGGTTTTGGGAAATCGTCAACTGG  
GACGAAGTCCGCAACGCTTTGCGCA

## SEQ ID 3470

VFNNAQTWNHTFYNLGTFPKQKPSGELAAIDAEGSFEKQZAFNACAAGTFGSGWAWLVKTPAGGLALVSTSNAAATPLATTENTPLLTCDVWEHAYIIDYRNSRPNYLEGFWEIVNM  
DEVAKRFAA

## SEQ ID 3471

ATGGTTACACCAATCCGTTAACAATAATTTCTACAATAATTTGATATTTTAGCGAATTTCAAAAACCAATTAAAGGTAAATATCGGCAAAACGCCCAAAAAACCAATAAATACAATCA  
TGTTA

## SEQ ID 3472

MVTPKSVNKLSTIISYSEFQKPLGKYRQNAQKNPINTIHL

## SEQ ID 3473

TTGTCCCGCATCTGAGCAAGAGACTTTGGAATTCCTACTACGCAACACCATCAAACTTACTACCAACCTGAACAATCAAAATCAAGGCACCGAATTTGAAAACCTGCTTTGGAAG  
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CGCGCATCGATGCCGAATGGGCGAGCTTCCAGAAATTCGAAGCGTTCAATGCTGCGCGCGGCACTTTCCGATCCGCTTGGCGCTGGCTGTAAGAACCCCTGCGCGCGGATGGC  
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## SEQ ID 3474

LSPHLSKETLEPHYGKHHTYITNLNQIKGTBENLPLEEIVKFI GRRVQQRGNSLPHLLAGFHAQRPRQTFRRTRRRHRCRMGQLREI PRSVQCLRGRNFRIRLGVAGKNPCRRIG  
FGPHFQRCNSADE

## SEQ ID 3475

ATGCGGGGACAAATGCGCTCCGGCTCATAGGCGAGTTCGGCGAGCTTATGTTCCATTTTGTGCTCCTAATGTTGTTTTGGATGTTGTGTTTTGGCAGTGTGCTGCAAAACGAATCGCGGGCT  
CACGCATTCTACCTGTTTTGAGTGATGGAAACCAATTAACCTGCTTTGCGTATATAAGAGATTGCAATTTCCGCATGACAGATTGGATGTACCATGAACGATTACCGAGCTATGCCGC  
C

## SEQ ID 3476

MRGQCVRLIRQLRQLMFHFVLLMLFLDVVFWQCCCKRIGSSRLPVLSDGNQLNLLCVIIEDCNFGHTDMYHERLESYAA

## SEQ ID 3477

ATGAACGATTACGCGAGTATGCCGCTGAAGCGCTGAGGTGCGGCGATTGTCGCTGCTCCGCATTCGATGGAGGCGGAACAATCCGTTTTGGGCGGTTGATGCTGGAAATCCGGCTT  
GGGACAGGATTGCGGATGTTGTTTTGGGAGAGGATTTCTACCGCCACGAACACCGCTGATTTCCGATCCATTGCCAAATTAATCAATGAGGCGCTCCCGCAGATGTGATTACGGTTCA  
GGAAGATTTCGACGCGAACGAAGATTTGAAGCGGCGAGGCGGATTTGAATATCTGATTACATCGGCGCAAAACACCGCTCTGCGCAAAACATCCGCGCTACGCGCAAAATCGTACGGAG  
CGTTCATTATGCGCCCACTCGCGAAGTGGGGACGGAATCGCCCGCAGCGCATACAATTCGCAAGGCGAGGACGCGGGCGGCTTTTGGATGAGGCGGAAACAAAGTGTTCAAATCG  
CCGAAAGCACCGCCAAATCAAAGCAGGCGTTTTTGGAGATGCGGATTTGCTGAAAGAGTGTACAGCGCATCGATATGCTTTTATTCGCGCGCAATCCCGATGAAGTTACCGCGTACC  
GACAGGTTTCATCGACCTTGATAAAAAAACCCTCGGGTCTGAGCCCGCGACCTGATTATCGTCCGCGCGCGCGCTCTATGGGTAAACCGCGTTCTCCATCAATATTGCCGATATGTC  
GCCATTGAAAAACATTTTGGCCGTCGCGTTTTCTCGATGGAATGGGCGTTCGCGATGTTGTCATGCGTATGCTCGGCTCGGTCCGAGCGCTGGATCAAAGCGTTTTGAAAAACCGCAGCG  
TCGAAGACGAACACTGGGCGCTCTGAACGAAGCAGTCTGCAAACTCTCAGACGCGCGCTGTACATCGACGAGACCGCGCGCTGACTGCGCTGCAACTGCGCGCGCGCGCTGCT  
CGCCCGTCAATTTAACAATAAGCTGGGATTAATCGTCATTGACTACCTGCAACTGATGGCGCATCCGCGCTTTCGGAACACCGCGCTTCCGAGCTTGGCGAAATTTCCGCTTCCCTCAA  
GCCCTGGCAAAAGAGTTGCAAGTCCCATCATCGCCCTGTCGCAATTCAGCCGCACTGTGCAACAGCGCACCGGACAAACCGCGATGATGTCCGACTCCGCGAATCCGCTGCTATCGAGC  
AGGATGCCGACCTGATTATGTTTCATGTACCGCGACGAATCTACAACGAGACTCACCCATGAAGGCGCTTCCGGAATGTATCATCGCAAAACACCGCAACCGTCCCGCTCGGTAAATCTT  
CCTCACAATGACGCGGACAAATTCACAAATTCGACAAATGCTGCTATATTTCCGAGGAGGCAAGATAGAAGAT

## SEQ ID 3478

MNDYAAMPPEGEVAGALSPLPHSMEAEQSVLGLMLENPANDRIADVSGEDFYRHEHRLIFRSIAKLINBGRPADVITVQEDLQRNEELEAAGGFYLITLAQNTPSAANIRRYAETVRE  
RSMRQLAEVGTIELARSAYNPQRDAGRLDEANKVFIESTAISKQGFLEMPDLKKEVVQIDMLYSRDNDEVTGVTGTFIDLRKTSGLQPGDLIVAGRPMSMGKTAFSINTIAYTV  
AIEKHLPLVAVFSEMGGQQLVMRMLGSVGRLDQSVLTKGRLEDEHWRLEAVVKLSAPVYIDETPLGLALELRARARRLARQFNKLGLIVIDYQLMAASGRSDNRASELGEISRLK  
ALAKELQVPIIALISQTSRTEVQRTDKRPMMSDLRESGAIEQDADLIMFYRDEYYNDSPMKGLABCIIGKHRNGPVGKIPLTWGQPTKPDNAAYTPEAKIED

## SEQ ID 3479

TTGAATTTAATCCATATACATTACCAATTAACCTCCTATTGCTTATGTGTACAGAAAACAACAGGTTTTCAGCTAACAGAGCTGCTCATCGTATGGCCATTGACGCCATTATGGCGA  
CGATAGCCCTCCCAATATGAGTGGGTGGATTGTCATCAGCGCGCATTCGACGTCAGCGGAGCAGGTTGCCAACCCTTTTGGCTTTTTCAGGGGCGAAGCGCTCCGCTCAATCTCCCTGT  
CTATATCTGCTCCTGTCAAGTTAAAAAGAGCGGTGCGTCCAAACAATAGATGTGACTTCAGCAAGAAGGGGTGGGAATGTTGGCTTTTGGCGCAAAAACCGCAATTAAGGAATATGACGGC  
GATGTGGCGGATGTTTTCTCCGCGCGTGGTATTGAATGATGATATCAATGATTAAGCGGATTGATTATGCTTCAACCATATCGCTTTCGGTTCGTCTCAGCGGACCGCGCGACCGGTGAG  
TTTGGAGCTTCAATCAAAACCGGACGTTTCGGTTATACGACGACGAGCATCTTACAGAGCATCCAGCTTTTATTTATCCGAGCGTTATATCCAAATCGTCTGACAGATGCGAGAGCAGT  
TTCAGATGCCATAGGAATTTCCGTTCCGCGGTGGTTTTGATTGACAGCAGCGCGAGGTCGAAGTTTGTGCTAAAAACGATACCGCGCGCGTATGCAACAT

## SEQ ID 3480

LNLHLYTLPIVLLMLCTRRQGGFTLTELIVMAIAAMATIALPNMSGNIASRIASHAEQVANLLRFSRGEAVRLNLPVYICPVQVKDKGASNNRCDPSKRGWMLAFGDKNGKEYDG  
DVADVFLRSVVLNDINDIKRIDYAFNHLAFGSSQPTADRVVMTFNQNGTGYTTQHLTERSSFFYSYDGYIQLVLTARAVSDADRFRSAVVLIDSSGRVEVCRKNDRVAVCKH

## SEQ ID 3481

ATGAAGAATAAGATTGCTTGGCGCTGAAAAATCCCAAGTCCGCTGATGGCTGTAGAGAATCTTGGTCCGTATGCTCTGACCATCGGTATTTGGCATTGCTGCTCCGTACAGTTGC  
GGACAGTCCGTTCCGTCAGGAGGCGGAAACGCAACCATCTGTCAGCCAAATCAGCGAAAACCTGATGGAAGGAATGTTGATGAATCCGACCATTTGATGGACAGCAACGAAGAAACATA  
TAGCTTTTACATGGGAAACAGACATATCAGCTGTGGATGTTGATGTTATGCTTGAATGCGGAGAAAGTAAGGCGCAGTTGGCAGAGGAACATGAAGAGATTAGTCATGAGCTGAAA  
AATGCTTTGCCGATGCGGTAGCTATTATTACGCGCTGCAAGGATTCGTCAGGATTCGTCGCGGATGACCGCGCATATTTCCGAGCAGCGGTGCTTTTCTTCAAAATTCGACAAATGAAGCAACCGGG  
ATACTTTGATTAAAGTATTGTTGGTAAATGATTCCGCGAGGGATTTCGGATATTTCCTGACGAATCTGAAGTGAGCGGCGCAATATCGTATATACCTATCAGCAAGGTCGAGGTCG  
TGAA

## SEQ ID 3482

MKNNDLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQNLMEGLMNPITDLDNKNYSLYMKGQTLASVDGEFMLDAEKSAQLAEELKRFPSHELK  
NALPDAVAIHVAVCKDSGDAPLSDSGAFSSNCDNKANGDTLKLVLWVNDASGDSISRTNLEVSNDNIIVYTYQARVGGRE

## SEQ ID 3483

ATGCTAAACGTACCAAGGCGGTTATGATGGTATGAAGGTTTTACCATGTTGAATTTCTGGTTGCGGGCTGCTCAGTATAATTTGCTGATAGCGGTGATGAGTTACTTTACAT  
CCCGGAAATTAATGATGTGCGCAACGAGCGCTTTCGCAATCAACAGGATTTGCGGAATGCGGCAACATTAATTTGCTCCGATGCAAGAATGCGGGGAGCTTCGGTTGTTTCAATATGTC  
CGAGCATACTAAGAGCATATTGTTGATTCAAGTAATCAAACTCAATCAACCTTTCGCAAAACCGGTGCGCAACGAAGAAATCCCTTTTTCCTTAAAGAGGCGGCGCATGGAATCAACAA  
CTGATTTCCGTTGCTGAATCCATAGATATTAATATCCGGGTTTTATCCAGCGCTTAAACGATGTTGTTTCCAAATACGGTATCGATGATCTTTGATGCGAGTCTGAGACTGTTGTAGTCA  
GCAGCTGTTCCAAATAGCAAAACCGGTAAGAAATATCTACCTTGAAGAAAGAGTTCGTCGCGGATGACCGCGCATATTTCCAGATGATAAAGGCAAGTGGGTAATCCCTCAGTTGCTCGTGAAGAGGTTAAACGATG  
GGTCAATGCCATATGCGGTGCGCAGTTTCGCAATAATGAGGAAAGTTTGTTCGCTTCCAATTTGATGATAAAGGCAAGTGGGTAATCCCTCAGTTGCTCGTGAAGAGGTTAAACGATG  
GATGTGCGGATATTTATGTTTCGCTTTCCTGAAGATGAAGATGCGCGCAAGAGGAAATTCAGATATACGAATAAATTCGACAAATCCAAATATGCTGTTACGCTGCGCGGGTGG  
AGGTTTTATTGGATAGCGGCTTAATGCCAAGATTGCGCTTCTTCAGACAAATAGTATTTATGCTTACCGTATCAATGCGACAAATACGCGGGGAAATGTATGCGCAACAGACACTT

## SEQ ID 3484

MLNVKGGYDGMKFTTIEFLVAGLLSITVLIIVVSSYFTSRKLVANERLAIQDLRNAATLIVRDARMAGSFGCFNMSSEHTKIDIVDSNQTQSNLAKPGAKQENPLFLSLKRSMDKQ  
LIPVARSIDIKYPGFIQRLNALVFQYIGIDLDASAEVTVSSCSKIAKPGKISLTLQAKSALQITNDDKQNGNITRQKHVVNAYAVGRFGNNESLFRPQLDDKKGWENPQLLVKKVRM  
DVRYTVSSCPDEDEDAGKEKFRYTNKFKDSKNAVTPAGVEVLDDSGLNAKIASSDSNIYAYRINATIRGGNVCANRTL

## SEQ ID 3485

AATCCCTCTGCGTATTGTTATCTACAATCATATTATCTGTCAGTAACTGCTCCGCCCCAGCGGAAGTTCCGTATCCGAAATCAGCATACGAGAGACAACTTTTGTGCTGACGATCC  
ACGGTCTGCTGTCAAATACGTCCTGCGCTTTCCGCGCAAAATCAACCGGAAAGGCGTTGCTTGAGCAGTTCTTTATAGGGAACACTACCGGGTTCGCGAGCGCATACCATATGCC  
CTAGCGGTATGATAGGGAATACGTGTGACGCGGTAGCAAAAGCATGCGGGCTGTGCGGTATTAACATTAACAATACCATCCGCGGTAAAGTGGCTTTGCACTGTTTTAAAAATTC  
CGCACTCAACAGGTTAGTGAATAGGACGCCAGTACCAAGTCGAATTCATCAAACTCAATCAACCTTTCGCAAAACCGGTGCGCAACGAAGAAATCCCTTTTTCCTTAAAGAGGCGGCGCATGGAATCAACAA  
ACACGTTTGTCTGCAAAAGCGGTGCGATTTGCGGCTGCTCCGCGATAGGCTACGGTATGCGGATGATTTCGCAACGATCATGCTGCTGCTTCCGGAATGCGAGACAGACGCGG  
CCACGAACCTGCTACTCAATCAACGACGAATAATGCGGCTATGCGGACTTCAGGAGGGTAGCAGATAGGCAAGTTCGATGCGCTTGCACATTTGAATATATCGGTATTTGATGCGCG  
TCGTATACATTCGCCCCATAAACACCTTATCACCATCTCTATGTTAAACCGCAACATGCCGTGTTTGTGTTTCAATCAACCTATCCGAGCGGCGCAAGATTTTGAAGACAGAAATCC  
GGCAGTAGAACATAGGATGCCGAACATTTAGGGAACCTGCTACCGACACTGCAATTCAGTTCGAGACTTTTTGGAACAGTGTACAAAAACAAAGGACAGCAGAGAAATCAACAGATGA  
GCAGTAAATCTGTGGGTGACAAAGAAATCAAGATACAAAGCGGATAAGGACCGCAATTCAGTCTGCTGCGGCAACGTTGGCGAAATAAACATTTGGAACCTGCTGCGGATTTGTT  
GCCATCCGTACCCACATGGTGTACAAAGTGGGAAATCAACCCCTGACGACGCGCAGCAGGCTAATGAAGATACCGCGTGTGTGACGAAGCGGAAACCGGTCAACACACCGCAGCA

CCCAAAATCAA AAAATCGGCAATACCGGCCCAAGAAGCACTGCCGATAAAGGGAATATCAACAAAGCGGCTCGGGCAAATCCGTTTGCCAAAATACGGCCGACGGGOGATACCGGTCA  
GAAAAACAGGCAGAGTAAATGAAAAATGCCTGAGGCACGGACTGTCTGCGAACGAAAAACATCCTTACCCCAAGACTTCTATACCAAGCTCAATAATCCGTTAAGGAAGAAAGCATATA  
AATCAAAC TAGTATTCGGTTTAGTGTTCACCATATCCATCCTTCTGTAACGCGCCATACTGAAGCAGCAA

**SEQ ID 3486**

NPSAVFVFNHILVSNDFRPSRRFRHPNQHTRDNLCCSIHGAAVKVYPAAPRPNQPGKALBQFFTIRENTRGCRADEYHMPVAVCIGNTVYGGSKSMRAVRGKIKHYNTIRGKVALHLF\*KF  
 RTQVQSGIGTVPSPRIHQNVQVEFFIRMATQPPPTWIQYNFNTVLQKRCDLRLVRDKATVCRIDFNDRHLHFFNNGRQDARPRCTQSDNEAATAGLGG\*QIGTFDAVDTTIETIGIVCA  
 WYIRPINNLITISMVNRNNAVFPVNPQIRTAFTNLKDIRQ\*EHEDAHH\*GNCYRHCIQSEFTLEBQCTKQRDSSRNQTDQVNNLLGGQIKYHKADKRTQCTAGNVGEINLIGSSGFP  
 AIRTHMVKWENQPPDDGRQGNED\*GVVDEAGKTRQPRSTNQKIGNTRFPQALPDLNINAKAAANPFAKIRADGDTGQKTGKSK\*KLRLHGLCCERKHPYQPDPTTQYQ\*SAKERKHT  
 NQTSIRFSVHHIHPFCNAALKKQ

SEQ ID 3487

ATGTGCGAGTTCAACGAGTATTTAGAGAAACATCCCTTGTGTTTGAAGCATGATGACGAAATTCATTATTATGGCAAATGGTATGATGACGGGGTGTGGGATGATGAAGAATATTGGAAGCTGG  
AGAATGATTTAATCGAGGTTAGGAGAAAAATATCCCTATCCGATGGATATACCAAGGGATATTGTGATTGGAATCGGTACCATTTATGATTTTTTAATGGTTTCCAAATTTGGGAGCTTTTTGA  
AATTAAGAGTCTCCCTTGGTTGCCTGATAGCGTGGGAATTCATGAACGTTATGAAAGATTCACAACGATGCTCCGTTATATTTTTACCAGAAAGACATAGTCAACGTGCGATTGATTAT  
TACAACAAAAA

**SEQ ID 3488**

SEQ ID 3486  
MCEPQDFRRNIPCFREYDENSFIGWKYDDGVWDDDEYWKLENDLYEVRKYPYPMDIPRODIVIGITIIDFLMVPNWELFEIKASFWLPDSVGIHERYFTTMLRYIFTEKDIYNVRFDY  
YNKK

**SEQ ID 3489**

SEQ ID 3489  
TTGACTGTGGAATATTTTATGTGTGCTGGCAACAGACGGGGAGGATGTGCATGAAGCGCGTATGGCGGCACGTCOCGAACACTTTAAACGGCTGGAACCGCTGAAATCGGAAGGCCGTCTGC  
TGACGGCAGGCCCCAAACCTGCTGCCGGAACAATCCCGAACGTGTTCGGGCAGCTTGATTGTGGCACAGTTCGAGTCTTTGGATGCGGCGCAGGCTTGGGCTGAAGACGATCCCTATGTTC  
TCCCGGCGTGTACAGCGAAGTGCTGATCAAGCCGTTTAAAGCGGTGTTCAA

SEQ ID 3490

1ATVEYEM.I.A.TDGETVHREARMAARPEHFKRLETLKSEGRLLITAGPNLLPDNPERVSGSLIVAQPESLDAAQAWAEDDPYVHAGVYSEVLIKPFKAVFK

**SEQ ID 3491**

ATCCGCAACAGCAACACTTTGACAGGAATCCCAGACTTCTGACGGGACAGAGGGGGTCCGCACTGTTTATCGTGTCTGATGGTGATGATAGTCGTGGCCCTTTTGGTGTAACTGCCGCCCACT  
 TCTACAATAACCGAACAGAGGATCAGTGCCAAACGAATCAGACAGGAAATGGCTTTGTCTTTAGCCGAGGCGCGCTTTGCGGAGGGCGAAATTCAGGTTTTGGATTGGAATATGCTCGGGA  
 CAGTAAGGTTACGTTTAGCGAAACATGTGAAAAAGTCTGTGTAACCGCAGTGAATGTGCGGACAAATAATAATGGTAGTGAAGAGGCTTTTGGCAATACGTGGTGCAAGGCCAAGCGCGCC  
 GTTGAGGCGGTGAAGCGTCTTGCCTGCAAAAGTCTGGCAAAATCTACCGACCTGTGCAATTGACAATAAAGGGATGGAATAATAAAGAGCGCGGAGGCGCTGACAAAATGTGCGCGCT  
 ATATTATCGCAATATTTAGCGGTGAAGACGGGACAAAATGTTTATCGGGTTACTGCCAAGGCTTGGGGTAAAGATGCCAATACCGTGGTCTGCTCTCAATCTTATGTAGGCAATAATGATGA  
 GCAA

**SEQ ID 3492**

SEQ ID 3492

MRKQNTLTGIPSTDGQRGSALFIVLMVMIVVAFVLVTTAAQSYNTEQRISANESDRKLALSAAEALREGEQVOLDLEYAADSKVTFSENCEKGLCTAVNVTRNNNGSEAPGNTVVQKPA  
VEAVKRSCPAKSGKSNSTDLCIDNKGMEYNKGAAGVSKMFRYIIEYLGVKNGQNVYRVTAKAGKNANTVVVLQSYGVGNNDQ

SEQ ID 3493

SEQ ID 3493

ATGATGAGCATAAAAATGGAAACAAAAAGGGTTTACATTGATTGAGATGATGATAGTTGTCCAGTACTCGGCATCATCAGCGTCATTGCCATACCTCTTATCAGAGTTATATTGAAAAAG  
GCTATCAGTCCCAGCTTTATACGGAGATGGTGGGTATCAACAATGTTCTCAACACAGTTTATTTTGAAAAATCCCAGGACGATAATGATACCTTCAAGAGCAAACTGAAAAATATTGTGTC  
AGGCTATTAAGATGAATCCGAAAAATGCCAAAAAATATAGTGTTTTCGGTAAGTTTGTGCGATCGCGAAAAAACCAAGGGGCATACAGGTTGGTGGCGTCCGGAACCGCGGGACGGGTTATATC  
TTGTTCGGTATGGATGAACAGCGTGGGCGACGGATACAAATGCCGTGATGCCACTTCTGCCACAGCCTATTTCGGACACCTFTGTCCGCAGATAGCGGCTGTGAAGCTTCTCTTAATCGTAAAAA  
AA

SEQ ID 3494

SEQ ID 3494  
MMSNRMEQKGFLLIEMIVVTILGIIISVIAIPSPYSYIEKGYQSQLYTETMVGINNVLKQFILKNPQDDNDTLKSKLKIPVSGYKMNPKLIKKYSVSVRFDVAEKPRATRLVGVVNAAGTGT  
LSVWMMNSVGDGYKCRDATSAQAYSDTLSADSGCEAPSNRKK

SEQ ID 3495

SEQ ID 3495

GTGAGCCTTCTCTAATCGTAAAAAATAGGGCTGCTTTTGCCAAATGCCGCTGAAAGATCAATTTTCAGACGGTATTTTTTATGGGCATTTTGAAATGAATTATGCCATCAACCATCCCGAGA  
TGCCCTGACGAGGCCGACCCCTATCAATACGCGTAAACAACATGAAAAACGGCAGGCCGCAAAAGCGCGTTAACCGCATGGCAATAAGTTTCGTGCGGCTTCTGCGGATACAAA

**SEQ ID 3496**

SEQ ID 3498  
VKLSLIVKNRAVLPMPSDQFSDGIFYGHFEMNYAINHPMPDEPTPIINTVNNIEKRQAAKAVNMAISSCGLSDTK

SEQ ID 3497

SEQ ID 3497  
ATGAAAGATTATTGTGTCGTCGCCCATCATCTCTGCTGTTTTCCTGTATGCTTGC CGTTACCTGCCTACCCGGTTAATCGGCTTTTTCGACTCGCTAACCGAACCCTTAAGCCGCCCGCGCC  
AAACCGTTATGGAAGCCGCGCGCGCTGCGTCTCTCATTTTCCTGCTATTGCCCGCCATTTTGTGATCCGACAAGCCGCACGAACCTATTGGCATCGCGTTAAACCGCCTTTCGCCCTGCGCGTTT  
TTCATATGTTGTTCACCGTATTGATAGGGGTGGCTCGTCAGGCATCTCGGGATGGTTGATGCCA

SEQ ID 3498

SEQ ID 3498  
MKDIHSSPSLELFSCLAVTCPTRLIGFFALRNRTLRRRAQTVNEAAPGCVLISVIAPYFVSDKPELLIALALTAFAACRFSMLFTVLIGVGSSGISGHLEA

SEQ ID 3499

SEQ ID 3499  
ATGATGGGGACGCAATAAATCTTTTCATTTCGCGCCACTCCAAAAATAAGCGGACACAGGCCGGACAGCGTGCCGGCGGGAACATACACGCGCGGTCAACGGTCAAGTAAACGGCGGAT  
CGGACAAACAGGTTGACAAATCAAGGTAT

SEQ ID 3500

MMGTTINLSFPPTPKISGOOAGORAGGNI PRAVNGQVNGGCDKQVDSRY

SEQ ID 3501

SEQ ID 13501  
ATGGCATTCTCCGAAATCCAAAAACGGAAAGCAGCGGTTTGCCTCGATTCAAATATGCCTTTTATATGGGCGCATGCTTTATCTTCTCACTACTTGGATAGGTTTTCGCGCAFTTCGCG  
CGCATGAGCGCCCATGTTCCGGCAAGCTGGCAGCTTGGGGTTTCGCGATGCGGTTTCCTGCCGATTTCTGTTTACTGAGGGGAATGTGGA AAAATCTTTCGCGATCAATACCT

SEQ ID 3502

SEQ ID 3502  
MAESEIQPKAAGLPAENMPFYMGACPIFYITTWIGFAAFRAAVAPMPGNVAANGFGHAPPAVFLVLLRGMKNLSASIP

SEQ ID 3503

SEQ ID 3503

GTGGCAATTCGGAGCCGCGGCAAAAGTTTCATCCCGTCATCAGCAGCATTTCCAGCCGGCCCATACCTTTTTCGCGCGCTGCATACCGAGTATCAATGCCCAAGGCAAAAGCCAAATCA

GCATGGGGAAC  
SEQ ID 3504

SEQ ID 3504

## SEQ ID 3505

GTGTTACCATATCCATCCTTTCTGTAACGCAGCCATCTGAAGCAGCAATCAGAAGGTTAAGGCAGGCTGTGAGCGCAATGTTTGGGAGAGGGTAAAAAGACGTAGAAAAATTCGGCG  
GCGGCAAGCGATCCGAGTGC CGCACCCAAAGTGTGAAAAAATATAAGGTACCGATAGACTCGCCAACTTATGTATTTTCGGTTTAAAAAACAGGTGAGCAAGGTCGCGCCCA  
TCATAAAGGTAGGAAGCAGCAATAAGAGAAATTTGGCAGCAGCGATGATGGGCAATCAGCCCTCAACTAAAAAGATGCCCAAGCGGAATCAGACCTTGCTTACCAACCGAACAGACC  
GATGGATACCTTCAGCGATGCAAAACAGGGGATGATCTTGAAGGAAAAAGGTGAGCAATGCGTCCGCCGAAATACGCACCTACACCAAGCGGACCATTAATACAGAAATAATGACAGTA  
ATCGAACTCAAAATCGATACCTATGTGGCTGAATAGAAGCTCTGCCAGCTGACCTGGTAAATCAGGCGCAGAGCCAGAGCGAAAAACACAGCGACAATCCTTTACGGGTTTACTTG  
CGGTGCAATTCATATTTTCTATTTTCAA

## SEQ ID 3506

VFTISILSVTPY\*SSNQKVKAGCQRNGLGEGKDVKEFGGKRSECRTOSEVKI\*GTDRLANIMYFVKKTGQQGQGRAHKGKQQ\*KEIGSSDDQISLN\*KMPQAGNQTLAYQTEQT  
DGYPSDAKQDDT\*RTTVNSASAEIRTYTQADHKYRNNDNSRTQIDTYVAE\*KLPADLVNQGAEARGEKHQRQSFQGTFCGRHIFYPQ

## SEQ ID 3507

ATGGTCGACGCGCTGCTAAAACTCCCGAATTTTACCTTTTACTTCTGTAGGAATATTCGGTTTGGTGCTGATATAACACAGTACAAAAACATACGGAACCTTTTATGTATGAACCTC  
CTGATGAGTTTGAAGCAGAAATATTGAATCTCCGACTCAAATTTACTCATTTCCGTCGAAAAAACAATTTATTCGATATTTGTGTATCAGGAGTATATTTTATGGCGCTTAATAT  
AATAGGCTGAATTTGAAGATTTTAAACAGCTTTCCATCACCCTAAATCATACGTTGTGATTAATATTTATTTATCAATGAATCTTATCCGACATATGCTATGAGTTTGTGAATA  
GGAGTACAGCATGGGAAGCAAAAGGAAAAATTTGTACTATCATTCGCGGGGCAAGACAATTTATTCGACAGAACCTTACTACGATGAA

## SEQ ID 3508

MVDVAVKTFEFLPFTSVGIPRFGADITQKNILETFMYEPPDEFTEYYESPDSNLLISVEKNKII SIFCYQELFMGVNIIIGLNFEDFKQLFHHKSYGVDKYILSNESYPTVYEFDEI  
GVQAEAKGKI VPIIAGGKDYSTEPTYDE

## SEQ ID 3509

TTGCTTTCTCATTGGATATGAAATTTGTACGCGACCTTTTGTCCGTCATCTGTGTTTTGCTACTTATACCGTTACCAAAAAATGATTTGCCGCTGCGCGGTTGCTTTGGTTCAGGCG  
TGGTTCAGCGCGCTTTCTGTATTGGAAGCATAAAGGCTGGATACGATCGATGGGTGCGGACTGGTCTGATTGTCGTTTCGCGCGGCAACCATTTGTTTGGCGACACCGCTTCAT  
TATGTGAAGCGCAGTATTGTTCTGGTGGCGGCGCTTATCTGCTGGGACGCCACTTTCGCGGTAAAAACGCGTTGAAAGCGAGTATCGGCAGGAGATTCAGCTTCCGGATGCCGTA  
TGGGAAAAATTCACATATATGTGGTGGTCTGTTTTCTGATTTTATGGGTATTGCCAACTGGTTTGTGTTTACTAGGTTTGAAGCGCAATGGGTTAACTATAAGATGTTCGGTTCGACTGCC  
TGATGCTTTTCTCTTATTTATTCAGGGTATTTATCTGAGTACCTATCTGAAAAAGGAGGAT

## SEQ ID 3510

LLSHLDKMPVSDLLSVILFFATYTVTKNMIAAAVALVAGVVQAAFLYWKHKRLDTMQVGLVLIVVFGGATTVLGDSTRFLMKPTVLFVCGALFLLSSHLAGKNGKASIGREIQLPDAV  
WGLFVYMWVGLIFLPMGIANWFVTRFEAQWVNYKMPGSTALMLFFPIIQGIYLSYLLKKED

## SEQ ID 3511

GTGTATAATCTCAATCTTTGAAACCGCGCTATGCAGGAGCAGGACGATGAATATTGAAGTAGAAATGAAAGTGTGGACGAGAGGATGGCGGATTTTATCCCTGCCATTCGACCGGAGG  
GTTCTCGAGGTTTGGATTTCGCGCGCTGTGTTGGATGAGGAAGTCGTTTTCGAGCGCGGCAACCGTTCTGTCGCCACAGGTTTGGCAATTTATTTGGCGAATCCCGCATATGCCGCTGT  
TTTGTGCCAGCTTCCGGCTTGGGCGATAAACACGCGCATTTGCTTGGGCAATTTGGTTCGTTGATTGACTCCGATTACCAAGGGGAATGGAAGGTGCTGTTATGGAACAGGGGTAGCGAA  
CGTTTTCGCGTAAGCGGTCGAGCGTATCGCACAAATGTTATCGTCCCGCTGTACAGGCGGGCTTCAACGTGTCGAGGAATTTGTGCGAAGCAGCGCGGTTGAGGCGCGCTTCGCGCA  
GTACGGGTCTCAC

## SEQ ID 3512

VYNLSLPAVCRSRMTNIEVENKVLDERMADFI PAYATEGSAGLDLRACLDEEVVLQPGETFLVPTGLAIYLANPAYAAVLLPRSGLGHKHIIVLGNLVGLIDSDYQGLKVS LWNRGSE  
PPAVKPFERIAQWIVPVVQAGFKRVEEFVGSRRGEGGFGSTGSH

## SEQ ID 3513

ATGCCGCTGAACCGCTCTTCAGACGGCATTTCTATATCTTATGTGAGAACCGTACTGCGGAAGCGGCCCTACCCCGGCTGCTTCCGACAAATTTCTCGACAGCTTTGAAGCCCGCTGT  
ACGACCGGCACGATAACCATTTGTGCGATACGCTCGAACCGCTTGACGCGCAACCGTTGCTGATCCCTGTTCOA

## SEQ ID 3514

MPPEPSFRHSISLVRTRTAEAAITPAASDKFLDTFEARLYDRHNDHLCDTLERLDGKRFATPVP

## SEQ ID 3515

ATGAATACCTTACTCAAGCAGCTCAAACATATCCCTTTGCCCGACTGCGCGAGGCGATGCAGGCGATTTCCGCGCTGAAGGCATGGAAGCGCTCCCACTGCATATCGGCGAACCGGAAAC  
ACCCGACACCGAAGTCAATACCGGATGCGCTGACCGCTCATTTGCGCGAGTTGGAATAATCCGCTGACTGCGGGTCTGCCGTAACGCTGCGTTCAGGCGTGTGCGAACTGGAACCGCG  
TTATGACGGCTTGACGCTCAATCCGGAATAAGAAATCTGCGCGTTTGGGCACTGAGGAGCGCTGTGTTTCTTTGTTCAAAACCGGTGTAACCTGTTTTCAGACGGCTAAAAACCGTA  
ATCGTCAGCGCGAATCCCTTTATCAGATTATGAAGTGGCGACACTTTTGGCGCGCGGTGAATCCATTTTGCCAAATGCCCCGCGCGCTTCTCAACCCCGATGCGCGCAGTATTTCG  
AAGAGGTTTGGGAACGCACCAAACTGGTGTCTGCTGCTCGCCCAACACCCAGCGGAGCGTCCCGGATTTGGACGATGGAGAGAAGTTTGTATTTACAGGATAAATATGTTTTCAT  
TATTGCTCGGATGAATGCTATTCCGAAATCTATTTGACGCGCAACAACTTTGGGCTGCTGCAAGCCCGCGCACAGTCCGGGCGAAGCAGGCAAAATGCTTATGTTTCAACAGTTTG  
TCCAAGCGCTCAATGTTCCGGGCTGCGTTCGGGTTTGTGCGCGGTGATGCGGAATGCTTANGAACTTTCTGCTTTACCGAACTTATCAGCGCAGCAATGAGTATTCGCGTGCAGC  
GTGCCAGTATTCGCGCTGGAATGACGAACAACAGTTATCGACACCGCGGTATGATCAGGAAAAATTTGAGCGCGTTATCCCATTTTGCAACAGGATTTGACGTTAAATTACCGAG  
TGCTCGTTTATCATCTGTTGAAAGTCCCAATGGCGACGATTTGGCATTCGACGCAATTTATGGCAAAAGCGCTATCCAAAGTATTTGCCGCGAGCTTTTGGCGCGGATACCGAG  
CAGGGGAATCCCGGGAAGGTTATGTCCTATCGCTTTGGTTCGCGATGTCGCACTTGTGTCAAAGCTGCGGAAACCATTTGTTCCCTATATCGG

## SEQ ID 3516

MNTLLKQLKPYPPARLREAMQGISAPEGMEAVPLHIGEPKHPKVIITDALTSALRELEKYPLTAGLPELRQCANWLKRRYDGLTVNPDNEILPVLGSSREALFSVQTVLNFVSDGLKPV  
IVSPNPFYQIYEGATLLGGGEIHFANCPAPSPNPDWRSISEEVWERTKLVPVCSNNPSGSPVDLDGMRVFDLQDKYGFIIASDBCYSEIFYDGNKPLGCLQAAAGSGRSQKLLMFTSL  
SKRSNVPGLRSGFVAGDAELLKNFLLYRTHYSAMSIPVQRASIAWNBQHVINDRRMYQKPERVPILOQVVDVKLPDASFYIWLKVPNGDLDFARNLMQKAAIQVLPGRFLARDTE  
QGNPBGYVRILVADVATCVKAAETIVSLYR

## SEQ ID 3517

ATGTTTTTTGTCCTTTCCCTCGGAAAAACCTTAAACGAAAAAGACCTTTCCTGTCAGCGAGTTTACCAACCCGATCTTTGGCGGAATCTGAAATCTGATGCGCCAACTGAGGGAGC  
TTGCCCTCAACAAATGACAGATTGATGCAGCTTTCCGACAAATCGCACTTCTAAACGCGGACGAAATGACGCTGGCACACCGCGTTTACGCGGAAAAACGCCAACAGCGCGTCTT  
TATGTTCAACGCGGATGTTTACGAAGTATGATGCAACACATGAAATACCAATCAAAATCAATATCTGCAAGGCGATGACGCTGCTGTCGCGTTTGTACGGTCTTCTTCCGCCGTA  
GACCTGATACAGCTTACCGCTCGGAATGGGAACGCTTTCGCCAATTTGCGCGCAAGAACCTGTATGAGTTTGGGCGCGCATCATTACCAACCTTTTAAATGACACGCTTGCCCAAG  
CAGGCAGCAATACGCTTGTCAACCTTGCCTCACAGGAATATTCAAGTCGCTCAACAGAAAAAATTTCCGGCGCGGCTGATTACCCCGATTTTAAAGACGAAAAAACGGTAAATATAA  
AATCATCAGTTTCTATGCCAAACGCGCGCGGATGATGGTCCGCTATGCGCGAGAACCAATATACCGATCTTGAAATGCTGAAAAATTTAATTTACGAAGGCTACGCTTCAATGAC  
GCGGCTTCCAATGAAAGCGAATGGGTGTTATGCGCTCGGAACAAATAAG

## SEQ ID 3518

MFVFLSPAKNLNEKPCVSEFTQPDLLAESEILMRQLRELAPQQAELMHVSDKIALLNERNAAWHPTTPENAKQAVFHFNGDVYEGMDANTLATNQIQYLQGEVRLLSGLYGLLRPL  
DLIQYRLLEMGTSFANLRGKNLYEPWGGIITNLNDTLAQAGSNTLVNLSAQEYFKSVNTKKLRARLITPIFKDEKNGKYKLIISFYAKRARGLMVRYAAEHNTDPEMLKNFNVEGTAFND  
AASNESEWVFMRSQIK

## SEQ ID 3519

TTGGCAAATGTATAAACTTCATTATTATCTCTACTCTTCAAGAAGACGGAAGCGTGGCAGAGCGGTTTAAATGCAACGGTCTTGAACACCGTCGAGGGT

## SEQ ID 3520

LAKCINFIIIPTLQEDGSVAERFNATVLTVEG

## SEQ ID 3521

GTGGGTTCGAATCCCGCGCTTCCGCCGCAAAACGCGCTGATTAGGGCGGTCTCTTTTGTTCAGGTGTGTAAATTACTATA

## SEQ ID 3522

VGSNPAVSAKQNRPSGRFFVQVVLITI

## SEQ ID 3523

ATGCAAAATATGCACAGATGTTTTGAAAAAGATGGAATATGTCATAATTTATAAAATGGCTTTAAAAATACAGCTTCGGCCGGAACCTTGCTATCCGCACCCATCGTCGGTATTCG  
CTATGCTGATGACGAAATTTACAGACTGTACGCGGTCAACCGTATTACAGCGCCCAACCCAGGGGATACATCTGCAAAAACAACAGACAAATCAAC

## SEQ ID 3524

MQICTDVFEKRRKVIYIKIGFKIQLRPEPLPIRTLSSVLEMPDDEIYRLYAVKPYSAANPQIHLAKTTLSN

## SEQ ID 3525

ATGTGTAACATTGTATTAGCCGTAGGAAATCACCAGATTGCTCAAACTGCAGCGCGGAAAATAAACTCGTAAGCCCGCAACCGGTATCACTGTTCAAACTGCTGTGCGGCTTCAT

## SEQ ID 3526

MCKHLY\*P\*EITALLKQAGKINS\*ARKRRITVQTAVRLE

## SEQ ID 3527

GTGTGGGTTCATAATCTTGTTCGCCCTAAAAGAACAGGAAGCTCAAGAAATGAAAAACATGGAGACGCGGTTCGAAGTCAAATATCAGCGGAATCAAAAATGCTGAATTAACAAATAAAA  
TTATTCCCGGAATGTCAAAAATGAACGCTTAAAGATTAGCAAAAATCAAAAATATTGCCAAAATGCCAATCGAAAAACAAGGAGAGAGCATGGTCGACGCGGTCTGT

## SEQ ID 3528

VVWHNSCPPKRTGSSKNEKHGDGRSQISARSKIAELTNKIIPGMSKNERLKIQKIKINIAKNANRKTGEEHGRGR

## SEQ ID 3529

TTGTTAATGAGTCTTTGTCTCTTATGCGGCGGATTCTACTTTGCAAGAAGTAATAATGGCTCTTATCATGGAAGCATAAAGCATCGGCATCAAAATGAGTGGCATGGGTACTTC  
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## SEQ ID 3530

LIMSALSSYGADSTLQEGNNGSLSWNDKASAKIEWHVVLLMHRILVFP

## SEQ ID 3531

TTTTTTCAGTTTTTCTAATCAAGTTCATGTTTTCAGCTTTCTTTTACCCATTGAGAGAAGTCAAAATATTGGAATAATCAAAATTTAGCTTTCTTTTTCAGTGTAAATGAAACGTGC  
TTTAAACGCGCTTAGATTCTGATGCTTTTGTGATTGTTTGGTGGGTTCATCTTCCCCCTGTGTGAAAATAATCGTAGATACATTTTACTCGATTTAAATCAT

## SEQ ID 3532

FPQFF\*FKFMFLFFYPFGEV\*LIGKQ\*ISFFSVK\*NVL\*NALRFVAFGLFGWVHSSPLLKIIVDTFYSI\*NH

## SEQ ID 3533

ATGGATGCTTTAAATATTATGACGAACCCCGCATCTTCCAAAAGCTGAAGCACCCCGCCCGCATGCGCGGAGTTGGAACAAATATGCAAGCGGCAACCCAGTTTCCGATCACGGCA  
ACATCGCCCTTCCGCTTTTACCGGTATCAAGCGAGGTAGGATTGCAACCTTTTCGCGATGTGTGGAAGCAAAACGGTTGCCGAATGAATTTCCGCGACGATGCGATGAAAAAGCGGA  
AAAAGTGGGCAATATGCGCGCATGCTCATCGGGTAACGTTTGTGCCGAACCGCATGTGCTTAAGCGGAACCGGAATGGAGGAGCATGCTGACGCGCGGTGTGTCGGCGTATGCGCTG  
CACTGCGCGCAACCGCTCAGGATTCGCAATATGCTGATACGGGATGTGGGTCAACAGCCCATGTGTGCGGAGGCTTTCGTTGCGAGGATAAGGATAAAATCATCGGCTGATGA  
TGTGCGCACGCGCAGAGGAAGTGCATAAGCCCAAGATACCGATTGGAAGCGTTTGTGAGCCATTGG

## SEQ ID 3534

MDALKLITNRRSSKKLHPADAAEQLQAATQVSDHGNMPPRFTTVIQEVLQRFVRLVQTVABLNFGDDAMKKAIEKVGNNMAMVIVGVTFVPRNDVPKPKPEWQMLTAGCAAYAL  
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## SEQ ID 3535

TTGCAATCTTGGCGCATCTCTTATTGCAATTTTTATGGTAATGTATATGTAATTTTGGACAACCGGAATTTACCATAATGCAAAAATCATCACGCGCTGTGCGCAATCAAGT

## SEQ ID 3536

LQSCGIFLLHFFMVMVNFQGTGYHNGKNHAAVGVKS

## SEQ ID 3537

TTGTCGACGCGGAGGGTGTGGCTTTGTGGGTCTATCCGACGGGAGGCGGAGTTGGAAGCTGTGCTTTATGCAAGGACGGAAGGCAACAGACAATTTCTGCTGGGGCGGTATCTGATTTCT  
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TGTGCTTGTGCAAGGGGCGGTCTGAAAAGTATGCCGACAGGTTATCGGAATTTTGAACGGTGGGTTTTTCCGCTATCGGCAATCTTGATATCCGTCAAGTCAGGACGGCGGACGTG  
GTCGGCTGCCCTGCTGTGATGAGGCGCGCGGTATCGTTGATACGTTGCGCAAAACGAAACAGTCTGAAGATGGTGTTCGCTTTGCGGTTCGGGATGATGGAATCAACCTG  
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GAAGGTGTATAATGATGTGGCGGAAAGCTGCTTGCCTATCGTTGGGACGAGGACGCAACCGCTTACAACCGCTCGGAGCTTTGGGAGGAGCTTAGGATGCGCGGAGCGGTGGGG  
AATGATGTTTGAAGCTTCCGCAACAGGAAA

## SEQ ID 3538

LSGGGLALNVYPTGRRSWKLSFMQDGRQPTLSLGRYPDFSLAEAREWREVRKRAHGVNVNKKVRADFAFEKVARDMFVWRSKGRSEKYAQVMNRNFERWVPAIGNLDIRQVRTADV  
VGCLRVMEARGIVDPLRKTNSLKNVFAFVAGSGMMEINPVAQIGSGVFERVKTNTALSPLEPLRIDFLBQRNEFAVYAGRVHHPVTRFCIYVLLITMTRIREALMEHSELDCGEVW  
RIPAEKKERRRGDVPPLSRAMRWLDQARGLVNNGRPFVSVNFQGHINKSPHVMRRSGLDITAHGLRLSLARTYLREVLKVYNDVAEKLALHSLGTRTQTAYNRSELWEKRDAPERNG  
NDVLRADNGK

## SEQ ID 3539

ATGAACATCAACACCGGGCGCAAGGATAGACCGCCGACCATCCGCAACTGATTGCTACGCAACCTGCGCAACCAACCCCAATTCAAATCGACACTGCTGCGTATGAAAAAGACG  
GACGGATACCGTCCGCTGTAACCCCTCGCATCCCGGTATGGACACCGCGAAGTTTTGGAAGCATTAGGGTTGCAGCANTAAAAACCGCGATTAGGGCGTTTTACATAATGC



GGAAACAGCTTTCCTATCATCATTTCCACATAAACGCAAAACACACAAAAATCATTTTCGCTGTGCGGAAGCCTCAAAACATCATTTCCCCACCGTTCGGCGCATCCTTACGCTCTCT  
CCAAAGCTCCGAGCGGTGTAGACGGTTGCGCTCTCGTCCCCACGAATGGGCAAGCAGCTTTTCCGCCACATCATTTATACACCTTCAGAACCCTCGCGCAATTAAGTAGCGCGAAGCGAG  
CGCAAAACCGTGCGCCGTGTATCCAGCCCGACCGCGCATCGCCACGTGCGGAGCTTTCCTTAFTGATATGCCCTTGAAATTCACACTTTCAAACACAAACCGCCCGTTCACATTCAGCC  
CCGCGCCTGATCCAACACCCACCGCATCGCCCGCAGCAGCGGCACATCATGCCCGCCGCGCTCCTTTTTCGCTTGGGGGGGATACGCCAAACCTCCCGCTCCAATCTCGACCACTCCAF  
CAACGCCGCTCCGGAATCCGGGTATCGTCAACAGCAGCCAAATAGATACAAAACCGCGTACAGGATGGATATGCACCOCTGCCCGCATAAACCGCAATTCATTGCGCTGCTCCAAAAAA  
TCAATCAGCGCGGCAATTCGAGCGGACTCAACGCCGTATGTTTTGGTTTTTACCCTGTTCAAACACACCCGAAACCGATTGCGCGACAGGGTTGATTTCCATCATTTCCGAACCGACG  
CAAAACGCAAAACCACTCTTCAGACTGTTTTTCGTTTTGCGCAACGTATCAACGATACCCGCGCGCTCCATCACACGACGCGACCGACCATGCTCGCCGCTCTGACTGACGGGATATCAAG  
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GTGCTCTCCGCTCGCATAAACGACAGCTTCCAACCTCCGCTGCGCGTTCGGATAGACCCACAAGCCAAACCTCCGCGTCCGACAACCTATACAGCTTATCGCCAGGCTTCGCATTTT  
AACTTGATTTGCCGACAGCGCGTGATGATTTTTGCCATTATGGTAAATTCCTGTTTGTCGCAAAATTTACCATATACATACCA

**SEQ ID 3540**

MNI TKPGARIDRPTI RELIAYATCRNHPISNS TLLRMEKDGRI PCRLNPPRI PRMGHPRSFGS KIRVAALKKRPITRAF SHNAETAFLSTF PHNAKHTKKSFSVVGKQPMI IPPFPFRILFLK  
 PKLRAVVSRLRPRPQRMGKQLFHHI ITHLQNLAQISTKRKAQT VRRRIQPPRPHRHVTFTLIDMPLKIHTFKHKP PVHIIQPPRIQLQHPHRRPQRORHIMPPFLFPFGGDTPNLVPQLRPLK  
 QRRLPNPHRHQQQPIDTKPRYRMDHHPARINRKFIALQKINQARQFGRTORRHVFGFHPPKHTKTDLDRVDVPHHSRTDRKKHKLQTVFRPAQRINDTARHLHITQAADHVRFLPDITK  
 IADSRKNPPFKI PHNLGSLFPPRLPPTHKPTI TRHLLKSKIRPHILLIDIPFCVPSAHLPPFPRLSPQREIRIPQORNCLFPSVLHKRQLPTPPARRIDPQSQPSAVERQLIQLIARLITP  
 NLI CRQREDDFCHYGKFPFVQNLPTPLT

**SEQ ID 3541**

ATGAGTCTTCCTCGACGTACAAGGCGGATGGAAACACTGGCATTTCGAACCGCCCCGAAAAAGGCGGAATCCGGAATCCGGATTTCGGCCGCGTTAFTCTAATCAAAAGCGGGCATATAG  
TTATTCATAACGCTGATGGCGACAGCTTTGCCACCGGCTAGCGCGTGATTGCCGCCGACATCGTCAGTCCCGATTGAAAAACAGACTTTGACATATTCTTCCCGCCGGAAGCTTGTTCG  
ATATAAAAAAATCGGGAAGAAGAA

**SEQ ID 3542**

MSGSDVOGRMETLAFATAPKKGGIRKSGFGRVILIKSGHIVIHNADGDSFATGYGVIAADIVSPDLKTDFFDIFPPESLLRYKKIGKKK

**SEQ ID 3543**

SEQ ID 3543  
ATGCGGAATATGAAAGACGCAATTCGCCCATGCGCAAGCGGTAAAAAAGCGGAAACCCGGACAATTCGGAATCAACGGAAAGAGGATTGAAGACATGGAATACGAAGTATTTCANTAAACGCC  
TCGCAAAAAAGCGGTGCGCGAAGCAATGGAGTCTTCCGACGTACAAGGGCGGATGGAACAACATGGCATTGTGCAACGCCGCCGAAAAAAGCGCGAATCCGGAATTCGGATTTCGCCCGCGTT  
ATTC

SEQ ID 3544

MPNMKDAIAACQAVKKRKPQOIGINGKRIEDMEYEVFNKRPSKKRSKQNSLPTYKGGWKHWHLQPPRKAESGNFDSAALF

SEQ ID 3545

SEQ ID 3545

TTGTACGTCGGAAGACTCCATTGCTTCGCCGACCGCTTTTTPGACGGGCGTTTATTGAATACTTCGTAATCCATGTCTTCAATCCTCTTTCCGTTGAATCCGATTTTGTCCGGGTTTCGCT  
TTTTTACGGCTTGGCATCCGGCAATGCGCTTTCATATTCGGCATATCCTTTCCCCAATCCGCGGAAGTTTCCGCATCCGCGCGCTCGATTTCATGTTTGCCTCCGATTGTGTTTAC  
GAAGCCCGTACCGTTACGGCA

**SEQ ID 3546**

SEQ ID 3548  
LTVGLHCFADRFDDGRLLNTSYSMSSILFPLIPICPGFRFTTAWHAALASFIIGLSFPQSAEVSASAAVSIHVCPPICFTKPVPTTA

**SEQ ID 3547**

TTGGACGCGCAAGCGCGTCATTGCGGTTTCTTCGCGACAGGCAGTCCGCGATCCCCTCTTGTTGGTGTCCGACATCGGTGCGAGGCGCGCAGGTACCGGAATACACCGCCATCCTCGATCCTGTGCG  
GCTGCTCGCCCAAAACCAAACTCTGCATTTTCAGACGGCAAGACACACCGCAAAACCGCTCCGGAAGCAGAGTCCCAAGAAATACAAACCGCCAAAGCGCCTCCGCAAAACCGGATAAAAAAGT  
CAGCGCAAACTCTAGCGGTCAAACCGCGCGCATACCGGCAAAACCCATACCGTCCGCAAGGCGAAGACGCTCAAACAGATTGCCCGGCCATCCGTCGGAACACCTGACGCTCGAACAGGTT  
GCGCATGTGCTGTGTAAGGCGAAACCAAAATGTTTCCGCGACACGGCAGACTGCGTGCGGGCAGCGTGTTCACATCCCGAATCTGAACAGGATCAAAGCGCGCAGCAAAAAAATTCAGAG  
CGGAACACCCCAACCGCAACCGCGGAAACCCAAAGCGGAATGTCATTCATGCGCGTCTGAACCTGTCCAAACAGGACCGGTGAGAGAACACCGATAGAGAACTCTGTGCAAAAAACCGGTTGA  
AAAACTCTGAAGCAAAATCTGCGCGCGCCGGAAGCGGAAAAAGCGGAAAAACCGCGCGTCTGCAGCCGCAACCCAAACCCGCGAGTGTCCGAACTCCGCGCTTCGCGCAGAGAACGCCAACCGGACCT  
GTACCCCTGAGCAAAATCTGCGCGCATCGGAAACCGCTGCCGAATCCGCGCCCCCAAGAACCGCGCGTCTCTGCCATCGACACGCGGACCGGACGAAACCGG

SEQ ID 3548

LDGKAVI~~AVSSAQ~~VRDPVLVFRIGAGAVREYTAILD~~PVGCSP~~TK~~SKALS~~SGDKTH~~RKTAP~~KAE~~SQENQ~~NAKAL~~RKTKD~~KSANS~~AVKPA~~HNGK~~THV~~VRKGET~~LQIAAA~~IR~~PKH~~I~~LEQV~~  
ADVLLKANPNVNSA~~HGR~~L~~RAG~~SV~~HL~~PNL~~NR~~IKIAA~~PK~~KIKAE~~QPKP~~Q~~TAK~~PKAETAS~~MPSE~~PK~~QAT~~VE~~KPI~~E~~KP~~VE~~KP~~VE~~KP~~EA~~RVAA~~PEAKA~~EKPA~~VRPE~~PKPA~~VSETPASATER~~QPGP~~  
VPAANTAASE~~TA~~APPSRR~~PF~~CHRHADRRNR

SEQ ID 3549

AAATGGAACAAGAACTTTTATCTCACTGTTGTATAAACGCCGCTTCGCACTCTCTTAAATACGGCTCAAAATGCTCTTTGGGAATGCCGCTCAAACTTCGCTAAATGACGTTTTCGCCGGTTC  
CAAAAGTTCCTCAATTCATTAATATGTTTTCGTTTCGCGAAAAATGTGTCTGTGATTGATACGGAAATGGCTAAATTCGCTGCATCCAATACATCATAGCGACGATAACAATCCGTAT  
AAACAATGCTGTCAGGCTCTGTGTCGTCTCTTCAGTTACGGCTCGGCAAAACAGTTCATGAGTTATTTTGTGTTATACCGGCTTAGACGGCTTTTCTCAT

SEQ ID 3550

SEQ ID 3550  
KQNKNEVLTVVKTPRALI.\*TRI.KMLFGNAVKLA\*MTFCPVKVPNSINMVL SFGKMCVIDTETMAKFACTQYIIATITIRINNAVRLCCSCSYACDKQFNEFILFIPA\*TAFSH

SEQ ID 3551

SEQ ID 3551

ATGGCAATAAGAGAAAGTCCTTAGACAAAAATCAAGAAATGTTTGGCTTTGGGTCGGTCGGTAAATGAACATGAAGCCGCACAGGCGTTAAGCGAGCGCAGGCTTTAATGGAAAAGTCAAAAG  
TAAATGCCGAGGATATCGCTCTATCAAAAGTCTCCGAACAGAAAGCCGATCGGAAAATGGCTTTTAAATGGCAGGCTGGCAATGGGGCGTTCGAAATATGAATGCGCATATATTCGGGTG  
CAAATCTTACCAACGCGGAAAAACAATGATGTTTTCAGGCATTGGAATCGAGCGGAAACCTCAGCCTTATGCTTTGATGTAGTCTATCGTCAGATTCCCGCGACCGCCGCAAAATTTTG  
AAACCTGCGCGGGCGGAAAGCCCTCGACAGAACTTATCTTTCGCGACCGATTTTTCGCGCGGTGGATTGCGAGCGCTTGGGAAACAGTCAAAAAATTTGAGATTCAGATGAAGAAAAAG  
CCATTATGACCGGATACAAAAGAAAGAAATATTCGCGATATGCGCGAAGCAAGCAAGATAGCGAAATCGCTCAATGCTCAAGGGCTCAAAAATGGGAATATGAGGCATTACCGCGGAAAT  
GGAATTCGCGTGAAGCAAGTGAAGTATCACTATGCTCGTAACCGGATCGGGCTCTGTAACAAACAAATCGGAGGGCAACAC

SEQ ID 3552

SEQ ID 3552  
MDKEKVIDDKIKKCLALGRSVEHFAAQLRQALMEKYKVNAEDIALSKVSEQADRKRAFKLAGWQGVANMIADIFGCKSYQRGKTMFYGITGNAETSAYAFDVVVYRQISADRRKFL  
KTCRAGKPSHRITYLADRPCGGNWLASAWETVKFPEMSDEEKAIMDGYKKKEYPDWAEARTRDAKSSILQSGKMEYALTRGMEGKQVKLHYAVNGTGFVKQIGGQT

SEQ ID 3553

SEQ ID 3555  
TTGCCGCCAAAGTCCGCCGATACTGCGCGGAACACCCGGCGTATTTCAGCGCGCGGACGAGCAGCTTGACAGGTATATTAAAGCCGCTCTGAATTTTCACGCCGTGGAGATTCAGCC  
CGAAGCCTGCAAGGCTTGTTCACAAACTACCTGCCCGCGCGGTAAATCTCGGCAGGCGGAAACAAAAAAGCCCGAGTTCGTAAAGCGTATCAGCCCTAGCCGAATGGCCCGACCGAAT  
CGAAGCAAGCGAAAGACGAATGGGCAAGGGTGGCAAAAT



## SEQ ID 3554

LPPKSADTAANTRAYLTARQEAGSLNGLSRNFTPWRYSPKPAKPCCKTTLPRPVISAGGNKKSPEFVSVALAENPDRIESKARDEWARVEN

## SEQ ID 3555

ATGTTGTCTGGCGCAAAGGTATCGGAAGACGAAGCCCTGACGTGCGGCATCATGATGCGGCTGGTTGCCGCCAAAGTCCGCCGATCTGCGCGAACACCCGGCGGTATTGACGGCGCGG  
CAGGAAGCAGGCAGCTTTGAACGGTATATTAAGCCGTCTGAATTTACGCCGTGGAGATACAGCCGGAAGCCTTGTTCGAAACTACCTTCCCGCGCGCGGTAAATCTCGGCAG  
CCGGAACAAAAAAGCCCGAGTTCGTAAGCGTATCAGCCCTAGCCGAATGGCCCGACCGAATCGAAAGCAAAGCAGAAATGGGCAAGGTGCGAAATTAATAATACCGGACAAAT

## SEQ ID 3556

MLSGARVSEDEALTCGIMRLVAARVRYCGEHPGVFDGAAGSRQLEKRYIKPSEFHAIVEIQPEACKALLQNYPAAGNLGRKKQKPKVVRKRIKSPSRHARPNRQKQSERRMKGAKLKYRTN

## SEQ ID 3557

TTGACGGCGCGTTCTGCCCGGTGATTCCTTCGCCCGCGGTTCGGCGGCAAGCATCTGTTTGGCGGTGGTTTGTGCTACTGTTTGCAATTTGTTTCTCGATTTTGTGATGCGGTTC  
TCTAATGCCCAATCATAAAGCTGTATCTCTCAGAGGTCCGCGAATTTAAAT

## SEQ ID 3558

LTPARSCRVDLSFAARLAASICFAVGFTVTCILFSRFFDAVLSPHAKAVSLTRSPMLN

## SEQ ID 3559

ATGAGCTATTGGAAGATGTAATAAACCGCATTAAGGGTAATAGATAACTTATGCAAGAAGCATTAAAGAGCCTGAATCCTTAGAGGGTTATATAGACGAAATTAGGGATAAAGCAGACG  
AAGCGGATACCTCTTTTGAATTTCTAAAGGATGTAATAAATTATGATATTAGCGATTAAATAATGTAATTGAGGTGTTTGAAGATTGCGTT

## SEQ ID 3560

MSYLEDVKNALRVINDLCKEALKEPESLEGYIDEIROKADEADTSLEFLKDVINYGISDLKNVIEVFEDCV

## SEQ ID 3561

ATGACCGCCCTCGCACTCTACCGGTGCGCGGAGACGTACAGCGCGCGTGGATTACTACTTTGACAGCGAAACCGAGCGGAAGACACGCTGGAAGCCGTTATCGGGCAGTTTCGAGGTCA  
AAGCGCAATCCGTTATCGCTTATATATAAACCAAGAAATCAGGAAAAATGCTTGAAGGGCAGATCAGGCGGATGACCGGGAAGCTCAAGGCGGTAAAGCGCAAAATCAAAGCCTGAA  
AGACTACTTGGCGCGCAATATGACAGCGCGCGGCAATACCGAAATCAAAGCGGACGACGCGACTTTTAAAGCCTCGCTCCGCAATCCGAAGCGCGTGTGATCTTAGACGAAGCACAAATC  
CCGCGCAATTTATGCGTGAGGCGGTCAAACCGAACCGGACAAACCGCATCAGAAAAGCGATTGAAAGCGGTGCGCAAGTAGCAGCGCGCAAGATTGAAGGGCGGAAGAAATTTGCAGA  
TTAGA

## SEQ ID 3562

MPALALYRCADVDQALDYFDSETEREDTLEAVIGQFEVKAQSVIAYIKNQBITKMLBGRHRRMTGKLVAKVQNSLKDYLARNMQAAGITEIKADDGTFKASFRKSEAVVILDEAQI  
PAEFHREAVKTEPDKTAIRKATIESGRQVAGAKIESRKNLQIR

## SEQ ID 3563

TTGCAACTGCTTCGGACGGCAACAGAGAAAGGAAACAAAAAATGGCAACATCGACCTGACCCATGGGACGGGAAAAACCATTTGGCGCGCGGCCAATCCGGAACAGGGATACATCAACA  
TCACCATCGGCAGCGACACCTATTATCAACATCGAACAGGCATACGCCATACACGCGCGCTTGGCGAAGCGGTTCGCCAATATGAGGAGGGGACAA

## SEQ ID 3564

LQLRTATEKGNKMANIDLQWDGKTIGAAANPQGYINITIGSDDLFINIEQAYIAHALGEAVAEYEGGAQ

## SEQ ID 3565

GTGCTCTCCAGTTTGGATATGTGCGGATGGCTTTGTAGCCGTCTGCCGTTTTTGACCAAGGTGCTGCCGTGAAAGGGCAGGTGTAGGATTTTTGAAGAACTTAGTTTTCAATATCTGTTTC  
AATGAAGGAATGCCGCTCGAAAAAT

## SEQ ID 3566

VLSSLMDGDFVAVCRFDQGAVERAGVGFLKNLVFNILPQMKEMPSN

## SEQ ID 3567

CCCGATAAATTTCCGCAACGACAGACCTAGATTCCCGCTGAGCGGGAAATGACGGTTGCGGTATTTCTGACGATTTCATCGAGCCGTAGCAACTGTATTTCCACCCCTCGGGCAAAAAATA  
CCAAACTCAAATCAAGCGTCCGAATACCGTTTTCGCGGTATGCTTTGCGGCAAAATAATCAACGATCCGGGCAAT

## SEQ ID 3568

PDKPFRQT\*IPA\*AGMTVRVFLTIHRAVATVFTSPSGKNTKQLKPSYRFRYRLRQNNHASGH

## SEQ ID 3569

TTGATTTTAAAGTGTGAAGAGCAAGCAATTTCAAACCATGCCCGGACAGGCATCAGCCACCTGCATCCGCATCATGATTGGGTACGACGCTCGTCAGTACCAAAACGAACAA  
AGCGGCAGCACAGATTTTGTGTCAGTGGGAATCGACCTGAAAGCGATCCGGAAATGCTGATGCCGAGCGGAGGCCCTACCTCATCAGCCGACGATACAGCCAGCCTGCACAGCAA  
AAGCCAATCGGCACAGACCTCAAAGCTGGCGGGAAGGACTTTACCCGGAAGAACCGGACAACTTCGATTTCGCAATATTTGGGCAAGCCCTGCTGTTGATATCGCCCAACAA  
GAAAGCAGCGCAGGCAAAACACCTATGCCAACATTTCCGCCATCAGCAACAAGATGAAGAGCTACACCCGAAACATCCGGAACAACCGGTTTTTGGCTTCGACCTGTGAGACCCGATT  
GGCGAATTAAGCGCTCTGAGCAGAACTGAGGAGCAGATTGCCAAAGCCCGGAATATGCCGAAGCCGTAAACGGCGCCCAACCGCGCGCGCGCAGAAACAGGCCCAAGCGGC  
GGAAGGGCGCGGGAACACCCCAAGCAATGCCGCGCTGCCGAAGACATCGAGGACGACATCCCTTTTAAT

## SEQ ID 3570

LILSVKDESNFKPCPAGSHATCIRIIDLGTQVYQNEQKQKILVQWEIDPEGDPEMLMPDGRPYLISRRYTASLHKSQALATDLKSWRGRDFTPEERDNFDLRNLLGKPCLLSIAHQ  
ESSDGKTTYANISAI SNMKSYTPKHPDNVAFDLSDPDMANYGLLNEKLRQIAKSPYEAHVNGRQPPAPPQKQAQAEGRPEHPQGNAAPEADIEDDIPFN

## SEQ ID 3571

TTGCTTTCGTCCTTTCACACTTAAATCAATGACATTTTCGGTCTCTCTGTTAAAGGTCGTTTCGTCATCGGTCGCGCGTGTATATGCTTCGCGCGGCGGTATCTGATAATGCTTT  
TAATGTGGCTCTTCGCTGTTTTTCGGTCATCCGCGGTGTTTGGCGGTTTTCCGGGCTTTCCGGGTATTT

## SEQ ID 3572

LLSSFTLKINDIFGLLLKVVSSIGLALFYALRGGGYLIMLLMPSACFSVIRRVSAVSGALPGI

## SEQ ID 3573

GTGGCCTTCGCTGTTTTTCGTCATCCGCGGTGTTTCGGCGGTTCGCGGCTTTGATTTCTTCGGGCTTGGTCCGTACGGCTCTGTTTCTCCGCGCGGTTA

## SEQ ID 3574

VAFCLFFGHPPCGGFRGAGYLISSGLGPGYGSVSPPL

## SEQ ID 3575

ATGAGCTTCATCCCGAAACCGCTTATAACGGCGGCGGAAACAGAGCCGTACGGACCAAGCCCGGAAGAAATCAAATACCGCGCAAGCCCGGAAACCGCGAAACAGCGGGA

## SEQ ID 3576

MSFHPETAYNGGETEPYGPSPEELKYPKPKPKHGG

SEQ ID 3577

TTGGTCCGTACGGCTCTGTTTCTCCGCGCCGCTTATAAGCGGTTTCGGGATGGAAGCTCATTCCTTTACCTCCGGCACTTCGCATCGCGTGCAACCCGCGGCAACCGGGCTTCTCTCC  
GCAATTCAGATGCCGCTCTCCAGCCAAATCTCGGCGCTCAATTCGCGCAACCTGCGCTGCTTTTGAGCCAAACCGCATACGCAATTGCGCAATATCGCGGGGTTTCTCCCTTTGCGGTACGG  
CTTCCGCGCTTCCCTTTGGCGAATCCGAAGGCATAGCCCGCCCAATACCGCGGCCAATACCGCGAACT

**SEQ ID 3578**

LRVTALFLRRRYKFRDGSFFTLRHFRIVHPPATGFFFRIQMPLFQPNLGAQFRNLRLLLSQRHTHCRNIGGVFPLPYGFRLPWRIRRHSPPIPPPIPR

**SEQ ID 3579**

TTGCGGTAAAGTTGCGGATTTGGCGCGGTATTGGCGGCGGGCTATGCCCTTCGGATTGCCAAGGGAGGCGGAAGCCGTACGGCAAAGGGAAAAACCCCGCGATATTTCGGCGAATGCGTATGGCGTTGGCTCAAAAACAGGCGCAGGTTTCGGGAATTGAGCGCCAGAGATTTCGCTGGAAGACGGCATCTGAATCGGGAAGAAGAAGCCGGTTTCGCGCGGGTGACGGCGATTCGGGAAGTCCCGAGGGTAAAGAA

SEQ ID 3580

IRISRYWRRYWRAMPSPDSPREAEVRORENPAIDIAAMRMALAKQAQVAELSAETIWL EERHLNAEEAGCRRVHGD AEVPEGKE

**SEQ ID 3581**

SEQ ID 3581  
ATGAAGACAAGGAATATTGCGTTTAAGTTTCGCGGTATTGGCGGCGGTATTGGCGGCGGGCTATGCCTTCGGAATCGCCAAGGAGGCGGAAGCCGTACGCGCAAGGGAAAAACCCCGCGAT  
ATTGCGGCAATCGCATATTGCGTTGACTCAAAAGCAGGCGCAGGTTGCGGAATTGAGCGCGCAGATTGGCTGGAAGAGCGGCATCTGAATGCGGAAGAAGAAGCCGTTGCCGCGGGTGC  
ACGGCGAATGCGGAAGTACCGGAGGG

**SEQ ID 3582**

SEQ ID 3582

MTKTRNLAPKFAVLA<sup>1</sup>AAVLAAGYAFGFAKGGGSRTAKGKPRRYCGNAYGVGSKAGAGCGIERRDLAGRAASECGRRSRLPAGARROGSAGG

**SEQ ID 3583**

GTGAAATATTACGGCACGGCGGCTTACGGCACGCCCGATTGGGGGATGGAAGATATTACGGCGGGAGGATATCGGCAGGCTTTGGACGTTGGGAGGCGGAAAACCGAATCTGCACG  
AATCCGGCGCTAATTCGGAATCGCCAAAAAATCGCGCGGGAGTTTGTCGCCGATCGGCACGGCGAACCTTACAGCCAGGAGGATTTGGGAAACGTACCTTACGGAAGATGTTCCCGTGTCGG  
TAAAGATACCGGAAGCCGCGATGAATACGCCATAGACGAGCGGGAATGGTTCCGGCTGGCGGAGAACATCGCAGGCTGGCCAAATCA

**SEQ ID 3584**

SEQ ID 3584  
VKYYGTAAVGSPEWGMERYYYAREDMROALDGEAENRIIHESALIGIAKKSAREFVRDADGEPYSQEDWETYLTEDASRVGKDTAAAMNYAIDEREFALAENIGRLANS

**SEQ ID 3585**

SEQ ID 3585  
ATGACGGTTCGGGTATTTCGTGACGATTCATCGAGCCGTAGCAACTGTATTTTCCACCCCGTCGGGCAAAAATACCAAACTCAAAATCAAGCCGTCGGAATACCGTTTTCGGCGGTATCGT

**SEQ ID 3586**

MTVRVFLTTHRAVATVFTSPSGKNKTKQIKPSEYRFRRYRLRQNNHASGHSISSAVCAIMP

**SEQ ID 3587**

SEQ ID 3587

ATGCGGTTTTGCGCGGCTGCCAGGCTGTCGAAATCCAAGTCGATGCGGTTTGGAAAGCGTATCGGTTTCGACATCGAACGTTTGGTTTTCGCGATAACTCTCTTCAGATTCCCCACCTAAGG  
CAAGTGTGTCGTTTACATCGTTTTCGGAGCGGGTTTCGGGCGTTTGCCGGAGTTTTCGACTTCGGCAAAGGTGATTTTATGCCGTCGTCTGCCGCGTCGTCAAGGTCAGGCTCTTCTTCAGG  
GACGGATTCTTCGGTACGGCGCGCGCGTTTGGATTGGGCAAGCGTAAAGACGACGACGACGAGGCGCATCAATGCCGTGCCCTCCGCGGGCAAGCAGCAGAGGTTAGCAACCGCCGAACAGA  
CCGTCAAACAGTCCGCTTTTCGGTTTCTCTTCGCGAGAAACCTGTCTGCACAGGTTTCGGCAACGGGTTTCGGCGGCAACTTCACTTGGCTGTTTCGCGAACAGGTTTCGAAACGGTTTACCGG  
TTTCTGTCGGTCGGCGTGTGCAATGGCAGAAGCGCGCGCTTCTTGGGGGGCGGATTCGGCAGCGGTTTCCGATCGCGCAGTATTTGCACGGGTACAGGTCGGGTTGGCGTTCTGTCGGG  
AAGCCGGAGTTTTCGGACATCTCGGCTTCGGTTCGAAACGCGCGGTTTTCGCCGTTTTCGCTTCGGCGCGGCAAGTTTTCGTCAGGTTTTCGACGTTTTCGACGGTTTCTC  
TATCGGTTTCTCTACCGTTGCGCTGTTTGGACGGTTTCAGAGCGCATGTCGTCAGTTTCGCGTTTGGGTTTCGCGGTTTCGCGGTTTGGGTTGTTTCGCTTGTGATTTTTTGGGTGCTGCGGCT  
TTTCAGTCTGTTTCAGATTTCGGAATGTGAAGCAGCTGCGCGCAGCAGCTCTGCCGTGTGCGGAAACATTGGGTTTCGCTTCAGCAGCACATCGGCAACCTGTTTCAGCGCTCAGGTGTTTCG  
GACGGATGGCGGGCGCAATCTGTTTGGCGTTTCGCTTTTCGCGACGGTATGGGTTTTCGCGTTTATCGCGCGTTTTCGCGC

**SEQ ID 3588**

SEQ ID 3588

MPFCAARLSKSSMRLEGVSVSTSNVCPADNSSSDSPPKASVSFTSFFGAGSGVAGVSTSAKVIFMPSSAASSRSGSSSSTDSVRRRLDWRKKSSSSRAINAVPPAPSSKVYEPFNR  
YNSPLSVSSSAETCSTGSATGSAATSLAVSATGSETVLVPSSVGVSMIAAAASWGGFGSGFRGCSICSGYRSLGLAFRRSRFCHGCGFGSGNRFFRCFGRGNCFRFFNRFFDRFL  
YRPLVYCTEGCFRRHCGCSFGFGFRRLRFLGLRFFDFGCCRRPDPVQIRNVKHAARTOSAVCGNTIWCVLCQHI GNLFRQVFTDGGGNLFRFAPADMGCFAMVRRFDG

**SEQ ID 3589**

SEQ ID 3589  
ATGAGTTATCTAGATCAACCACTTGAAGCACGGCTACGGCAACGGTAGCGGCAACGGTAGCGGCTATGGCAACGGCTACGGCAACGGCTACGGCAACGGCTACGGCGCGCGTCGGCG  
CGCGCGGTAGCGCGCAGCGGTACGGCAACGGCAACGGCTACAGCAACGGCAGCGCAACGGCGCAGCGGCAACGGCAACGGTAGCGGCAACGGTAGCGGCTATGGCAACGGCTACGG  
CAACGGCTACGCAACGGCAGCGCAACGGC

**SEQ ID 3590**

MSYLDQPLKHGYGNGNGSGNGSGYGNNGYGNNGYGNNGYGGVGGGGSGSGYGNNGYNGYNGSGNGDGDGNGNGSGNGSGYGNNGYGNNGYNGSGNG

**SEQ ID 3591**

SEQ ID 3591

ATGGAAGCGCAATAAATTGGAAGTGAAAAGTTTGTGCAGACCTTATAAAGTCTTTGCAGGCAATTGCTGCCGATTTCGAAGCGGCAATGGGTGTAAAACGCCCGACATTTCAACCGGAATTTG  
ACGAACCCCAATGTAGCGCGCAACCGCCGGTAAACAGTTGCCGAGCAAAAAGGTATCAACGACTTTGCCATCGGCAAGGAAGTCATCATCGCACTTATTCGGCAGGCGTTTGGTTTGGTGT  
GTTGAAACAAAAGCGAGGCAATGAAGTGATTCTGACAAAAGCGCGCGGAATGTACAGCTGGTGGGCAAGGAATCAATCAGCTGTGTCAGGTGTGCGACGACACGGCATCAGGCAAGACGCGC  
AGCCAAATTTGGCGCGAGCTTGATTCCGTATGGCTCGAGGCGATTGACATTATCCACAGTAACAGGCGCGCGGCTGAATCAATCCGCAACCGCGCTGGAAGGTGCGCCAGTCA

**SEQ ID 3592**

MEANKFEVKSLSDLIKVFAGIAADFEAMGVKRADISTEFDEPQHEPQPVTVBQKGINDFAIGKEVILIRTSAGVWFGVLKQKAGNEVILTKAREMYSHWAKESISLSGVARHGIRQDG  
SOICGELDSVWLEPAIKIIPVTGGAESIRTALEVAQS

**SEQ ID 3593**

SEQ ID 3593  
ATGAACGAATTAAATCAGCAGAATAAATCGGTTTGGCGCGAGGGCAAAAGGACGAGCAAAAGCCTTTTATTGAAAGTTGGTGAAATCTGCCCGACGACGACGACGACATGGACCCTAGAAAAA  
GCGAAAGCCCTCAATCACACCGCCTTCACTTTTCACTGTAAGAAAAAGACGGCTTAAAGAGAGAAGGTAAATGATTGTTTTG

SEQ ID 3594

SEQ ID 3394  
MNELISRTNRFGARAKDEOSLLIKVGEICRDAAATWTRKSESINHTAFTFTVKKDG LKEKVMIVL

SEQ ID 3595

SEQ ID 3595  
ATGATTCACCTAAATGTCCACTATTGGCATGAAATTTATCCGCCATCGCGAAATGACAAATACAGCCTGATAGTTATATCCCGATATATGCCATATCCGACACCGCAGGCCATCTAG  
GCCGCCGTGCTGCTGTCGTGTTTCATTTTCCGCCGAAGGCATGGATATACAGACTATGAAACCCTCAAAATTTTCTGGAATTCGTCGCAACGATGATGTAATCTCTGCACTTGAGATCC  
ATCATATGACGCCAGTGATACAGAAAAACGTGTCATTGCTACACCAAACATCAGCGGACTACCCGTTTCAGACAACGACCGCATTTATGTAAGAATGACAACACACAACCATATT  
CTCTCCGAGAGCCGCTCTTGTCTTTTCTTGGCTCTCTTACCCTCA

## SEQ ID 3596

MIHLNVHYCDRIIRHAENDKYSLIGIFPDICHIPTPQAILGRLCLSVSFABGMDIQTHKTQGIIFLEIVRNDIVISALEIPSYDGSDEENVSFMLAQITISGLPVSDNDRIYVRMTTTHNI  
LSRSRPLSFSLPHYHS

## SEQ ID 3597

ATGAAGAAGTGTACTCAACTAACGGCAGATGGTTCAAAATGGGTGCAACACTCACTGTTGCCGTGGCGCGCTGCACAGTATCAACACCTACATCCGCCATCCCGCTTACCCACATAAAAT  
GCCTGCGGATAAACGGGCAGATTAAATGCGTCAAAACCGATAAGCCCTAACACTACCCCTGCCGAGAGCATATTGAGCATGTGCGGAAAAATCCGCGCCGCAAGACGGGATGGACAGGGC  
GGCAGCAAGATTGCGGATAAAATAGCCCTCAAAAGCAGCGCGGGAAACATTGTGAGCTTAAGGATGAAAAAGGGGTTTACCCAGTCCGAATTGGCAACCGCCGAGGATTGCTTCAACCC  
TATCTGTCCCGCATCGAAAAACAGCAAAATCCCTGCAAGATAAGACTGTACAAAAATTGGCAACCGCATTAGGCGTTTCCCGCGTTGAAGTTCCGCGAGCGTTTCAACCGCGGTACGAAT  
ATATGGAGCAGGCA

## SEQ ID 3598

MKNCTPTNGTWFKMGATLVAVAACVTSTPTSAIPVTHIKCLRINGQIRCVKPLSPNITPAAEHIEHVKNPRKKAAMDRAAARIADKIALKAGGETTVSLRMMKGTQSELATAAGLPQP  
YLSRIENSKQSLQDKTVQKLANALGVSPLEVRAAFERRRYEYMEQA

## SEQ ID 3599

ATGGAGCTGACCGTCCACTTTAACGCGGAGCAGGATTTAGACCGCTCTTTGAAAAAGACGAAGAAGCGGTGCTTATCTCGAGAAATGTATTGCGATGATTACGCGGACTCTGCTATFTT  
TTGACGGCTTATACAAAAACAGATACCTTCAGGGAATATGGCGAACCCATAGGCGCGATTGACTTGGAAAGTGAACCCATATTGTTCATTATGGGGAAGAACATCAAGATTTTACGCGTCCG  
ATTTGACAGCGAAGAAGCGCGGATACAGAATAATTATCGCACCATGCCATGAAAAACAGCAACCGGACGATATCCGCGCATAGATATATTGGCTGTTGTAACAAGAGACAGAC  
GAATTTGACTATCAGGCAGAACCCCAATCAGAAACGATTATCAAGACTATGAAGAAGTCTACTCCAAC

## SEQ ID 3600

MELTVHFNAEQDLRLFEKDEEAVGYLENVIAMIQADSAIFDGLYKNRYFREYGEFIGIDLEVPKILSLNGKDIKVLVRVPDSEEAAGYRIIYAPCHEKQPNGTYIRRIDILAVNKKTD  
EFDYQAEHPITKRIIKDYRELYSH

## SEQ ID 3601

ATGCTTTTATATCGATTACCAATGCTTATGCGCAATTAATTCGGAGATCAAAATGTTTCAGCGCAACAGTTAGGACAAGCAATATCAGAAGCGATTAAAGAAAAATGTCAGTCAAA  
AGGAGGTTCGCGATCATTTTGGGGTGAACAGCAAGCGTTTCAGGTTGGATAAAAAATGGAGCAATAGATAAAAAACATCTAGATAAATTAATGATTATTTCTCAGACGTAGTAACGCC  
AAGCCATTTTCGCAATTGAACATTGAGAGTCTTAAATCGAATGAACAAAGTAGCATACGTTTCCCGCGCTTAAATGCCGAAGCGACTCGCGCGCAGGCACGATTAACGACCATATATC  
GAGGTGTGGATTATGTAACCGTTCGCTGCGCATGGCGCGGGAGAACTGGGCGGAAACCTCAACAAAATCCAAAGTCATTACAGCCCGTGGCGCAGACATGGAGCCACCATCGAAAAAG  
GCGACGTAATGTTCCTGTATACCGCGCTCGAAGCCTTCGATGGCGACGGCTCTACTGCTTTGGTATATAGACGGCTTAAAGGCAAGCGGCTCAATCCACCGCTCGCGCGCGCGCTGAT  
GATCATCAGCGACAGCTCATACCGAACCGAAACCGTGGCGCGGAGATTAAACGCGGTACGCATCATCGGACGCATACGCGCGCATAGCGCGCGCATGGCGTTTGGAGCGATTTC

## SEQ ID 3602

MPFIIDYQCLCAINSEIKMFSGEQLGQAISEAIKRNVSQKEVADHFVGKQPSVSGWIKNGRIDKHLKLDIDYFSDVVTPSHFGIETFRVLKSNQSSIRFPRINAATCAGTINDHYI  
EVVDYVTVAAAWAREKLGGLNLIQVITARGDSMEPTIENGDMVFDTAVEAFDGLYLLWYIDGLKAKRLQSTVGGGLMIISDSSYRTEFVRGDLNAVRIIGIRGAWRLSQF

## SEQ ID 3603

TTGCGCATACATGCGTAACGGCAACCTTATACGCTTACCTTGTATGGCGATTAAACAAAATCAGGACAAGCGCGCGCGCGCAGACGGTACAAATGGTACGGAACCGATCCGCTGG  
TCTTTCATCACCTTAGGGAACCGTTCCTTTGAGCGCGGGCGGGCAACCGCTACCGGTPTTTGTTAATCCGCTATACAGAGCGGTGGTGGAAATCCCGAA

## SEQ ID 3604

LRIHAVTATLYGLPLVGLGLIRTRRRADCTNGTEPIRLVLHHLREPPPLSRGATPYRFLIRVITAGVGNPE

## SEQ ID 3605

TTGAAAAACCTGAAGCAAAAGTTGCGCGCGCCGAGCAAAAGCGGAAAAACCGCGCTTCGACCGCAACCCAAACCCGAGTGTCCGAACTCCGCTTCGGCGACAGAACGCCAACCCGG  
ACCTGTACCGCGTCAAAATCTGCCGCATCGGAAACCGCTGCCGAATCCGCCCCCAAGAAAGCGCGCTTCGCGCATCGACACGCCGAGCAAAACCGGTAACACCGTTTCCGAAAC  
TGTTCGGAAAAACAGCCAGTGAAGTTGCCGCGCAACCGCTTCCGCAACAGTTTCGCGCAAGAAAGAAACCGGAAAGCGGACTGTTTACGGGTCTGTTCCGCGGTTTGTACACC  
TTGCTGCTTCCGCGCGGAGGACGCGATTGATCGCCCTGCTGCTGCTTTTACGCTTGCCTCAACCAACCGCGCGCGCTACCGAAGAAATCCGCTTGAAGAAAGCGCTGACCTTG  
ACGACCGCGCAGACGCGCATAAAAATCACCTTTGCCGAAGTGAACCTCCGCAACCGCGCAACCGCTCCGAAAAACGATGTAACGACACACTTGCCTTAGTGGGGAATCTGAAGA  
AGAGTTATCGGCAAAACAAACGTTGATGTCGAAACCGATACGCTTCCAACCGCATCGACTTGGATTTCGACAGCTTGGCAGCGCGCAAAACCGCATTTTGTCCGCGCACTTACGCAG  
GATGAAGAAACCAAAACCGCGGATGCCGAT

## SEQ ID 3606

LKNLQKQLPRPKQKRNRPDPNPNPQCKLRLRRQANPNPLPLQLLPHRKLPLNPPQEAASAIPTDETNTVSEFVAETAESAEPVAPVBPQVSAEETESGLFDGLFGGSYT  
LLLAGGGTALLALLLLLRQAQSKRRARTEESVPEEPDLDDAADGKIITFAEVETPATPEAPKNDVNDTLALGGESEELSAKQTFDVEFTDPSNRIDLDPSLAAAQNGILSGALTQ  
DEETQKRADAD

## SEQ ID 3607

ATGGAACATTAGACGAACGAATAAAGAAATTTAGGAAATCTCTTGAAGATAGAATTGACGCTAATCTAATGTATGCCACACTAGAGTACATTACTTTTTCAGAACGTTTGTAGCTTTTG  
AAACCGTATGTGATTATTTGAAGATTTCATATCCAGCTTACGGAAGAAAGATCCCAAGAAATCTCTTTTATTAATAAGGAATTTTGAATTTGAAGTACATCAGAT

## SEQ ID 3608

MEFLDERIKNLGKSLREDRIDANLIDATLEYITPSERLAFETLCDYIEDFNILQTEKESQRIISPINKPFIESTSD

## SEQ ID 3609

ATGAGTATCCAAAAAGCAGTTGATTATTTGGTAAATGAATCCCGACTTGCACGGCGGATCGGAGTTAAACAACCGACGGTGTGGCTTGAATAAAAAAGGAACCGCGCCCCGATCATTC  
GGTGGCTGCAGATTGAAAAATTAACCGGAGCGCGAGTGAATCGAAAGACTTACGCTCTGATGACTGGCATCTAATCTGGCCGGAATTTGCCAGCGGACCAACCCAAA

## SEQ ID 3610

MSIQKAVDYFGNESRLARAIGVKQPTVWANNKGTTPPIILRCVQIEKLITGAVNRKDLRPDDWHLIWFELAGDQPK

## SEQ ID 3611

ATGAAGAAGCAGGACAGAAACCGCTGTGCAAGAAAGACAGACGGCTGATTAAGAAAGCGGATGCTGAAAGCGCGCGCCAAAGGCTGCGATGAGGTTTACAAAATCGCGCGGTTTGAAG  
ACGGCTTTGAATTAATTGGAAGACAGCCGAT

## SEQ ID 3612

MKKQDRNRLSKDRRLIKKAMLKAAAGCDEVYKILAPGLKDFELLGKQPD

## SEQ ID 3613

ATGCGGTCGACTTATCTTCTACTACGCAAGAGCTTATCCGAGCGGTTCTATCCGCTTAAGCGCGAGTACGGCCAAAGGACAAGCGGAGAATTGGCGGTATTCATCCGAACACTTC  
GTCAAAAACCGAAGATCGGAGCCAAATACCGATGACGAATATTTAATCGGGCTGCTTTCCAAG

## SEQ ID 3614

MPSDLSPILAKELIRSGSIRLSGSTARGQAGELAVFIRTLRQKPESEPNITDEYILGLSK

**SEQ ID 3615**

TTGTTTGCAATTGCGTTTGTGTTTTGATTCATAATCGCCCTTTCGCCGTTACCTGAACCGCTTCCCTGCAATTTCAGGGGGGATTACCGCCCGCTGCGGGTTTTTCTTTATCGGCCGCCCGCTCTG  
TCCGGGCGGTCAACCGTCTTTCCGATTTTCGCCGTACCCCGTTACAAACGGGTTTCACACAACGGCCGACGGAG

**SEQ ID 3616**

LFALRLFLIHNRLSPLPEPLPCNSGGLPAPCGFFFIGRPSVRAVNRLSDLPSPRYNKRVTQRPT

**SEQ ID 3617**

GTGACGACGCTTCGGCACGGATAACCGACTTGGAAAGGCAGGGGCTTCGTGTTTGCCAAAGCCGAAATACAAGGTCGGTAACCTGTAAAAATCCCGTTGCCCATTTACTCAATCGCAAAGTCAG  
GAATTGAACCA

**SEQ ID 3618**

VTQLAARITDLEGRGFVFAKPKYKVGNCNPFVAHYSIAKSGIEP

**SEQ ID 3619**

ATGAGCCGGGAACAAAGAATACGCGGAGCCCGCTTCCCGGTGCCGGCTCATATGCAGGCGGAAGCGCGGGCAAGGCACGGGAAGCGTTGGACGGGCGGTCGAAGAAAGTGAAAGGGGTG  
ATGATGAAGCCGTC

**SEQ ID 3620**

MSREQRI~~RGARLPVPAHMQAEGAGKAREALDGRVBEVKGVDDEAV~~

**SEQ ID 3621**

TTGATGATGACAGCGCTCTGAAAGTTTGAGAGCGGCAGGCAGGCCAATCGCGTATTACCCGAAATTGGCAAGGCTTTGGCGGTGTAAATTCGGCGAATATTATTTCGGGCATTTCCTCTACT  
GGAACGATAAGACGAGTAGTATGAATCAGGCATTATCCGACAGCGGAAGAAATTGAAATTGAAACCGGGCTGTCCGTTTCAGGAACAAAGAACGGCACGGGCAAGCTGAGGGAACCGCGCGT  
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TTATAAGACAGAAGATTTAACAGAAGATTAGCAGTATATACCCCTTACCCCCAACCGCGGAAACGGCAAGGGCGTTTGAACGCTGACCGGCTTTGTTCCGCTGAACGGCGAAACGCTG  
CGGGCGGAAACCGCGAACCGCAGTTTCGCCGAAGCGCGAAGCGACGATACCGCAACCGCGCGCTTTTCGGGAAACGAGAAATTCGGAATTCGCGCGCGCGCGCAAAACCGCAGCGGTA  
CCGCTTCAGGAATTCGCCAGTTTGTAACAACGAAGTTTGGCGCGCGGTGCGCAACGCTGACGCTGACGACACCGCGAAACGGGCGATTGCAACCGCTGTCGAGATGCTGGGA  
CGCGCGCGCAACCGCAAGGTGAGGTTTCGGGACAGGAAACCGGTTTGGCTTGGTTTTCGCGGTTTCTTCGGGAAATGCGGATGAACCGGTTTGGATGGGCGAAACCAACAGGGTT  
TGCCTCGGCTTCGATTGGATTTCACAGCGGGCAATTCGTCAAATCCTTGAATGCGATCCGCTTAAACGAACACGGCGCAAGGGGAAGGCA

**SEQ ID 3622**

LNMPKSESLRAAGRIPIAYFKLAKPLGGVNAAILFGHFFYWNDKTYQESGIYRTAAEEIETELGSVQEQRTARAKLRERGVLITETKRIEHRITYKLNLAFFDMLQHSGGGSESTAPKCN  
INSPELQNHSGGGGESTAPKCNINSPELQNHSGSEESTAVIRTELDTEFLAVYTPPLPNAGNKGGLNADAFVSADETCGRETGEPTSPKAESDSNGNGGLSGKPKNANVPRRRKTHGV  
PLOEIALDYNEVLGGRLPSQVVLNDRKRAIANRWCEMLGTAAPNGKVRPGDKETGLAWAGF7PKVAMNPFWMUGENQNGFVAVGFDWTFKAGNFVKILEWHPPKTNQAARGRA

**SEQ ID 3623**

ATGCAATGGAAGAAATTTGAAGATCCTCAAAATPACTGCTGTTATTACCACCAGAAGAAATTTGTCTAAAAAACCAGGAATCTTAGAAGTATGGCATGATGCTGATGGAATGTGGCAATTCCTAGATATGCGCAATGAAATTCATGAAGGAGATGCTGTGATAGTTAGTTTAAAAAGAAATGTCACATTGATTTCCTCAGTCAATCTCTTAAGTAATTTACCTCTTGTTGGTTACGCTTGGAGAAATACTATATCGGAAAAATGGAATTTTGAT

**SEQ ID 3624**

MOXKPEDPONTAVITTRILSKKNGILEVWHDADDGMWQFLDGNIEHGDVIVSLKEIVTIDSSVNLNPLGGYAWRNTISEKWNFD

**SEQ ID 3625**

ATGAACCGAATTCGAGGAAACGGAAGCGGTCCAATCACTGSCCAGCGTAGGGGGCGGAACAGAACAATTTGGGCGGCATCTTGATTGAACCGCAGCGGATTCGCGGGTGCACAACTCCTGAAOCC  
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 GGAACACGCGGGTGGCTTGCCTTACTTGATAGACCTGAAACAAACACCCCAAGCGCGAAGAAATATCAAGCGGTACGTTGGGATTGTGAACGACAGGTTTGTGAGCGCGCGCTTGTCTGAG  
 GCTTCGCGCGGATTTGAAAAATTCGCGTTTCCAAGACGGCGGGACGGTCGCAGAAAAGCTGTCTAAGCGCGCGCAAGAAATTTGGCGCAGCGCGGCAAGACGCGGTAAAGCGTGAARCCA  
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 AAGCAGGCAGACAAACGCCGAACATGGCAGACATTCGCGGCAGCGCGCGATTGAGCAAGACGCAACATCATCATCGCCAGCCGGAAGCTTATACGACGGAACAGAAATCCGA  
 GCATTTGCCAGATGTACCTATGCCCAAGAACCGGGACGGGAACGGTGGTTTTCGCGCTGGAAGGCGAATTTATGAAGTTTCGAGGAAGCGCTGATTGTCGATGGCAGGCCGCCAA  
 ACATGATGAATATGACCTTACAGTCTC

**SEQ ID 3626**

MNRIBETFAVQSLASVGAQBNILGGILIEPTAIARCAILTPKFYQACHRIIFRALLDMAAANEPIDIITLNDKLEARGEAEANAGGLAYLIDLNQNTPSAKNISRYVGVNDRFVVERGLLK  
 ASAAIEKLEKSLKDGQGTVAEKLSKAADELAAGKDAVKRETKTFQGTVEDLIGGLDKRLDGVRFGLPTGLMKLDGMTGGLPDGNLIVIAARPMSGKTVLAENIARPAKQKQKAVHFPQSYEMS  
 AVELARRGMAAECNIPMQNLKTNGLTQSDYANMPTVVSQAKEWKFDVNCDDLNVDELCLFAKEKLLTGLDILLVVDHLHIMPAGRDEVAELGNISRLKLNLAELNTPVVLVQAQKHNCGMT  
 KQADKRPNMADIRGSGATEQDANTIIMPHRESYDNGENPISIAELITAKNRDGETGVVCGWKQGMKPEEBPDLAQAPKHEIDYDPYSV

**SEQ ID 3627**

SEQ ID 302:

ATGCGTGAAACCTGTGTTCTATTGCAACCATGCCGACTTCAAAACCAACACCGGGCACCGCGGTGCGCGGTTTTCGGAATCGCGGAAGGCGGGAAATGCGGAGGAAAAAGCGAGCTACTACC  
CGCGAACAATTCGTCGCGCGCGCGCGCGGTTTCAGACGGCATCGGGGGCGCGAGTCGCAAAAAGGACGGCGGTGCTTGGGGAATATCCCCCGCGAATGCGCGCAATTTGAGCGGGAAGGC  
GGGTAAACGCTTTGGGAATATCCAGCCTACCGAGATT

**SEQ ID 3628**

MR ETC FYC NHA D E K T N T G P P V R G F A K C A K A R N A E E K A T Y Y P R T N P C A A G A F O T A S G A A V A K R T A V L G E Y P P R N A P N L S G K A G K T L W E Y P S L P E I

SEQ ID 3629

SEQ ID 3629

TTGCGTTTAAACGCGTTTAAAAATCTCGGGTAGGCTGGGATATTCCCAAAGCGTTTACCCGCGCTTCCCGCTCAAATTGCGGCGCATTCGGGGGGGATATTCCCAAAGCACC GCGTCTT  
TTTTCGCACTCCGCCCCCGATGCGGTCTGAAACGCGCCGGCGGCGCACGGATTGGTTTCGCGGGTAGTACGTCGCTTTTCTCCGCAATCCCGGCTTCGCGCATTTTCGAAAAACCGCGC  
ACCGCGCTGCCGGGTGTGGGTTT

SEQ ID 3630

I-RFNAFFKSRVGVNDIPKAFYPPSRNSAHCGGDIPOAPPFLRLPPMPSETRRRRTDNFAGSTSLFPPHSAPSRLSQNRAPACRCWF

SEQ ID 3631

ATGACGGTCCGAACACGCAAAACCGTCGGAGCGGCGCGCAACAAGGCGCGCAATACCAACCCGGGCTATTACAAAAACCGCGCTTCGAGTCGTCGGGTTTTCGCGAAT  
ACCTCAACTTCAACCTTCGGCAACGCCCTTCAAAATACATCTGGCGGCACAAGGAAAAAGGCGGGCGCGAAGACTTGGAAAAAGCCCTCGCGTACTTGGAAACGCCAACGCGCGCGCGCGCGAA

GTTCAGAACTCAAAACACCGCGCTATGAAAAATGTACGCCGCTGAAAGATTGCGGGTTCGACGGCGCACGGAGGCGCGCTGCTTGCCTCATCTCCGCGCTTATTACATCCGC  
GACGGCGAAGACAATTTCGCTGGGCGCGCGCTGTGTCGAAGATTGTGGAATAATGCCGCTGAAGCGGGCGGGCCCCGACCTGAAAGCCCGATGCCGCTGAAACGGCGGGCG  
GAGGCATT

## SEQ ID 3632

MTVRNTQTETVRTEAPQQGGNTNPGYYKNRAFEVGFAYLNFNLGNAPKYIWRHKEKGGREDLEKALRYLERQRAGAPKPKLKHRRYKMYAGLKDCGFDGSTEALLAVISAAYYIR  
DGEDNFAWAAACVEDLLEKMPPEAGRAPHPEPMPETAGGGI

## SEQ ID 3633

TGTGTTTATTTCTTCGCTGCTTTTATGGGTCGGGTCGGATTCCCGCGCGCTCCGTCATTCCCGCGCAGGCGGGAATCCGGACCTTGAACAACAGCAATATTCAAAGATTATC

## SEQ ID 3634

LFYFLSVGFMGRGRIPAASVIPAQAGIRTLEQQYKII

## SEQ ID 3635

ATGGATACCTGTTAAGCATCATCACCGCGCTGCTGCTTTCGCGGGCGGCGACGTTGGCGGTATGGCTTTTGGTGAAGCCGCGACGCGGTTTGGCGCGAAGCGGAAGGCAAGGCG  
AAGACGACTTCGACGGCTTCGGATAT

## SEQ ID 3636

MTLLSLITALSFGAATLAVWLLVEAADAVLRKRKRGKGGDDFDGPGY

## SEQ ID 3637

TTCAGGTGCGCAATTCTTCGCGCAATTTGATTTTCTTTTGTGTTTATATGCTTTAATATCCGAAGCCGTGGAAGTCGCTTCGCGCTTTCCTTCGCGCTTCGCGCGCAAAACCGCGTCG  
CGCGCTTCCACAAAAGCCATACCGCAACGTCGCGCGCGGCAACGACAGCGCGGTGATGATGCT

## SEQ ID 3638

LQVRISALLIFFVFMCLISEAVEVVFAPAFALAAQNRVGGFHQKPYRQRRRPGKRQGGDA

## SEQ ID 3639

ATGGCGGAAGAAATGCGCACTGCAAGGCTGCGCGGGGACCAAGCCGTGGAGAAAGGGTTAATGCCGTCCCGCGCAAGGAAGGGGGGCTATTATTACAAATCGTGCAAAACCTGCC  
GCAACAAGGCACTCCCGCAAAAGCGCGCGGAAACGCGCGCGCGGGAGCGCGCGATGACGGCGGCAAGGCTGCACGGATACATCCCGCGCGCACACCGCGCTGCCGATATTGGG  
CGCGCGCTTGGACGCAACCGGCGGGAATGCGCG

## SEQ ID 3640

MAEEMRTKACGGTKPLEKGFNAVPRKEGVIYYKSKTCRNKAVRQKRAEKRAAAGAGAMTAARLHGYIRAAHAACPILGAGLWTPPAGECA

## SEQ ID 3641

TGGTGGAAATCCGAATAAGCGGTTCAAAACGTGTCGCTGCCGCGGACCATATACAGTTGGCAACTGTCCGTTGTGCGGATGGGTTGCCCTGCCCTCCCTGAGCTACGCAACCGTT  
GTCTGCCCTTGGCGGGCGCGGTGGCGCGCGGCGGTTGTGCTGATGATACGGAAGTTCCGATATACAAGGGCGGGCTTCAGCCCGCCAAATCCACCACTCCCGCGAATCCCGCGATT  
CCGCGCGCTCATTCGCCATAGCGGGAATCCAGACCTGTGCGGTGCGGAACTTATCGGA

## SEQ ID 3642

LVEIPNKRFTKCRGSHIQLATVRLCRWVALPLPELNRGCLPWAGAGGRAVCRYDTEVPIYKGLQPAKSTNSAESADSRHRHSRISGNPDLSVRKLIG

## SEQ ID 3643

GTGGACGCAACCGCGGAGGAATGCGCGTATACGCTTATCTGCTTACCCGATCGGCAAAACCGATATGGCGGATTGGCGCAACAGGCGCGTCAGGAGCGGAGGCGCGCGCT  
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GATCGATTGGACAACCGCTGGAAGTTGCGGTGACGCGCTTCAAGCGGTGCTATCACAACGACAGGAGGTCGGCGCATTTGCCCGCGAATATGGCGCGAGCGCGTCCGAGGCGG  
GGTTTGGCGGTGAGGTGGGGAATTGGATGAAAAG

## SEQ ID 3644

VDATGRGHRVIRLILPYVPSANRYWRIWRNRRAVSAEAAAYKETVRRIAQGAGAMPSEBGFVAVRLRLIPKANKDGGANKTVIDLNALKVALDALQGVAYHNDQVRRIAAEYGGEPVAGG  
GLAVEVGLDEK

## SEQ ID 3645

TTGCGGCAACAAATACAACCTATATCCGCCACTTTTTCAGATGTGATTTTTCGCTTCGGTTTTACTTTTTATCCAATTCCTCCACTCCACCGGCAAAACCGCGCTTCGACCGGCTCG  
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GCTCTTGTTCGCTTTGGGAATCAGCGCGACCGCGCACAAAGCCTTCGGACGGCATCGCGCGCGCGCTTTCGCGGATACGCGGAGCGTTTCTTATACGCGCGCGCTTCGCGCT  
CCTGACCGCGCTTTCGCGCAATCCGCCAATATCGGTTTTCGCGATACGGGTGAAGCAGGATAAGCGGTATCACGCGCATTCCTTCGCGGTTCGCTTCACAGCGCGCGCGCAATATCG  
GGCAGCGCGCGTGTGCGCGCGGATGTATCGGTGACGCTTTCGCGCGCTATCGCGCGCTCCCGCGCGCGCGCTTTTCGCGCGCTTTTCGCGGACTGCTTGTTCGCGCGGTTTT  
GCACGATTG

## SEQ ID 3646

LROQTIPISATFCRCDFSAVLLFIQPHLRQTAACDRALAAIFGNAAPHLVUVVIGNALKRVQRNLQGVVQIDHRLVCAAVFVRFGNQQAQHRHKAFGHRHARPLRDTADGFLIRRLRA  
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## SEQ ID 3647

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GTGACGGCGCGGCTGCGGTAGAATTGGGAATATTGGAGTTTGTATGATAGAACCGCTTGGCGGATTGTCGGAAGGGGAAATTCAGACGGCGCTTCGCGGAAGGTG

## SEQ ID 3648

MKSKTEAKSHLQKVADIGCIVCRNCRFGVPAEVRHIRNGAGAGCGRIWNHLGLVHYRTANRIVRKGRFRPSRKV

## SEQ ID 3649

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## SEQ ID 3650

MQQNQSPHYTFREGRLNFPRTIRQAVLYIKTPK

## SEQ ID 3651

TTGGCGGATTGTGCGGAAGGGGAAATTCAGACGCGCTTCGCGGAAGGTGTAATGCGGACTTTGGTTTTGTGTCATGAAAAGGGTTAATCAAGCTA

## SEQ ID 3652

LADCAEGEIQAFAPGVMRTLVLLHEKGLIKL

## SEQ ID 3653

ATGAATACAAGAANTTGAATTTATGAACGACTTGGCGGCTGCTTTTGGCGGCTTACCGTGATACGCGCAGCCTAAATAGATGTTTCAGTATCAAGGCGCTTATATGGGGGAGGAAG  
CTTGGCCGCTAAGCTGAAATCGGCTTGAGATACGCGGAAGATGCCATGTTCTTACTTTACAGGATGGGCGAAGGTGGATGCGCGCAACAGAGGCGCTTCGCTATTTCGTTCCGCTAT  
CGGTGCGAAGTGCAGGCGAGCTACGAGGAAGCTTTCAGGCTGAAATCAGGCGCGCGCGGAGGGGCGCGCTTCGCTATGAGGCGGATACG  
CAGGCGCGAGGAATGATTTGATTTGCTGTTGAGAAGGT



## SEQ ID 3654

MMQEFPEFMNDLARAFFERRYDRSLNRCSIEGRYMGEKACPHKPEIGLRYGEDAMFLTLQAWKVDAPOQEAVERISFGIGAKSQAAVEERLQAKIRRRREGPLHLQTDLGLAANYRAIR  
QAAGNDFDLLEKVV

## SEQ ID 3655

ATGCTGAAGCACATCAAAGCCCTTAGATTTTGGGGTAATATCATTGTGATGAGTGGGATTTTTTTTGGCCGTGTCATTGGCTGCAAAAGCGGGCGCTCACGAATTTCTTTATTTTG  
TTTTTTGTGTTATGATAGCAGGCTCTCTATGAG

## SEQ ID 3656

MLKHIALRFLRWISFVMSAIFPCPVIGCKRRGRHEFLYFVFCVIDSRLSYE

## SEQ ID 3657

ATGAGTAAAGCTATTAAACAAGTTAAATGAAAAGGAAAAGGAAAAATACGCCCTGCTTTTCGCACAAAGAGAAAAATTTATCGTATCTTGGAAAAATCCGGAACAGGGATTACTCCTCTA  
CCGCTCTTTTAAAAAGTGGCGAAACTTGTTTTGTGATTGATTATGTTAATATGGCGGAGGTGGTTACTGAGAGGGTCAGAACCTATACAGGGACAGCTTTAAACTTGGCTCCACACCGGT  
TTATTTAGCGGGCGGGAATCCGTAGCAAATGAAAACAGAGAATGTTGGCTACGGAGAGTTGGTATTGACGAATTTACAGTTGATTTTGTAGGGAATATGAGAAGTATAGATTTCGG  
CTGGATAAAATAAACAGCGTGAATGTTTCAAAGCAGCATCCGAATCAGCCAAAGCGGCAAAAACAAACCGATTTCCTTAATACCGTTTAAATCCGAGTTATGAAAGAGGCTATAT  
TGGTACTTTCCGATAAGAAG

## SEQ ID 3658

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LDKINSVECFQSSIRLSQSGKNKPIFFNTPVNPQLNKEAILVLSDKK

## SEQ ID 3659

ATGAACAATTCAGTTCAAATCTCTAATATTCTATCCATCAAACCGAAATCGGCTTATTCACTCTGAATGATTACACCGCGCTTCAGCGGAGAAGACAGACACGACCGCTCAAAGCG  
CCGCAACCGCCCTCGAAGCCTTAAGCGCACACGCGGACCGGAAACACGAGAAAAATCCGCCGATACCTCCCGGAATCCGCAACCTGTCGGCGGT

## SEQ ID 3660

MNNSVQISNISIHTFELFSLNDLHRASGGEDRHRALKAAANALEALSANADAEHAEKTRPILPEIRNL SAV

## SEQ ID 3661

GTGTACGAGCTTGAGACCTTCAACCGGTACAACCTGTGAAATCGTCAATCGACACGCGCGAACCAGGAATCTGTGCGCCAACTGCGGAAAACAAACCGGAAACCGTCGATACCGATTCT  
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AACAGTTGCGGAAGTCAAACACCGGAAGAGTTGCAGATTTCCTGAAAAGTGTACGAAACCGGTGCGGTCGCGGAAATGCGCTGAAACCGCGGATTTCACCGCGCGCAGACGATTG  
TCCGCATGTCTCAACCTGCGGAAGCACCGCGCGTTGAGGAAATGCGAGCGAAATCACCTTTGAAACCGCTGATCCAAACACCTCTGAGGCGAGACGCTTCCCGGACTTCTGAAAGACA  
GCGAGGAGGAAACCGGTAGATTGGAGCATCTACCTCTCGGAAGAAATATCCAAATAATGCAGATACCTGTTCCTCTCGGAATCTGTAGTTCTGACGCGCTTCCGAAGCGAAATACGA  
CCTTCCGGAATGTATCTCGAAATCGCGACCGCGATGCCGTGCCGAGACAGTGCAGAAATGCTGGAAGAAGCGGAAGCGGACTACTCAAACGTGCCCAAGCATTGGCGCAGGAATTG  
GGTATT

## SEQ ID 3662

VYEPETFPNPNFVIVDTFPEPSVAQTAENKPEVDTDFYNNLFSNNHIGTEETASAKPAAPSGLAGFLKASSPETILEKTVAEVQTPPELHDFLKVYETGAVAETAPETPDFNAAADDL  
SALLQPAEAPAVEENAAREITLETDSNTSEADALPDPLKDSEETVDWSIYLSEENI PNNADTFPSBSVSDAPSEAKYDLAEMYLEIGDRDAAAEVQKLLERABGDVLKRAQALAE  
GI

## SEQ ID 3663

CGCAACGCTGTCTGCGCTTGGCGGGCGCGGTTGGCGGCGGGCGGTTTGTGCTATGATACGGAAGTTCCGATATACAAAGGCGGGCTTCAGCCCGCCAAATCCACCAACTCCGCGGAAT  
CCGCCGATTCGCCCGCGCTTATCCCGCATAAGCGGAATCCAGACCTGTGCGTGCAGAACTTATCCGATAAAACGGTTTCTTTAGATTTCGCTTCGCGATTCACCATTTCTGTGGGA  
TGACGAATGTAGTTTCGCGGAATGACGGCGCGGCTGCGGCAAAATTGCCCTTCCCGTTTCAGACAA

## SEQ ID 3664

RNGCLPWAAGGGRAVCRYDTEVPIYKGLQPAKSTNSAESADSRRRHSRISGNPDLVRKLIG\*NGFFRCVPDSHFRNDGM\*VRGNDGGCGKIALPVFRQ

## SEQ ID 3665

TTGTTATGTACGGCTTAAAAATTCATATCCTTCGGCGGTGCGAAAAATCCCGCAAGGGTAAACGATTGGAATTATACACCTATTGCCGGAATAAACAGCGCGCTGGAAGATTGAGAG  
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GCGGCTT

## SEQ ID 3666

LLCTGLKIHILRACENPRKGNLDNYTPIAGKNRPFSEDSGICIPYCIKPPTGCGFRAVSGGFLRVPRRRVRLRLRGLRLRL

## SEQ ID 3667

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TGCCGCAATGAAACTATTTACCGTTGGTTGGAAGCTAATGAAGAAATTCGCCACCAATACGCGCGCGGAGAGAAAGCAGCGGACTATTTCCGTGAAGAAATCATCGAGATTGCCGA  
TAGTGCAACAGCAGAGAGCGCGCGGTTCAAAGCGGAAATTCAGATAGATGCCGAAAGTGGCGGCTTCCAAGATTGCCCGGAAGAAATACGGCGACAAATCGGAGCTTGACGTTAA  
TCCGGCGATGGGAGCATGAGGGCGGCTGTACGGCTTGATGCTGAGGAATATCCCAAGATAGCGGAAGATGTGTTCGCTAGGGT

## SEQ ID 3668

MSGTKRKLGRPTDVKMDADKICEKIANGRSLRSICAEDGVPPMKTIYRWLEANEFRHQYARAREKQADYFABEII EIADSAQAESAAVSKAKLQIDARKWAASKIAPKYGKSELVVK  
SGDGSMAAARLDABEYRKIAEDVLRV

## SEQ ID 3669

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CGCGTGGCGCATGGGCGCGTGCCTGATTGCGAGTTTATCCAGCGAGCTATTTCGCGCGGCTGGCGGTCAATAACTCCGTACAGATTTCGGAATTTGTCGCAACAGAGAGTATCGCGG  
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CAGCCCTGACACGCGGATTATCTGATTATGCAACGCTGCACGAGAAAGACTTGGCGGGCTGGCTGCTGACGCGGCAACCGCGGAAGAGTGGGAACATTGTGCTGCTGCTCATCAG  
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GTACGTTCAAGCTTGACAACCTGCAATTTGTCAAGCGGTGCTGCGGGAATATCAGATGGGTACGCGGCTGGGACTTGGCTTCAACCGCAACCGCGGCGACTACACGGCAGCGCGGAG  
GCTTGGCGTTACGGAAGACGCGGCTATATCATCGCAACGCTGCGCGCGCGGTACGCGCGGAGCAGCGGAGCAGGATATTACGCAACACCGCGCAAAAGACGCGGTGAAACGAA  
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GACCGTTTCGCGGACAGGTCAACATCGGCAATGTGATGTTGTTGATGACGGCAGATGGGACAGGACGCGCTGATTGCGGAAATGCGCATGTTCCGGAACGCGCGCATGACGACCAAT  
AGACTGTTTGGCGGCTGCGTTTGGCGAGCTGCTGATACCGGAGCGCATGATTGATTCTCGGATTCGAGTTCGAGGCTGTGAA



## SEQ ID 3670

MALGQFDVDETSVIRSLSSASLYMFTRRMFPYQRRGVWQRANHHAPICNALERVFNGETKRLIINIIPRYSKTEIAVWNFLAWAMGRVDPCEFIHASYSAAALAVNNSVQIRNLVQHEEYRA  
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EDGTALWPEKHDIEITLRMEQAAPIYVAGQYLQKPAPPDGGTFKPDNLQPVKALPAGNIRWVRAWDLASTANGGDYTAGGRLGVTEDEGRYIIANVVRGRYGADERDRILRNTAQKGVKTK  
ISIPQDPQAGKSQYLITRQLAGPSVSAGPESGDKVTRAGPFAAQVNI GNVMVLDGTDWTDALIAENRMPNRRHDDQIDCLGRAPGELLDRTRGMDFLRSQVRAVK

## SEQ ID 3671

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TGTATTGCGTTTGGTGTATCGAGGCGCTAAGACCAATGGAGTGCTTAAAGTGACCAATCAAAAGCGCGACGCTCGAATCAACCGAAGACGAGCAATCGCAACGGAAGACCGAAAGGTC  
GATGAAGCCGTGCGTTCTCCGCTGCGCCGATAAAGAACATACGTGGCGGACTGGCTGCGCATCTGCTGGAAGACCTGTTTGTATTGACGCGCGGTGCACTACCGCGGCAAAACAC  
TGGGCGGCGGCTTGATCGCCCTCGAAGTGATGACGGGCGACGATTAAAGCGGTTTGGACCAATACGGGCGGTATGCGCTTACCGCCGATACGCGTATCAGCAATCTGCACGGCAT  
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TGATAGGCTGGGAAGGAAGCGCGCTGCTGCGCGCAAGCAGTGGATAACCGCAAGACGCAAGGTGCTCGATGCTGCAATGCCAAGCGCGGATGGCGGTAATCGGTTTGCACGAGCC  
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## SEQ ID 3672

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RQVHALEYTAGSVPDALVGPETWADDIRRPQYEWDLISGETAQRKRMRFPVGEISRNFRRETKQPLKDVYDEWLARVVCFAFSVEPTFPVQVNRSAETSREQLSDGHSGLKMHV  
KALIDVLYARMMAAYEFVWKGESLNPKEQAEIYAIYKNAGILTADEIRAEIKKEPLPGQGPEDPKQDGRKPEEPNQAELKGRSPMSSEDESAALIEAYLLTRIDGLAEQIALI  
EGAAVDMQAGDLAELSRAGVANGLDPGWGLSDVVEPIIRVAEDGVAALLKRVPEPAAGNVNIRSAVKWAHERAAEMVGMKRAAGGLVRNPAAEWQITFETREMIKRAQVAEAM  
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## SEQ ID 3673

TTGGTTTGGCTCCAAAAAAGCGCGCCGCGAAGGGGCGGCAAAACACACCGCGCTGACCGCAAGGAATCAAGATTACGGCATATCCCTGCCAAAAAGGACACACCGCGCAGT  
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## SEQ ID 3674

LVCSSKKPPREGAAKHTRLTRRNQDSGLSPARTGTTAHRQPG

## SEQ ID 3675

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CAAAGCACAGGCGGAAATCGAAGGCTGAAGAAACAGGCGAGTACCGCGAAGGCGAGTACGAAAGCTATCAGTAAGGACAGGAATAACGCGGAGAGCGGCTTAAAGGTTTTCAGCGGATT  
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## SEQ ID 3676

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KLFEISLVDRPANPDVPTCFKADKPKDEAGAADKDGKPSDKPTEEDENPKDGKPKTEKDGKDGKDEAGKSASVNLSESEIAALKAVALAKADKPKGGPAAKSMYQVSPADVLHS  
LKWLVEDASYDNIDEAVTAQIKESAAGLAESLKALAASEADKPADGLAAKAGSGDLAKAESADELAKAQDALKKSNDALAKAQAEISLKKQAVPPKSGTKAISKAEDNGEDPLKGFQPI  
VKNDGTLDDVATLILAKQTRGL

## SEQ ID 3677

TTGAACCGCACAGGCTCAAAACAGCAGGCGCTCGGCAACAAAATGCGCTCCGAAACCCCTAAAGGCTTCAGACGGCATTTGGCGGCGCGGATCAGGTATTGCGCA

## SEQ ID 3678

LNRHLKQQAQVGNKMPSETPKGFRHRHRRRYQVFA

## SEQ ID 3679

ATGAATAGAAACGAGGGGTAGTGAAGTCTGACCAATCTGGAGAAGTTTGGTTCGCTTAAAAAGAGCCAAAAAGGTATCACCCCCCATCAATGAATGCGAGATTGACCATGTGCAAG  
CAAAAGTAAAGAGGTTCAATAGTTTATAAATGCACAGGTTTATCCAGAGAGAAATATTAGAAATCAATAAA

## SEQ ID 3680

MNRNGGVKSDQSGEVLVRPKSKQGITPPSNQWQIDHVAQSKSGNSYKNAQVLSRRENKIKSNK

## SEQ ID 3681

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## SEQ ID 3682

LCLELVHLSLLIILKPPVSGVTDGLFVLP

## SEQ ID 3683

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CGTGGCGAACCAACGCGCGCGGTATCGCGGAAGGACAGGCGCGGCGCTCATCAATCAGAAACGGTGGAAACGCGCAATTCCGCGCCATCGGCTGGAAAAACAAGTAACCTTTGAA  
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GCGTTACACCTACACGACCGCGCTGTTTCGCGCGACGCGCGGGGAAAATCAGCGTCAGCACTTGTCTGTAATCTGTGTGGCTTTGGGCTTCAGGCGGTATTTGGGACGTGGCAGGCGC  
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GCGGCGGCTTCGGTTTCGCGTATTTAGGCGAGCGAAAAAGTAACCGCGGTGATTCGCGCTGTTCGCGCGCGGTTGCCCTATGCTTGGTACTGGGTGCGGCGCGGTTCTGAAAACTGGGCG  
CGGTATACACTGCCGCGCAAAGTGGAAATTTCCGGCTGATGCCGAAGGTACCCAGACCGCGGCTTCCTCGCGTCCGAAGACAATTCACACTCTATTTTGGAAATTTGACGCGCTGTGACCCA  
AATCGCCCTGCCTGATTCGGGCGGTTCTGGTCGAGACAACAAGGCGGCGGCTGACTTCCGACAAACGCGGCGCGGCTGATGAATTTGAAGAGGCGTTCGCGCATTTCTTTACCCGATAC  
CGCTGTTCGCCGATACCGCTACTGCTCAACGCCCGCGATTTGGCGCGCTGCACCAAGCTGATTTATTCGAAACACGCGCGCGCGCTGTGATTAAGTTGAACGTTGACGTGAACAATACGGCGA  
ACATCCGCGCGCGGTGTCTGTGCGTTTCGATGACAACAGATATGACGCGCGGACGACCTGAACTCATGTGGTTACACCCGAAACCTGCCTGCCGGTACTTACCTGTCTTACTACTAAGCGCGCTGCC  
CGCTACGTTTCAGGCGCTCGGCAATCTCGTGTCAAGTGGTACGCGCCAAGAGTATTACCAATCGAATGGCCGCTCGCACCCGATGTGTACGAATACGGCGCTCATGCGGACGAGGTGCTG  
CAAGGTATGTTTCAAGCTGCCCTTCGGTATGATTACCAACGTGGGT

**SEQ ID 3684**

MNVNQLTQETIELMKSAQAGGGPPDKGFTQPSASFTAGLQTYDLSAPSKLYPVLTLPLNRRIPRVGGGRTIISGNWKAVTMINVGNQIRAGIEGEGRRGGVINHETVERNAQFRAIGLENVQVTFE  
ADYAARGFEDVKALAVATQTLQATWVAEEMILLGGTSLKAGVTPPTPAVVSADAAGKISVSTLSVICVALGLQAYWDVAGANNAGATQSPNIKTAQVPAKITERRADGTDTFPGGSGARKS  
AAASVSGIEAGKKVTAVIPAVRGAVAYAWYWGAAAGSEKLGAVTTAAKVEISADAEGTQTAASLPSEDNSTILEFDGLLTLQIALPDSGAFWSDNKGGLTSDNAGVYFEFRAAGVFPFTTRY  
RLSPDTVYVNMARDLAALTCLIIGNSGAPLILKLVNDVNTANIRAGVVGVSVMNKLITGDLLNI VVHNLPAAGTYLYFSRRLPAYVQGVGNLLQVRTRQEYTLQLEWPLRTMYEYGVYADEVL  
GCHMFPAPFAGMITK

**SEQ ID 3685**

ATGCGCGTGTGAAAATCAGCAGCGCTTTTCCTTTTGGAGATTTTGGATGACAGTCAAATTAAGCGCCCGAAGGGTTTACCGAGCTTTCCCTTCGGCAGCCAAAGCTACGCGGCAGATGAAA  
ACGCTATCTGGAAGTGCCGTGGGAGCGCGCGGAATTCCTGTATCAGTTTCGGTTTGGCAACGTTGCCCTCCGAGCCTGCCGAAGGGCTGAAAAGCCAAGCGCGGGCGTAAACCTAAAC  
CGGCAGCCGGCAGGACAAATCCGAACCTGCCGAAGTGCCTGCCGAACCTGCCGAAGCCGAAGCGAAGCTGCCGAACCTGCCGAAGCAGAAGCCGAACCTGCCGAAGCCGAAAAGGCTGAA

**SEQ ID 3686**

MPSENQAFSEGDFFMTVKLKAPEGFTDVSFGSOSYAADENGIVEVPSEAAEFLYQFGFGNVASEPAEGPEKAKRGRKPKTCQPAGQSEPAEAAEPAEAEAEAEPAEAEPAEAEAEAE

**SEQ ID 3687**

ATGCGCGCCGCGGTTATCGCTTGAGGAGTTC AAGCAGCGTATCGGCGTTGAACATGACCGCGGGGACGATTCTCTCCTCAGCGTCATTGACGGCGTGTGCGGCGCGCGGAAGCCTATATCG  
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CGGCGGCTGGGAGTTTGACAACATGCGCTGCTGATCGCCGCCCAAGGTTTCTGCGCGGGGGCTGAAAATATCTGAGGATATCGTACCGCGCCGCTTATGAGCGCATGCCGCCGACATACGGAA  
CGCGTGATGATTATCGCGGTGCAAGCGCTGAACGAAATCTGGCTGAGCGCAAGGCGTACGGAAGCAAGACGCTGCAAGCGGAAACCGTCGCTTCTACGCTTCGGTAAATCCGCGGTTATCGCC  
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**SEQ ID 3688**

MAAPVSLSEEFKQRIGVEHRRDDFFLSVIDVGSAAAEAYIGRSLAADYVGRYDNGKDRIVLDNYFVLSSVVKINGADAGGWEFDNWLLMRPEGFARGLKNVEVSYRAGYERMPADIRE  
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**SEQ ID 3689**

SEQ ID 3689

GTGTTGGGGGTAAGGACGGGGGACCTGCGAGCGCTCGGTACACGAGCGGTGAATGTTTCCGGCAATTCGTTTCGGGCGAAGTCGATACGAACGTCGGTTACGGCATCGCGCATGAAGTATG  
GTTTCGGCGGGCAGGTGTCAAGGTTAAGGCTTCGCTGCGGCAGGTGAGGACAGCGGTCGGCAAGCGCGTGAAACCGCGCGATATGTCAAGCTCGCGGCCATACCCGTGATGTGAAGTTGCC  
GGAGCGCTCGTTCTCCGTTTCGGCATTTCGCGGATTTCGAGCCGAAGTTCGCGGACGACCTGCAAAAAATCGATTGGAAGGTGTTGAAA

**SEQ ID 3690**

VLGVRTGDLRRSVHORVNVSGNVVSGEVDTNVRYGLAHEYGFAGSVNVKASLRQVRQAFGKPLKPPRYVNVRAHTRDVKLPERSFLRSALRDLTPKFADDLQKSIGKVLK

**SEQ ID 3691**

TTGCAAGGTCGTCGCGCAACTTCGCGGCTCAAATTCGCGCAATGCCGAACGGAGGAACGACCGCTCCGGCAACTTCACATCACGGGTATGGCGCGGACGTTGACATATCGCGCGGTTTCAGC  
GGCTCGCGCAACCGCTGCTTGACTGGCGCAGCGAAGCCTTAACGTTGACACTGCCCGCGAAACCACTACTCATGCGCGATCCGCTAACGAGCGTTGTTATCGACTTCGCGCGAAACGACAT  
TGCCTTGGAAAACATTCACGCGCTGGTGTACGGAGCGTCGCAAGTCCCCCGTCTTACCCCCAACACCCGCCGATAACCGGTTACGCACAACCTTCGCTTTGCAAGCGCAATGCCGACCTGCCCA  
CGGATT

**SEQ ID 3692**

SECRET  
LQVWRELRLQIAQCRTEERPLRLQHITGNGADVDI.SRRFPQRLAERLPDLAQRS.LNVDTARETILMRDAVTDVRI.DFARNDIAGNTHALVYGASQVRFPYPQHP.PITGSAQLRFAGANPTCP  
PI

**SEQ ID 3693**

TTCCCGCATGAAGCGGGATCCAGACCTGTGCGGTGCGGAAACCTTATCGGATAAAACGGTTTCCTTAGATTTTGCSTTCCGGATTCCCACTTTCTGTGGGAATGACGGAATGTAGGTTTCGGGG  
AATGACCGCGCGCGCTGCGGCAAAATTGCCCTTCCCGTTTTCAGACAACATATTGCTTGTCTTGTCTACGGTTTTTTTGGCGGTAGTGTGGGAATCTCGAATCCGACATTTCCAACACGGGTT  
TTTTCGGAACCGATAAAACCGCTCAAAAGTTTTTTTTTTGTGCGGATACGAATATCCGGCTGCATTTCAAATTTACATCGCTTCCAATTTTCGCA

SEQ ID 3694

SEQ ID 3694  
RTHKDESRDNGAETTPRIKPEI.\*II.PSGEPISWE\*RMVCSRE\*ERRI.PONCPSREOFFTICLVLATVFCRRSDSRIRHFOORFFGNDRVKCFFCRIRISGLHPKFTSLPISO

SEQ ID 3695

SEQ ID 3695

ATGANTCGTAGAGCGGTTTATTCCGCGCTGTGGCGAAGCTGGACGCATTGGACGGCTTCGTAACCAAGAGCCGGAAGCTGGTGCATGGAAACGATGTGAACCGCTACGATCAGCCTGCCT  
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GAATCCGCTGATTGAAGCGGTTGTGCATATGCCCTGAACGCCCTCCACCCCGTTACGGGCAAGACGGATTAAACGGCGGACGGCGCGGATATCGAGTATTGCCCGCTCGAGGGTACGGTGGAA  
ACGACGAGGGGAGCGCTTGGCGAACAGCGCGGTTGTGATTATTCGGATTGTGATTTCGGCCGCG

**SEQ ID 3696**

**NRREAVYSALNAKLDALDGFVTKSRKLVHWNVDVKRYDQPALFMAQGDHQAFLTGRETKWILRADVYLYVQTAGQPPAPVMNPLIDAVCNVAVNHPVTGKTDLTADGADIEYCRVEGTVE**  
**TDEGTGEGEOAVCLIPIVICAA**

SEQ ID 3697

SEQ ID: S937

ATGCAGTGTGACGPTTTGGCAGCGGCGAAGTGTTGCCCAATGATTACGGATGCTTACGGCAACCGGTGTACAGAACGCAACGCCCGTGCGGATTATGGGCTTGCAGGAATGTCGGTCGATT  
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CCTGTTTTTCGGTACGGAATATGCAACCGGCACGATGAAGCGCGCTTTGGCGGAAATACGGGCAAAATGCTCGATGCGGCACAATTAATCTTACCTTCAGGCAAGCGCGCGCCGGCGGGGCGC  
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CGGATAAAGGCAAAACGTTTATCCGAGCTTTTACCTATACGCAAAACGATGCCCCGGCGAAGAAAAATCGAGCTGACCAATATGGCGAGGGCAACACGCGGACGTTTAAAGATGAGGTACT  
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ACCGGACGAGGCGGGCTTTGAATACGGTAGCCTGTGAGGATTCAGGAG

**SEQ ID 3698**

NQLTFGSGEVFAQMITDAYGNRVONATPVRIMGLOEMSVDLASAEIKFYGQNRYPYLAOVAQGVKVSQKMGALINGLTINTLFPGTETATGTMKALHAFTTGRVLDGDNYSYSLQAAAPGGG  
KFAEDAGVGMQDGTAYIKVASSPKQGQYTVSESGVYAFNSSDKGKTVPYSFTYTTQTMPPAKKIELTNMATGNTPTFKHRYLTQFKGKKALLEBSVTSGLGLFSTKNDDFSVPEIDFTAS  
TDEAGFKIGTLWIOE

**SEQ ID 3699**

GTGGATTCAGGAGTAATGTTTATATGCCGCTGAAAAGGCGGCTTTTTTTATTCAACCAAAGTCAAGGAAATAAAAAATGACCGTACGGAT

**SEQ ID 3700**

VDSGVMPICRLKRRLLFLFNQSQGNKNDRTD

**SEQ ID 3701**

ATGACCGTACGGATTAAAGGCGTAAACGTAGAACTGAACGGCGGGATTATGTGATTCCGCCATTTCGCGCTGGCGCGCTTGGAGCAGTTGCAGGAGCGCATCGGCTCATTTGACGGCAATG  
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AGTGTTTGCCGCCGTGATGGACGTTTCGGGCTTGAAACGCAAGGAGCAGGAAGCCGCACAAAGCGGGGAGGCCCGGGCGCGGAT

**SEQ ID 3702**

MTVRIKGVTVELNGADYVIPPALGALEQLQERIGSFDGNAADAGQISTVIDCAHAALKRNPDLTREAADLIDIGNMNEVFAAVHDVSGLKRKEQEAAQAGEARAAD

**SEQ ID 3703**

GTGATTGCCACCGTTTTCGGCCTCTACCGGCTGGACGTGGGAGTACGTGCGCGACAACCTTGGATTTCGGCGGTATCAAAACACCTGAACAGTATTGGCGCGAACATCCGCCCGTGCATATCT  
TGGCAGCGTCGTATATGGGCGTCAAGCCGTCGTGCGGCAGTGTGCAAAAGCGAAGCGGACGAAGCCGTCGGTATGCTTGGCGGCGGCGAACTCTCCGAAGACGAATTTGACGCCCT  
GCTCAAAGCGAAAGGAATCATC

**SEQ ID 3704**

VIAHVCASGTWTDYVADNLDLPRIKHLNEYWREHPVHILAASYMGVKPSSGSVQSEADEARAVGMLGGGELSEDEFDALLKAGTII

**SEQ ID 3705**

TTGCGCGGTGTTGAAAAACAAAACGCCCTTGTGCGTAACGGTGTAATCGCGCCCGTAGCCCAACGCCGTGCCGCCGACCTTGACGGCGGGCCGTTCCCTTGACGCCCGACACAGGCTCGATA  
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CAAGATATGCACGCGGAGTGTTGCGCCCAATACTCGTTACGCTGTTTGATACGCGGCAAAATCCAAGTTTGTGCGCGACG

**SEQ ID 3706**

LRRVENQNALVGVNGVIAPVRQRRAADLGGGFFLDRRHRLDKSAHPTDKLITRNALHRVSDRLVGYGVGVRFVKETPKFAAGVAGVESRQFQOLVYGRFCPOYLERQKPPFLRVGVVGSGZL  
TAAACRFLRPRTPYRRFLPPPLOAGELGENRIAHOMIPFALSRASSNSSSDSPSPSIPTASASSASLCTLPDDGLTPYDAAKICTGGCSROYSFRCRLRGKSLSAT

**SEQ ID 3707**

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**SEQ ID 3708**

MGNAVFPPEFGLKWRGKKTAVWSTGTQKASGREFRTAYTTPQWRPFLSFEVLRTKASVNELEKLAGPFNARKGSFESFLYEDPADNAVTDQPVGNTVQGVARYQLVRSNKGGFIEPVSAY  
KERPAVKVGGTALAYGRDYTVTDKGLVFNFTQPPGRPTTWGGFYFRVRPSTSDTVDFENVGLSLMAAKKIEFTSVKL

**SEQ ID 3709**

TTGAATATGGGCAATGGCTTTGTAGCCGCTGCGCGTTTGGACCAAGGTGCTGCCGTGGAAGGAACAGGTGTAGGATTTTGAAGAAGCTTAGTTCCCAATATCCTGTTTAAAAAAGGGGAA  
GGTGGCTTAAAAAT

SEQ ID 3710

LNMGNGFVAVCRFDQGAAVEGTGVGFLKNLVPNILFKIRGRSPEN

**SEQ ID 3711**

ATGAAACCTGCTCCGCCGAAAAGACATATCCGGAAGGCAGATTACCTTGCCCTCTGTCGGTTACGGGACGAAACCGACACCGGTTTTTGGAACTGACGCACAACCTGGGATACGAAACGAT  
ACGACTTTGGGCACGCCTACGGACACATCGCGGTTGAAGTGGACGATGCCTACGAAGCCTCGCAACCGGTGAAGCGGCAGGGCGAAAACGTCGTCGCGGAGCCGGCTGATGAAACACGG  
CACAAACGTCATAGCCTTCGTAGAAGACCCGACGGATGCAAAATCGAGTTCGTTCAAAAGAAAAGCGGCGACGATTCGGTTGCCCTATGCGCAATACC

**SEQ ID 3712**

MKLLRRKDYPEGRFTLAFVGYGDETDSTVLELTHNWDTKRYDLGDAYGHLAVEVDDAYEACERVKROGGNVVREAGLMKHGTTVIAFVEDPDGCKIEFVQKSGDDSVAYANT

SEQ ID 3713

GTGGCAFTGGGTACTTCTGCTAATGCATCGAATTTTGGTAFTTCCCTTAGGGAAAAGCAGTGCTGCCAGTGGTACGAAAGGAATTGCAGTGGGGACATCTTCTCAGGCAACAAATTTTAATG  
CGGTGGCAATTTGGTACTGAAAGTAAGGCACAAAATAAA

SEQ ID 3714

VALGTSANASNFGISLGKSSAASGTKGIAVGTSSQATNLSAVAIGTESKAONK

**SEQ ID 3715**

AGAAGTCCTTTTCGGATTGTTCTTTAACCCATTGGGAAAACTAATTTTATTGACCTTATTGACCTTTTTTATAAATATAATTCAA

SEQ ID 3716

RTLFQFVL\*PIGKN\*FYHLICTFFINLIQ

SEQ ID 3717

ATGAGAGCGCGACAAAAGAACTGATTGGCCCTGCTGCACGGCGGGCAGAGTTTCAGATGGCGGATTTTGTACACCATTAAGCTTTTCGGGCGGGCGGGTCTCGGGCATAACGGCGCGGATA  
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TGGTG



**SEQ ID 3718**

MKAATSGRLIGLLHGGDEFPQADLYTITLSGGRVLRHTGADMFVVDWQAYCAHELVIKRGATRTAVGLEVDNSHTLQISAAPDYRLBGLQWAEALAGVLGDARVKIDRVFFDAGLAPVGVAV  
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 QAGDAFKVYPGCDKRRDCTDKFDNVHFRGPPFPIPSADTFV

**SEQ ID 3719**

ATCCGCTCCGAACGCGATTTCAGGGCGCGGATCGTCGAAGAGGCGGGTCGTGGCTTGGCACGCGGTACCATCATCATGCAATGGTCAAGGGCGCGGGTGTGTGATTGCGCGATGCTCCTGGTCCGCTCTACGCGGGCGGTCCGACTGCTCCCGAAGGGTTCGACCCGCGCCCTTACCTCAAGATTGGCATCTGCACCGCGATTGCGAGCGCTTATTGGGGTTCGTACACGAATTTTGCCGTGAACCGGAATCGCCGAGGCGGGCGACATTGCAGTATGGCGTTTCGGGCGGTTCGTTTTCGCACGGCGGCAATTGGCGGGCGGGCGCAAGGTTATTACACGCTACATCGGGCGGGCGGTGTGTGCGACGACATCGGCCAAGCGAACTTATCGGGCGCGGGTTCGGTTTTTACATTTTCAATT

**SEQ ID 3720**

MPSEETDLRARI2VEKARSWLGTPIYHHHAMVKGAGVDCAMLLVAVYGAVGLLPEGFDPDRPIYQPDWHLHRDCERYLGFVTPQFCRETESPQAGDLAVNRFGRSFSHGGLLAGGGKVIHSHYIIGRV  
VSDDIGQAEILIGRGVRFFTFPSF

**SEQ ID 3721**

ATGGAGAAAGCCGAACCCCTAATTCCTCCGTCATCTTTGACGCACTGTGCGACACGGCTGCCAAAGCCGCCAATATGCGGTTGCGGCGCGGCGTGATGATGACACATGCGCGATACCGTCCGCGAAA  
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ACTCGGGCAGTGCATTTCTTATCTTGGCCCCGGG

**SEQ ID 3722**

MESEETLILRHLDALCDTPAQAAAMRLRAGLMMHIADTVRENGWTFQQAEEHCGLTRPRINDLLNGKIDKPSLDALVNINAGLGQCISLSFAPA

**SEQ ID 3729**

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SEQ ID 3724

LAFSGNCRROSNEPPEKFNGFIFYICPDISKLYRF

SEQ ID 3725

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 CAGTATCTCTGTTTCAGGAGGAGTTTAAATGACTCGCGTTCCGAAATCCAACCTGCTGTTTTCGTTGGAACATCTGGTGGCAGTATATCGAGCTCGCGCAATATCAGGTTCTGATTCGGAAT  
 CGCGCAAAAACGAGGTTTTCGCCCTTCGCTC

**SEQ ID 3726**

SEQ ID 3726

MGKSSVTYSAEERILSLQVQRSSQGLTLPTVYGRTRVAGNLIIWYDGFVTIEHKAVTRGGKGGGGVKQVGISYTYEAAVMLALCEGEIQGVGRVWRDKKFPSPAQRLRLTMRGGDQPL  
WHLQQAQKHQGOALNYSSTAYLCSNPYELTKSAQIYQHNFEVITGKSGYSNGIPDANPREITVLDLLTNQRYGCGPPSONIGDTRYSNYCRAVGIFLSPATYEQGEAQRNITSELLBQTNAA  
VFSQGLRLKIPYGDGSHSGNGAVVYADNKAAYDLTDDDFIVSQAQDPVKAGRKTNADAFNQIQVEYLDLRDNDYNVAIAEAKDQANIEQYGLRPKDAVRMHGICDAKVAQKVAQQLLQRLAY  
VRNEYEFLKWKYCLLEPMDIVTLTDAGLGLNKTPVRITKEEDGGVLVSKAEDCPAGVYVTSYPTQPSGGSADYNVSPGMAHVPLVIFAPALQLTGGEQPIWLTATAGGMWGGAEVWY  
SADGDSYTRVGA VNRKARFAGLADLPDGA VFFORTNTLTVGEISAGQLTGGTEQDSRDLLTLCYVDGEFLAYADAEKLGKVGRYTLGNLIRGAYGSAVNAHAAGSRFARIDEALFYKVA VPRNW  
IGTRVWVKLVSYNVFPGGIIQDLAEVPAYSYTTIEGAPLQIQNLRLTSSWAYGKEAVIANDKLDGADTDVYEIYAGCGSRRRLRADVGIVDINSYTTQADMKAQGVIRGIVFKVRGAVTIG  
TGWAAQIAAQNPOQLAQGISIDSJGRQAFPTQKPDDEAFAGIIVWCVCEACPAADNKA YDGAETPTIYAKCGGKPLEKGTGIVLTAAGYDSFGQDNLKI SSGISFTFVYDVASLTASE  
SSLNKLNDKLNILDNGAGSVNREVAEVRDGAAGAAAVDTARSINGLEAQYTVKPDVANKVAGFGLATTPKNGTPESKFTVNADRFGIGAAGKADVTPFVVDTRNRVNGINGELVWG  
KAVVDKLNAGDIHGKKIADLTDLANRLKAGSVTARETGAAAVTADKIGANAVTADKIQVADLSAVSSNLGSIPTGGSNLNIGGHNFTVSSDGIITADNAVIGRIEADSGYFNGTVRASSVGG



DVILRAHRLRLFTFEGNVVWLDLKDPLPRVLPLPIFYVSETFGNNRVRQAKLLINGGVLAPREVRETEYNTNYIWRGRFTGRFYEDLPFRARGGGDYTBQSGSRYRTRLEYQIQVIPAGKPVSLK  
LSLASHESVFSPPFVSYSYLAQSDYEYKQLGRMVNRTFAESFRYDSKQIYLGDDRVRVDYQNMVYKHNAYGGLQLPDDIYGISFEYRPTNADWSTMLAFDRSDKFPVVVKYRGHAPQ  
QYSLFOREFNTAVPKSNLLFFVEHWWQYIELNRIVLIPESRENEVWPSV

**SEQ ID 372**

TTGGCGCGCGCGGTATCAGGTATTTCGCAATAGGCAACCGAATCGTCGCCGCTTTCTTTTGAAACGAACTCGATTTTGCAATCCGTCGGGGTCTCTACGAAGGCTATCAGGTTGTGCCGTGT  
TTCATCGGCGCGGCTTCGCGGAGCAGCTTTCCGCCCTCGCGCTTCACGCGTTCGCAGGCTTCGTAGGCAATCGTCCACTTCAACCGCGATGTGTCCGTAGGCGTCGCCCAAGTCGTATCGTT  
TCGTATCCCAAGTTGTGCGTCAGTTCCAAACCGTCTGCTCGGTTTCGTCGCCGTAACCGACGAAGGCAAGGGTAAATCTCCCTTCGGGATAGTCTTTTCGGCGGACAGTTTCATACCCAA  
AACGTTTTGGTAGGAATCGAGGGATTTTTTCGAGATTGCCACGCGGAGCTA

**SEQ ID 3728**

LAAVSGSIRIGNRIVAFLNLNEDFASVGVFYEGYHGCAVFHQAGFADDVSALFLHAFAGFVGIVHFNRDVSVGVAQVVSFRIPVVRQFQNRVAUGFVAVTDEGKGKSAFGIVFSABQFHTQ  
 NVLVGIEGFFETIAHAEL

**SEQ ID 3729**

CATCGCTTCCAAATTTCGCAAACTGGTATCCAGCTCTTTACAGCCCTGTTTGCCGAAGTTGATGGTCAGTCGGCGGGATTTCGCTTTTGTCGCGGCATCGAATAATCAGCCGGTGCCGAAT  
 TTGCGCGTACGGAGCTTTTGTCCGATGCGGAAGCCGCTGCGTAGGTTTTCGCGCTGTTTGAAGTCATCGATGATTTTGTCCCGCTGTACCGTGGTTTGGCGCGCTGTGCGCGTAGCTGTGCGAAG  
 CGGGTTTTTTGACGGAACAGGTAGTGCAATACTTCTGCGCGGAATTTCTTCGACGAAGCCGGATGCGATGCCGAATTTGGGTTTGTCCGTGACGATGCGGTGCTGTGCCATGGTGATGTAGAG  
 GCGTTTTCGCGGCGCGCGGTGATGGCAGCTACATGAGGCGCGCTTCTTCTTCGAGGCCCGCGCGCTCGGCAAGGCTCATTTTCGCTGGGGAACCGCCCTTTCCATACCGGTGAGGAAGAGCG  
 GCGTTGAATTCCAAGCCTTTGTCGCGCGGTGAGCGGTCATCAGTTGGACGGCTTTTTCGCTGCCCTCTGTTGTTTTCGCGCGATTGAGGCGGGCTGTCTCAAGAAGGCGAGGATGGGGA  
 AGGCGGGATCGGTGCGAATATGTTTTCGCGCGAGGTTTTCAGAGTTGCTGTCTTCGCGTTTGAACATCGATGCGCGCGCTGTGACGAGTTCGTCAGAGGTGTGTCGAGGCGGCTTGTGTTGTCTGCCTTT  
 TTGGGTTTCGCTAGTGTCTGCGTCAGACCGCTGTCTTTGAGGATGCCAGCATGATTTCCGACAGTGCATTTGTCCGACTTGGTTGCGCAGGGCTTCAATCAGCGGACGGAAGGCGACGACT  
 TTGCGCGCTTTCGCGCGCGGCTTGCAGGCTGCCGCGCAGAGGGTGATGCTTGTTCGTTTGAAGCCGCTCTGAAGGTTTTCGACGGTGCGCGCGCGCATGCCGCGGTGGGAAGTTGATGA  
 CACGCAAGAGGGCGTTGTCTGCTGTCGGGATTGACGCGCAGGCGCAGGTAGCGCAGGGCGTGTGTTGATTTCTTTGCGGTTCGTAAGAAGCGCAGGCCCGCGTAGATTTTGTAGGGGATGCCGCT  
 GCGGAACAGCGCTTTGTTTCGATGACGCGCGATTTGGCGTTGCTGCGGTAGAGGACGCGCATTTCTGTCCAAATCCAGCCCTTCGCGTTTCGAGGGCTTTGGTTTCATCCAGCATGAACCGGGCT  
 TCTTCGAGTTCGGTAAGGCGGAGTAGTAGCGGATTTTGTGCGCTGCTTCGCGCTCGGTGCGCAGGTTTTCGCGAGAGCTTCGCTGTTGTTTTCGATAACGGCTTTGGCGCGCGAGGA  
 GTTTCGCGCAGCGAGCGGTAGTTTGTTCGAGTTTGAACGGCGCGGTGATGTGGAATTTCTTCATCAGTGCCTGATGTTGCCAGATTTTTCGCGCGGGAAGCGGTAATGCTTTGTGCTGTC  
 GTCCGCCAGCGAATAACCGCTGGCTTACCGCCGCCCATGAGTTTGAAGCCAGGCGTATTGCACTTTGTTGGTGTCTTGAACCTCGTCAGCCAGAATGTGGTTGAAGCGGTTTTGGTAGTGC  
 CGGCGCAGGATTTCTGTTACTTTTGCAGCATTTTCGTAGCTGCGGAGCATGAGTTTCGGCGAAATCGACCAACGCCCTTCGCGTTTGGCAGATTTTGTGTAATTCGCGGTAGACCAATCATGCGC  
 TTGTGTGCGGATCGGCGCGCCCAAGACGGAAGCGCGCAACCCGATTTCTTTTTCGCGGTGATGAAGCCCTTCGACGGAACCGCGCGCATGATTTCTTCGCGCATGTGAGGCTTTTGTAG  
 CAGGCGTTTGTATGAGGGGAAGCTGTGTCGCGCTGTCGAGGATTTGAAGAAGACGCGCAGGCCCTGCGTCGCGGTGTCAGGCGCAAAAAGCGGTGGCACAACCCGTGGAACTGCCGAG  
 CACATAGCGCGGAGCTTGATGGGAACTATTGCGCCGAGTCGGGTTTGCACTCTTTTGGCGGCCCTGTGTGTTAAACCTTACCGCCATATGCTGTGTCAGCTGTCGCTTTGTCCAAAG  
 CCGATCGGATACGCTGTGTCAGCAACGCGCTTTTTCGCGCTGCCCTGCCCTGCCAAAACGAGGGCGGATTTCGCGCGGCGAGTTTACGCGGAGAGTTGTGTTTCGCGGTTCAAGCTTCGACGAG  
 ATTTGGGGCGGATTTGGTGGGAACAT

**SEQ ID 3730**

HRFPRLKILQLFHALFAEVDGQSGGFVFCGIDNHAGAEEFGVTDVLSDAEACVGLRLFEVIDDFVPLYGGLARVAVAVEGGFFDQGVVQYFWRDFDEAGCDAELGLSVQHALLCHGDVE  
 AFAGAGDGDVHEAAFPEAAALGKAHFAGETPLFHTGEEDGVFEQAFGGVDGHQLDGFACPLVFAFEGGVAQEGEGEGGIV\*NVFGQGFKVAVGFELDGGGVDFVKVVEAVLVVAF  
 LGSVVLGQTAVFEDADDDPFGVHLSDLVAQGFNAQDEBGDDFGFRAGVAGCLPBGDALFV\*GRCLKVFDGARADAARWEVDTDQEGVVVGVLDGEAQVGVGEGVDFDLFAVFKAAQAAVDFVGDAA  
 AEQALFDDARLGVAAVEDGDFVQIPAPAFAPFGFGFIHDEPGFFFEVGKGGVVADFVACFPGVGAQVFAETFVVVFDNGVGGGEDVADGAVVLEFEDGRVDDVEFFHQCGHADVCAAEAVNALV  
 VADGKYRCVTARHEFEPGVLFQVGVKLVDQNVVEAVLVVPAQDFVTLQHFVAAEHFEGBEIDHAPALADFVVFVAPNHAACVRI GRAQDGSQAQTGF LRVDKALQTRRRDDFFGDVEAFB  
 QAFDEGLKVAIVEDLKGRRQACVAVVQAQKAVATVERAREPHSADVDGNHCAESGLHLFGVLGVGRYRHNAYVAGLSALQKPCDTRGGQHARFAAACACQNEGGLRFPYGGGELFGVQALQQ  
 IGGGLVGKH

**SEQ ID 3731**

ATGATATATCATATATGAAAAATATATAGGCACTATTTCCTCATGGCTCGAAAAGCGGATTCGGGAAGTCAGTACAAATTAATATATCGACGATTATCCCTCTTCOOCTAACAGGGATTAAAAA  
CTTATATTACTTTTAGGGTTAAGCAACATGATCTGAATTATAAAAGCAGATTGAAATACTTTTGTGATGTCTTTAAAATATGATGAAAATCAGATTTTCCCAITTTTAAAGATGGTATGC  
AGAAACCAATCATTTAGAGATAAAAAATCTCTCTCGGGGGCAGGTGTTTATTTCCTAGAGACATGTTAATTCACAAAAATGGATGCACTGTATTTTCCGCCCACTTTTATTTCGAC  
GATGATTTCCAAGTCTGTTATGGCGAACACTACAAATATTGTTTCCCTTTGCTGCTCCCTCTGTATTAACCAAGCCGAATTTGGTGAAAAAAGGTTTGGAAATCTTTTGACGAGTTCT  
TGCTGGATAATGAAGTTGGCAACCTTTTCGGATATGAATCGGGAAACCGTTTACTCTGG

SEQ ID 3732

SEQID 3752  
 MINHIKRYITGISHGSKSDSGSQYKLNIAAPSSPNRDLKTYITLGLSKHDLNYSKRFELLVCSLYDENQIPFPLRLWLAFTIIEKKILLRGQVVYLPRSTVNSTKMDALVVSAPPYFD  
 DDPOVCYGHEHYNIIVPLPLVPLYKOEAEILVEKKGNWAFEOFLLDNEVGNLSDMRKPFTW

SEQ ID 3733

SEQ ID 3733

ATGATTGAAGATAAAAAAGATTGTTGCCTTGAATTTTCAGTCGAGGACGGTATGACCGGCGCGAGTGGCGCCTACCACTGTCGAAACATATCGGCGCGGATTACCGCAACGGTTATGTGTA  
CGGCGACGTTGAACCGCTATGTGTCGGAATAATGCGTTTAAATCGGGCAACGCTACTCTGTTGGCGCGCATTTGGATTTTTCAGGAACCGGACATAACCGCGCCGACCCCGGTTGGGTGTA  
CGCGAAGCGCTTGGAAAGGTGCGGCGGGCATCCCCAAAGACGGCGCAACCGGTTTACCGGGAA

SEQ ID 3734

SEQ ID 3734  
MTEDKKTIVALNEAVEDGNTGASAAVHVVEHTGADYRNGYVTATLNGYVSENAPKSGKEYLLARTLDFQETDITAPDPGVYRKALEGAAGIPKDAOPVYAE

SEQ ID 3735

GTGACGGGTATGTTTGAGGTTTGTGACGGAAACGGCGGTTTTTGCCCGCGGGTTTCAGCGCTGTGTTTCGGCACGGCGACGCGGGTGCTGGAGGCGGTCACTCGGTTTGGGCTTGTGCGGTTACGCGCGCTGTTTCGCGCTTGCGCCCGACAGAGATTACGCGTGGCGGATTATTATCAAAATTCACGAGATATTCGCGAGGCGTGGACGCGTGGGGGTGCTGGCGCGCGCGGGGCTGCTTTCAGACGGCATGCTGTGTTTGC CGGGGCGTGAGGGCTGTGTGGCTTCGGCGTACCTGCTTTTGTGTTTCGGGCTTTGTGTGGTTTGTGTTTCGGTGGCGTTTGGGGGGCGTACCGGCTTTGAACACGGGTTATGGTCTTCGCGCGCTGTGGCGGTTTTTTCGCGCGCTGGCGGGGAATAATGCGTGTAGGTTTGTGTTTCGCGCGCAAAASTCGCGGGGTTTGGCGGATGAGGGTTCG

SEQ ID 3736

VTGMLRFLTERRFLPAGFQAWLPGTATRVLEAVIGLGLSGYAAVFPALAPDEIYANRIYYKQDIPAEAWTVGVLLAAGLLQTALLFARGVVRACVASAYILLFSGFVFWLVSVAFWGAYPPLN  
TGMVVVPLLAFCCALAGNNALRFLFSSAOKSRGLADEGS

SEQ ID 3737

SEQ ID 3737

ATGGGGTTTTCGAGTTCGGACTGCTGTTTCCCGCGGCGCGCGGCTGCTGGCGCGGTTGTGGGCAAGCCTTCAGGAACGCGCGCGCCCGGTGCAAGGCTGTGTGCGAGGCTTTTATTTCG  
CAATCCGCGCGCGCGCGCGCGGAGCGGCTGCTGCGCGCTGGATCAGCGCTGGACGTGCGCGCGCGCGGGGTGTTCGCGGGGATGATGACGGGACACGCGCTCGATACGCTGCGCGGCT  
CGCGCGAAAGCTTTTCGCTGTACTTCCGCGGCTTGGCGGAAAGCTTACCGGTGTGAAAGACGGAGGGTCTTCGGATGGAAGAAAT

SEQ ID 3738

SEQ ID 3738  
MGFIQEGLLFAAAGGVI GAVWASIQERGRPVOAVLEAFISAIAAAAAAERFVPLDOAWTCAAAGVFAGMMTGHALDTVRALAPKVLRGYLGGLAEKLTGVKDGSSDGKD



**SEQ ID 3739**

EQ ID 3739

ATGTGCTGCGTCAGCGCGGACGCTGCCCGGAACACAGCGTCTTCAGCGCCCGCCGATACCGCTCGAAATCAATCTTTTTCATCCGAAGACCCCTCCGCTTTTACACCCGTAAGCTTTTTCGCGC  
AAGCGCCCAAGTAACCGCGCAACACCTTTGGGCGGAGCGCGCACCGGTATCGAGCGCGTGCCCGCTCATCATCCCGGAACACCCCGCGCGCGCACGCTCCAGCGCTGATCCAGCG  
GCACGAACCGCTCCGCGCGCGCGCGCGCGCGCTGTCAGAAATAAAAGCTTCCAGCACAGCTTGCACCGGGCGCGCGGTTCCTGAAGGCTTGCCCAACACCGCGCCAGCACGCGCGCGCG  
CGCGCAACACGAGCTCGGAACCTGCAAAAACCCATTTCAGACCCCTCATCCGCAAAACCCCGCACTTTTTCGCGCGAAACAAAAACCTCAACGCAATTATTCGCCGCGAGCGCGCAGAAA  
AACGCCCAACAGCGCGGACGACATTCAGACCCCTGTTCAAAGGCGGGTACGCCCGCAAAACGCCACCGAAACCAAAACACACAAAGCCCGGAAACCAAAGCAGGTAGGCGCGAAGCCACAC  
AAGCGCTACGCGCGCGCGCAACAGCAATGCGCTCTGAAGCAGCGCGCGCGCGCACGCGCGCGTCCAGCGCTCCGGAATATCTCGGAATTTGTAATAAATCGGCCACGCGTAAAT  
TCTGTCGGGCGCAAGCGCGAAACCGCGCGGTAAACCGACAAGCCCAAAACCGATGACCGCGCTCCAGCACCGCGCTCGCGGTGCCGAACACCGCTGAAACCCGCGCGGCAAAACCGC  
CGTTCCGTCAAAACCTCAACATACCCGTACACACCCCGCGCAAAACCGCGAAGCGGAAGCCCGCAGTGTCCGACGCGCTC

**SEQ ID 3740**

SEQ ID 3740  
 MSCVSRTPGQRLHAPRYRSKSIFSIRRPVSFHTKILFRQAAQVTAQHLGRERAHRIERVPRHHPREHPRRARPRLIQRHEPLRRGRRDCRNKSLQHS LHRAAFLKACPHRAQHAAG  
 RGKQQSEIQKPHSPRLIRQTPRLLRKQKQPRILIPQRAEKRQQRNDHTVRQVRVPPKRRHRNKQPKHARKQKQVGRSETSPHAPRKQKQRLKQPRRRQHPHRPLENILEFVINPPRVN  
 LVGKRKRHRVTRAQATDDRLQHPRRRAEQPRLKPGGQKPPFRQKQHTHTTPPGKTPRSRSPAVSDAV

**SEQ ID 3741**

SEQ ID 3741

GTGCGCCGCGCCCTTTGACGGCGTTGATTTGGAAGCCGCGCGGATATTTTGAATGCTTTTGAATAGGGCGGGGTATGGAACCGGATGCTTCCCCCTGCGGACAGGCTTCGCACTCTGAAGTCA  
GTCGAACAGTACTGCGCGGATGCGTGCCAACTGCTTCAATCAGCTAATCGGGACGGTTTCGCGGAAGCGCGCGCGGATTTTCCAATCCAATGCCCTTACCCGGTGGCAGTGGACA  
TTGCTTTGTGTGCGCTTCGCCGTCCGCGGACGATGTGTGGAATCATACCGCCGCTTCTTGCCGCCGCCGCCCTGCCCTTGTAATCGGGCAGGCGTAAACCAAGCCGGTTGCGCGGTTGTAAAG  
CTCTGGCGGACAGCGGCTATGGCGCTAATGGCCGCCCTTTCATTTCGTACCGCGCGCGGGTTCGAAGGCAAGATGGAATAATGTCGCCCTCGCTCGGGAAATATACATCAAAAGCCCTCTGTCTCG  
ACATCGGGCATTTTCTTCCAGCCTTCCGCGCGCGCGGGCGGCTTCGGTTTCGCAAAAGGTCGGAAGCGGATAGCGTTTACAGGGGCGGATGAGCAGCTCGCCGTTGCGGATTTTCG  
TTTCCAGCGCTCGCCGATTTTGGCGTTGAGGGCGGTACGAGGCGGGCGGCGAGCAGGACTGCCGCGCTGTGTGCCCATTTTTCAGTCGCAACATGGTTTTCCTTTCGTGTG

**SEQ ID 3742**

**SEQ ID 3742**

VRRAFDGVDL EAGGYFECFEI GAGMETDAS PCGQASHSEVSR T VLRRCVP IRLQSRNRGRFRGRRRGGFSNMPSSGGSGHCLVLPPFCRAVWKSYRRFLPPPCLVKSGRRKPSRLRGCK  
LWATGLWRNGRLSPFYRRRRGRRODGKRIAREYTSNALLSDIGHFFPAPFRARRGGFRFCQKVQGAVAFDGADEQLAVADFCFORVADFGEVGEGQEAGQTDCRAVAPFLQSQHGFAPVL

**SEQ ID 3743**

SEQ ID 3743  
TTGATGTATATTCCCGAGCGAGGCGACATTTTCCATCTTGCCCTTCGACCCCGCCGCGGTACGGAAATGAAAGGCGGCCATTACGCCATAGCCCTGTGCGCCAGAGCTTACAACCGCGCAA  
CCGGCTTGGTTTACGCCGTGCCCGATTTCACAAGCGAGGCGCGCGCGGAAGAAGCGCGGTATGATTTCCACACTGCTCGGCACGGGAACGGCAACACAAGCGCAATGTCCACTGCCACCG  
GATGAAGGCATTGGATTGGAAAAATCCCGCGCGCGCCTTCCGCGAAACCGTCCCGGATTACGTGATTGAAGACGTATTGCGACGCATCGCGCGAGTACTGTTCGAC

**SEQ ID 3744**

SEQ ID 3744  
 IMVTPERGDIPLAFDPAAGTEMKGGHYAIALSPRAYNRATGLVYACPISQGRAAAARSGGHIISTLLGTGTATQGNVHCHERMKALDWKIRRAAFRETVPDYVIEDVLARIGAVLFD

**SEQ ID 3745**

SEQ ID 3745  
ATGTTGGCACTGCAAAAATGGGGCAACAGCGCGCACTCCGTCGCCCCCGCCCTCCTGACCGCCCTCAACGCCAAAATCGGCGACCGCTGGAAACAGAAAATCGCAACGGCGAGCTGC  
TCATCCGCCCCGTCAAAACGCTACCGCCTGTGCGACCTTTTGGCAGAAACGGAAGCCGCCCGCCCGCGCGGAAGGCTGGGAAGAAATGCCCGATGTGCGACAGGAGGGCGTT

SEQ ID 3746

SEQ ID 3746  
 MLRLKQWNSAAVRLPARLLTALNAKIGDALEIRNGELLIRPVKRYRLSLLAETEAAPPRAEGWEHMPDVGQEGV

SEQ ID 3747

SEQ ID 3747  
TTGGATAATAAAGTGGGTCGGATAGTCGGCAAACGTAGTCGGTTTGAACACGCTTTTACTTTTCAGACGGACTTTCTACCAATGGGAACAAGCGCTTTTCTCTCAATCGGTTTA

SEQ ID 3748

SEQ ID 3748  
LDNKVGRIVGKRSPFETLLLFRRTFYQWEQGVLSQSL

SEQ ID 3749

SEQ ID 3749

ATGGACAACGAATTGTGGATTATCTCTGCTGCCGATTATCCTTTTGGCCCGTCTTCTTCAGATGGCGTGTTGCCGCCCGCGTGGATATGAAAAACGATTTGAAGCAGGCAAAAAGCATCC  
CTTCGGGATTTTATAAAGCCTGGAGCCTTTTGGTCGACGGCAACAGCGGGCGCGCGCAAGGGAGTTGGCGGAAGTCGTCGACGGCCGGCGCAATCGTATGATTTGAACCTTACCCCTCGG  
CAAACTTTACCGTCAGCGCGCGGCAAAACGACAAGCCATCAACATACACCGGACAATGCTCGATTCTCCGATACGGTCGCGGAAAGCGCGCGCGCTCTGTTGAATTTGGCGCAAAAC  
TACCAAGCGCGGGTTTGGTCGATCGTGCCGACAGATTTTTTTGGGGCTGCAAGACCGGTGAAATGGCGCGGTGAAGCCAGCAGCAGCACCTGCTCAATATCTACCAGCAGGACAGGGATTGGG  
AAAAAGCGGTTGAAACCGCCCAACTTCTTAGTCACGACGAACAGACATATGACATTTAGAGATTGCAAGTTTATTTCGGAACCTTGCCCAAGCGCGCTGTTCAGTCCAAATTTTCGATGCCGC  
GCGTTTCAATGTGCGCAAGGCATCGAAGCCCAAAAAAATGACCCCGCGCAACATGATTTTTGGGCGACATTGAACACCGACAAGGCAATTTCCCTGCCGCCGTGGAAGCCTATGCCCGC  
ATCGAGCAGCAAAACATGCATATCTTAGCATGTGTGCGGAGAACTTTACGAAGCCTATGCCGCGCAGGGAACCTGAAGAAGGCTTGAACCGCTGACAGGATATATGCAGAGCTTTC  
CCGAACCTTGACCTGATCAATGCTGCTGTACAGAAATCCCTGCTGCTTAAGGGCGAGAAGAAGCCGCGCAAAACCGCGCTCGAGCTTGTCCGCCGCAAGCCGACCTTAACGGCGTGTACCG  
CTGCTCGGTTTGAAACTCAGCGATTTGGATCCGGCTTGGAAAGCCGATGCCGACATGATGCGTTCGGTTATCGGACGGCAGCTCCAGCGCAGCGTGATGTACCGTTGCCGCACTGCCAC  
TTCAATCCCAAGTCTTTTCTGGCACTGTCCCGCTGCAACAAATGGCAGACGTTTACGCCGAATAAAATCGAAGTT

SEQ ID 3750

SEQ ID 3750  
MNDRLWILLPPIILLPVFFTMGWFAARVDNMTVLKQAKSTPSGFIYKSLDALVDNRNNGRAARELAEBVDGRPQSYDNLTLGLKYRQRGENDKAINIHRTHLSDPTVGEKRAVLVFEQAQ  
YQSAGLVDRABQIFLGLQDGEHAREARQHLLNTYQDRDWEKAVETAQLLSHDEQTYQFETAQFYCLAQAALPKFSNFDAARFNVGKALEANKKCTRANMILGDI EHRQGNFPAABEAYAA  
IEQQNHAYLSMVGKELYEAYAAQKPKPEGINRLTGYMOTFFELDLINVVYKSLLSLKGEEAAQTAVELVRRKPDNLGVYRILGLKLSLDLPWAKADAMRVSIGRLQRSVMYRCNRCH  
PKSOVFFWHCPACNKNWOTFTPNKIEV

SEQ ID 3751

SEQ ID 3751  
ATGAAGAAGATTGAAATGGATTGAAGAAGCCCGTAAATACCTTGGCGCTCAGCAAAAAGTGAATGGCAAGTCAAAACCTGTGCTTTTAGCGATGCTGCAAGAAATGGGAAATTTTAAATCAGG  
AGCAGAAAGCGTGTTGGAAAGAAACAGATACGCCGTGGTGGCGGCTGTTTTCGCGATCTGCTTGGGCAAAAGCGGACGCGCGGTATCAGGGACTGGTATCGCGCCAAAGCCTGGTCAAT  
GTCGGGTTTGACGAAACTCGAAGCCCCCGCATACGGCTGCATCGCGGTCAAACCGCGCGGGCGCGGACACGTGTTCTTCGTGTGTCGGCAAGACGCGGAAGGCAGAACTCTTGGGCTTG  
GGCGGCAATCAGGCAATATGGTATCCATCATCCCGTTTGACCCCTCGGCACATTGACGGCTACTTCTGGCGCTCCAAGCTGATTGGCGGCAAAAGCCGTGCCTTCTGTCGCCCGCGCAAGGGC  
GTTACCGGTTTTCGGACGTTGCGCGCCACGGCGAAACAGGGCGCGGGCGAGGCG

**SEQ ID 3752**

SEQ ID 3752  
MKELKWIIEARKYLGAHEKVNKSNPVLAMHLEMGNFNQEQKAMWKEITPWCGLFVG YCLGKSGRAVIRDWYRAKAWMSGLTKLEAPAYGCIADVPRRGGGHVPFVVGKDAECRILGL  
GGNCGNMVSIIPDPADIDGYFWPSKLIGKAVPSSPAEGRYRLSDVAATAKQGAGEA

SEQ ID 3753

SEQ ID 3753  
ATGATTGGGGCTTTGCTGAAAAATGGAAGCCGCTGCTTATTTTGTGCGCAATCGCGTTCTTCGCCGTTTCTTGGCAGCTGGACAGGGCGGCGCAATACCGTCCGGATACGGTGCGCGG  
TGTGGAGGTTTTCGAACGCCCTCAAAGCCGCCGCGGTGAACACGCGCGAACACGCCCGCAAATCGTCCGCCGCTATCAGCGCGCAAAAGCGCGCGCGAGGAAAAAGAAAGGTCGCGTA  
TGTGCAACCGCTTAAANTCATTGAAAAACCTGTGTACCGCAATGCTGTTTGTGATGCTGACGGCGTGCGCGAATCAACGCCCGCGTGTGACGACGCGGCT

## SEQ ID 3754

MIGALLKWKPLLLLSAIAFFAVSNQLDRAAQYRRGYGAASEVSESLKAAAVEHAZHARKSSAAYQAQKAAREKERVRYVQTLKIIEKPVYRNACFDADGVRELNAAVDDGG

## SEQ ID 3755

TTGGCGGCCCATCGGGGAAGTGTGCGCATTCGCCCGGATTTTTACATATCGGGCGGACGCGCAAAATTTTCCCGTTTGTGTTCGCGAAGGGGGCGTTATACAAAATTATCAGCGC  
ACCAA

## SEQ ID 3756

LAAASGEVSAPFPPIFYISGRGKPLPFCLREGGVIQNYQAHQ

## SEQ ID 3757

TTGGTGCCTGATAATTTTGTATAACGCCCTTCGCGCAACAAAACGGCAAAATTTGCCGCTCGCGCCGATATGTAAAAATCGGGGGGAATGCGACACTTCCCCGATGCGGCC  
GCCAACCCGGAACCGACGTTTCGGTTGCAAACTTCCGGTTGACAACTCAATCCGCGCCCAACGCCGTACCGCGCGCCGTGCGCGCCCTGCACTGTTATACATACCGGCCGCTTCAG  
GGCCACCGGACGACGTCGCGCCCGCTGTTCCCTTCAAGGTGCGGCGATTTCGGGCGAGGCGCCGACCAATCGCGCGCGGCTTAACCGCGCTGCTCAACCGCGCGGTTGAGTTCCGCAC  
GCGGTGAGCATCAAAACAGGCATTCGGGTACACAGGTTTTCATGATTTTAAGCGTTTGCACATAGCGCACTTTCCTTTTCCCTCGCGCGCCGCTTTTGGCGCTGATACGCGCGCGAC  
GATTTGCGGGCGTGTTCGCGCTGTTTCGACCGCGCGGCTTTGAGGCGTTCCGAAACCTCCGACACCGCGCACCGTATCCGCGACGGTATTCGCGCGCCCTGTCCAGCTGCCAAGAAACGG  
CGAAGAACCGGATTCGCGCAAAATAAGCAGCGGCTTCCAAATTTTCAGCAAAAGCCCAATCATTTACGCGCTCGCGCGCCCTGTTCGCGCGTGGCGGCAACGTCGCGCAACCGGTAAGC  
CCCTTCGCGCGGGGACGAAGGCACGGCTTTCGCCCAATCAGCTTGGACGGCCAGAAGTAGCGCTCAATGTCGCGAGGGTCAAAACGGGATGATGATACCATATTCGCCCTGATTCGCCGCC  
AAGCCCAAGATTCGCTTCGCCGCTTTCGCCGACACGAAGAACAGTGTCCGCCGCCCGCGCGGTTTGACCGCGATGCAGCCGATGCGGGGCTTCGAGTTTCGTCAACCCGACACA  
T

## SEQ ID 3758

LVRLLILYNAPFAQTKRQKFAASARYVKNRGECHRFPRCGRQPGTDSVANFRLTTSAPNARTSAPCRALQSLYIPAAFRAGHSTSAFVFPSCRCSFGGRTKSAGGLTAVVNGGVEFAH  
AVSIKTLAVHRFPNDFKRLHIAHPFFLARRLLRLIRGGRFAGVFGVDRGGFEAFRLNHRRTVSATVLRFPVQLPRNGEERDCQGNQRLPIFQSPNHLRLARALPRGGNVQRVPT  
PFGGRRRHGFAANQLGRPEVAVNVNRVRKRDGYHIALIAQAQDSAFRVADNEHVSAAPARFDRDAAVCGGFEFRQTRH

## SEQ ID 3759

ATGCCGTCCGAAAGCCTTTCAGAGTGCAGAGCCTGCCCGCAGGCTGCGGCATCGGTTGTTCGCGATCGGTACGGCATTTTCATTCCGCCCATTTATTTGGTGCCTGATAATTTTGTA

## SEQ ID 3760

MPSESLSECEACPQGAASVVVRIGTAFSPFPIIGAPDNFV

## SEQ ID 3761

ATGAACGCCGAGGATTTTGTGAAAAACAACCCGCTGCCGCCGACGGGCGCGAAATCGGGCGATCGTCCCGATTGAAGGCTTTGAATTTGCCGAACAGGAATTGGCGAATTATC  
GGGAAATGTTGAACGTTATGCCGTC

## SEQ ID 3762

MNAEGFCEKQFACRPDGRNRAGDRADLKAPEFABQELANYREMLKRYAV

## SEQ ID 3763

ATGAGCGATTTTGAAGCCAAAGTCAGGATAACGCTAGAAAAACATACGAAGCAGGGTTTGTATTGCGCCGCCCGGATGCTGATAAGCGCGCGGAAAAGATGCGCAGCAGCGCGGATAATG  
CCGCAAAAGGCGTTTAAAGCTGCAATCGACAGTATGACAGAGACCATGCGCAATTTGCAACCGCGATGTGAAGCGCGGATTTGAAGCGCGCGCAATGAGCGCAACAGGCGCTCGAAAAGGT  
TAGGGCCGAAGTGGTAAAAATCGGCTCAGGCTTATCGGGCTGACCAAACTGCTGGCAGGATTAGCAACCGCAGACTTCGCAAAATCGGTCCTTGATACCGCGCGATGCGATGACGTCGATA  
AACAGCCCAAGTCCGACAACTACGTCGCTCGTGAACCGGAGTATCTGGCGCGTGCAGCAGCAGCTTTCGATACGCGCAACCGTACCGCGTATGACCATCGCGCGCTTGGCGCGCAACACAGCGCCCGCGCT  
CCACAAGCCGCGCTTGAAGAGTACGCTACACGACGAGGAAATTTAAATTTACCGAGCGCGCAACACCGGATGACCATCGCGCGCTTGGCGCGCAACACAGCGCCCGCGCT  
GATGCACTTATCGACGCTTTGGCAGCGCGCTATTGACGGCGGATGAATTTAAATCCATTTCGGAAGCGCACCTATTTCGCTGGATACCATTCGCGAATATATGGGCAAAATCCCGCGAC  
GAAATCAAAAGCTGGGCGAGCGAGGGAATTTGACGGCGGATGTGATTTTCAAGCCATTTCGCGCGCTCGGAGAAGTTTCGGGAGCAGCGCGCAAAATGCCCTGACGATGGGCGAG  
CTTTGACGGTGTCTCGAACAATCGGCAAGCATGTTTCAAACTGCTGAACGACAGCGCAACATTCGCGCGCTCGGAGAAGTTTCGGGAGCAGCGCGCAAAATGCCCTGACGATGGGCGAG  
GGCTGATTGCGAAATTCGCGGATGAATTCGCTGCGCGCGCTGACCGCACTGCTTGAATCTTGCACTGCTGGCAACCGCTTCGGGATTTATGCGCTGCAATCGGCGAGTGTGTC  
CCGTCAATCGTGTGTTGACGGGCTGACAGCGCGCTGAAAGAGGCGCGCGCGCTGCCGCTGTTGTTGCGCGCGTATGAGCGTCATCTCAAGCGCAATCGCGCGCTATGTAAGCT  
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ACGCGCGGCTTGGCGAGCGTATTCATGACAGCTTGACGAAGACCGCGCGCGCAATGGAAGTTCGCGCGCGGCAAGTTCGCGCGCGGCAAAATCGCGCTTCGCGCGCTCGGCGCGGCAAGACCGCATGACGCTTGGGAA  
CGGCGAGGACACCGCAAAACCGCGGAAAGCGCGCGCAATTCAGGCGCGCGGCAAGTTCGCGCGCTGAGGCGGAATTTGCGCGCTGAGGCGGAATTTGCGCGCGGCAAGCTTGGCAACGCTGAGC  
CCAACGCGCAAAACCGCGTGAATTCGCGGAAATTCCTGATGCTTGAAGACCAATTTATCGAAGCATCAACGAGCAAAATGAATCAGCGCGCGCAATGGGAGAAATTTGGAACAAGCA  
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ACGAGGCGCAACCGCAAAACCAACCGCGCAAGACCGCGCAACGCTCATGGAATGCTGCAAGACCGCGCGGCAAGCTTTTCAAGAGTGTGGGCAAACTTTATTCAGAAATGTTTACGAACTTTGACGGGCTTATGCGCGCATGCTT  
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CGGTTCTCAACAGCACCAACACGACGCGCATTCCTTCGCGCGGAGCGGCTGGGACATCCCGGAGGATCAACCGCTGACCAACTGCAAGCAAGACGAGATGCTTACCGCGAGAA  
CACGCCCAACCATCCGTGAATGGCGGATCAGCAGGAGGCGGAGCAGCGTCATCATCAATTCGACAGGAGCGGATTCATCCATAAAATGACTTGGCGAAGCTCTTGAAGCAGATGA  
AACCGGACTTTAAATTTGTC

## SEQ ID 3764

MSDLKAVRITVYENHTIKQFDSAAADAKAEKMRSSGDNAAGFKAAIDSMHETMRNLHADVKAGFEAGNQAQQAASEKVAEVRGKIGSGLSGLTKLLAGLATADFAKSVLTDADAMQSI  
NSQVRQVTSSETEYLAVDQQLLDLTANRTRASLESTANLYVSTSRALKDYGTYQQLKPTFAANNAMTIGGVGAQQAALMLQSLQALGSGVLQGEDEFKSI SEAPAILLDTIAEYMGKSRD  
EIKKLGESEKLTADVIPKAI SGASEKFGQAKNPVTMGQALTFSNNWQSMVSKLLNDSGTMGIAAVIKLIADNLNLVVPVAVGFAVAVAAVAPTALNALLANPFGIATVAIGTVV  
GLIAKFGDELDVFGGWSNLSDVIRAVVQIITETVGEAVGTVKSWFDGLTGRLEBAGGWNPSLPGRVMSVSSAIGAYVNVYINIPATGWMILKEAANDMPQFANLGRATGNVPIASIER  
MINKAVGMINSMIDPANKAASMAGISGIGKLNKVRMGRMDGGLGERIHDSLTKDRAGAMANAVERAADIHEADALKRGCGGGHAKTARKKPGANQGGGKGSRSRSGPGAARDPMQAWB  
GETKARKLAHREMQRETIAHQENDLAREAYWRAKLTAVDANGTGVIREKILNLEDQLSKQSTEAQMNQAAEWELDKHLEMEKDAADQALADGRISQLERLDELIEFENRRYRIAYD  
ALQERIALAEQDPAYSQAAITGKLAQMGEELGRGHERTQAKNEBKRENQRKDAPNVMEMLQDGGNRNVQEAQQQHQQAFTAMILARAQNFQAMNGFFKSNQGTQIQEMVTKPLTGLMRNV  
QESATYKMIPTKETLTAATAAKTATKATETTA VVSSNAVQAASGAASQAHIYVGPILAVAAAMMSAVMGLMGGGGGQTITTTTTRIPSAAGGWDIPAGINPLTQIHEHENVLPAB  
HAQTIREMADQGGGFTVIINSTGGDF IHKNDLAKLLKQMKRDFKPV

**SEQ ID 3765**

ATGCGCTATTTTAATAGAAACGGAAGGATGCTGACAACCTGATTTTGATTTCGGTTTGGCAAAGCCCTCGCCGACACACGCAACGCAAAACCTTGATAGGCGGATATCACATTGCGGCGT  
TCCAAACCGATTTTGGACGGACGCATCGACAGGATGCGGGCTGATTTGCCGAGCCTGACCATTGGTCAAGCTCGGAAGGCCCTTCCCCGTAAAGCGGGTATTGCAATAGGCTTTGATATCCG  
CCTATCGGTTGGGGAAATATTTCGGTTTGGCGCTGAACATAGGAATAACCGCTTTCAATTGCAAAACACCGAAATCGTACCGATTGTTACAGACACAGCCAAAAACAATGCCGCTG  
AAACCCGGATTGTCAGGCTTCAGACGGCATTTTTGTTCAGCGGGTTGCCGCTCCCTCCCGGAACATCTCCCGCCACAATTTC

**SEQ ID 3766**

MRYFNRRNGRMDNLILISVLAKPSPTHAKRTLIGGVHIAAFQTDLGGRIDMRADLPSTLTMVKLGKPLPRKGGIRIGFDIALSVGENTISVCRNLNIGITAPQFANNRNRRTDCSDTAKNKCRL  
 KPLSGFRHRHFLFRRLPLPRTLPTATIS

**SEQ ID 3767**

GTGCGAGAAAAGACTGTGGGATTTTGAAGTGGCAGTGTGCGGCAACGGTACATCAGCTGCGCTGGAGCTGCCGTCCGATAACCGAACGCATCATGTGCGGCATCGCTTTTCCAAGCCGGATCC  
AAATCGCTGAGTTTCAAACCGAGCAGCGGTACACGCCGTTAAGGTCCGGCTTTCGCGGGACAAGCTCGACGCCGTTTTCGCGGCTTCTTTTCGCGCTTAAAGCAGCAGGATTTCTCGT  
ACACGACATTTGATCAGGTCAAGTTCGGGAAACGCTCGCATATATCTGTGCAGACGGTTCAAGCCTCTTTCAGGTTTTCCTTCGCGGGCATAGGCTTTCTAAAGCTTTCTCGCGGACCAAGCT  
CAAGTATGCAAGGTTTGTCTGCTCGATGCGGCGCATAGGCTTCGACGCCGGCAGGGAAATTCCTTCGCGGTTTCAATGTGCGCCAAAATCATGTGTCGCGCGGGTGCAATTTTGTGTGGCT  
TCGAGTGCCTTTCGCGCATTTGAACGCGCGGCATCGAAATTTGGACTTTGAACAGCGCGGCTTTGGGCAAGTTTCGAATAAAACTGTGCAATCTCAAACATGATATGCTGTTCGTGACTAA  
GAGTTTGGCGGGTTTCAACCGCTTTTTCCTCAATCCCTGTCTCTGTGTAGATATTGAGCAGGTGCTGTCTGCGTTTCACGCCGCAATTTACCGCTTCGTCAGCCCCAAAAAATCTGTTCGGC  
ACGATCGACCAAAACCCGCGCTTTGGTAGTTTTCGCCCAATTCAAACAGGACGCGCGCGCTTTTCGCGGACCGCTATTCGCGGAGATTCGAGCATTTTCGCTGTGTGATGTGTTGTGCG  
TTTTTCGCGCGCTGACGGTAAAGTTTTCGCGAGGTTAAGGTTTCAATCATACGATTCGCGCGCGCGCTGACGAGTTCGCGCAATCTTCGCGCGCGCGCTGTGTGCGGCTGACCAAG  
CGTCCAGGCTTTTATAAATCCCGAAGGATGTTTTCGCTGCTTCAATACGCGTTTTCATATACGCGCGCGCGCAAAACAGCCCATCTGTGAAGAAGACGGGCAAAAGGATAATCGGCAG  
CAGGATATTCATATATCTGCTGTGATATCGCTTTCTTAAGCTGTTTGGCAGATTTCGCGAGCAATTTGTATTCGCGCGGTGCAGTCAATTTCTGTGCGCTCAAGCGCGCACTTTCTTCAC  
TTCGCGACGCGAGCGGCTGTTTTCGCGCGCAAGGACAGCAGCGCGCGCAACAGGGCAACATTCGGAACAGATCCGACGCAAAACGCGCGCAACATACGCAATCAGCGCGAGAT

SEQ ID 3768

VPEKDLGFPVAVAATVHHAALPSPDNRTHVHGIGFSPRIQLAEFQTEQAVHAVKVGLAADKLDGGLRGFFLALQKGQFLVHVIDQVKFGKRLHISCQTVQAFRFSRLRGIGFVKLLADHA  
 QVCMLVLLDGGIGFDGGRBIALSVFNVAQNHFVAGAPFVGFECLADIETRGIEIGLBQRLGKPAIKLNLKILCLFVVTKLGGFNRFPFIPVLVDIDIEVLGSGFTRHFTVLQPKNLFG  
 TIDQTRALVVLRFQKQDARALFADRIIGRIEHCPCVYVDGVVFAALTVKFAEGKVQIIEBLPAVDDFRLQPCRAPAVADQSVQAFIKSRDADFCLLQYGFHAGGKPAHREEDGQKDNRO  
 QDNPOFVVHIGFLKAVWQIRQHFVSAVQSISSVSSAHFSSSLPHAGGCFRRARTAAARTQFTTRTCRQTRTRTQSAAD

**SEQ ID 3769**

GTGTCTATGGACATAAAATTCATAACTTTGGGGTTATCTCGAATGGGGTCAATCTCGAAGAAAAATTCATAAAAAATTATTGATGGCCAGGAAAAATCCGGTGGATTCTTGATACGTGTAT  
CTTCAAAATGACAAAATCTTCATCATTTGACAGTTACGATGATCGGGTCGAAAACTAGAAATATTTAAAAGAATACCTGCAAGAAATCTCATTTGGATAATAAAGTGGGTTCGGA

**SEQ ID 3770**

VSMIDIKFNTLGVILNGVNPEEKFIKIIDGQENTGGFLILLSNDKPFSSFDSDYDDWVENLEILKEYLQESHWTIKRVG

**SEQ ID 3771**

GTGATTTCGGCCTTCAGACGGCTGGGACGGCAATGACTGACAACCTAATACAGATAGCAACGCGGATATTGACTGTTATCGCGCTTTTGTGTGCGGCTTACGGCATCATGAGGAATACGG  
AAAACGCCAAAAAGCGCGCCACCATCGACATGATCATGGCCGAAGCTAACAATGCGCGCCTTCAAGAAGCCATAACCATAGTAAACGGGGCTGGGAAAAACAAGACGGATGCATCTCGCCAC  
GATPACATCAGATACCCCGGACAAGAAGAAGACCGTGAAGCCATCATGACAGTGTTTAAACCAGCGCGAATTGTCTGTGCGGGCTATTGGCGGGCGCTGCACGAGAAAAATGTATAAA  
GATTTCGAATACTCCATGCTGTGTACCGGACTGGGACAACTTAAGCAGCTTCATTGTGAAATACGCCCTATFCAGGACGGCGCCGACGGCCTTTCAGAAATTGAAAGCCGTAGCCCGGAAAT  
GGAAGAAAAAGCCTCTGAAACCCAAA

**SEQ ID 3772**

VISAPQTAGTAMTNDLNIQIATPILTVIGVVAAYGIMRNFTENAKKRATIDMIAERNNAALQRAITIVNGLAKTDCILATYTSOTPDKKKDREALTVLNQREFVCAGVLGGALHEKHYK  
 DFEYSMLIRWDNMLSSPIFEIRIRISAPTAFQREFVARKKKKPLTKK

SEQ ID 3773

TTGCAACCGGAATTGCACCCGAATAAATATGGCAACCATCACTCAACGGTAACGGCAAAATGGCGCGTACAAATCCGTATGAAAGGCGTTTCCCGTTCCGCCACATTGTGACGGGCATCAGAAG.  
 CGAAGCGGTGGGCGCGCGCAATAGAGTCGCAAAATATGGACGGCATCCAAGGCAATGCCCGCGAAATACATATCTTTGCCGACCTTATCCGCGGTATTTATCCGAGGTTACACCATCAAA.  
 GCGGGGCGCAGCGGAAGAATCATACCGCATTTGGACGCGCACTAAAAACACCTTTGGCAAGGTTGGCGTTCGCGACCTTGCGCCCTCAAGACCTTCGCCGATTTGGCGAGATCAACGGTTGCAG.  
 GAGGTATCCCCACCAAGCGTTCGACGCGGAATTAACCACTTTATCCGCGCTCTCGGACACAGCCATGAAAGAGTGGGGACTTCTTCGCCGAAAACCTGTACGCAAAATCAGCAAGCCGAAAA.  
 AAGACCGGGCAGGACAAAGACGCCCAACCGAGCAGGAAATTCGCCGATATTTGCGCGGCCCTCTATACCGGCCCTAATGAGAAACCGAAAAATCGCGGTGCAACGGGTTGCCGTTGCCGTCCT.  
 ATTTGCCATCGAAACCGCCATTCGCGGCAGCGCAAAATCTCGGCCCTAAATGGGCAGATGGAAATCGCGCGCTGTATGTCGCCACTCCCAATCACTAAAAACGGGCACAGCGGTGACGTG.  
 CCATTATCTTTGCGAGCCGCGCACTAATAGACCAACTTCGCGCGGAATTTGATGACATCACTGGGTGTTAGCGCTGCAATCCAAAGCGCTTGATGTATTATCAGGCGAGCGCGGGAATTAFTTGG.  
 GCATACAAAGCGCTGTATTTTACGACACACCCGCGCGGAAGCCCTCACGCGCTATCAAAAAAGTGCCTGTGGAGTCTTGGCAAAATCAGCGGCATCGGGATTTAAGGATTTTACTCAA.  
 TGTTTTACTACCGCCCGACATGCGCGGATATTGCAAAAATGTTGGAT

SEQ ID 3774

LHPNCTIRINMATTQPNKWRVQIRMGVSRSATFERASDAKAWAARIESQIMDGIQGNAPRNTTIFADLIRRYLSEVTPSKRGAREESYRIGRALKTPLAKVRLADLRPQDFADWRDRLQ  
 EVSPTSVGRLETTLSAVCEHAMKEWGLLRBNPVKIKSPKKSRRARTRPTEQBIADIACALLYRPNKPKMAVQVRVAVLFALETAMRAGEICGLKQADVMRRRIARLHPITKNGDSRV  
 PLSIRAAELIOLRGIDDTWVPSLDAKSLDVLFRRARNCGIOGLHFHDTREARLRSKVPVVEVLAKISCHRDRLILLNVYRPMADIARLKL

SEQ ID 3775

TTGGGACAAATTCGGTGGCACAAAATATAAGCTGTCTGCTTTTCAGCGGGCGGCTTTTTATCTGCCTATGTGTTTCAACACACAAAACGGGCACA

SEQ ID 3776

LGOFGGTKYKLSAFQRAAFYLPFCFNTQNGT

SEQ ID 3777

TTGGCAGACGCGCGGAGGGGTTTTTTTGTAGCCATCATCAAAATCAATATTTTCTTCCTTCGCGTTAAACCCCGACATTAGGGCGGGCAATCCGATGCGGGCGGAAGCACCCGCTTC  
GATTCGCGTGGGAACAAATGGCGGTGCTTTATGTGCGGTTTGTGTGTGTAACACATAGGCAGA

SEQ ID 3778

1ADGRKGFFDALIKINIFFFPVKTPTLGAANPIAGGSTFRFGAEMAVLYVPPCVLKHIGR

SEQ ID 3779

SEQ ID 3779  
ATGCCCGCGCGTGTGGGTTTGGCGGGGCCGTCCGCAGGATTAA CGGCAGAAACCCCGCTGCCCTTCCCTCAATTCTCTATATATCGCGTTCCATCAAAAGACGCAATTGCTTTTCTTAA  
CCATTCTCTTTTGGCAGACGGCGGGAAGGGTTT

SEQ ID 3780

MPARVGGGAVRRINGOKPACPSPOFLIYRVPSKDALLFLTIPFGRRABEGFF

## SEQ ID 3781

TTGAGGGGAAGGGCAGGCGGGTTTCTGCCCGTAAATCTCGCGACGGCCCGCCAAACCCGACACGCGCGGCATATGGCGGATTGTTTACAATATTGTCTAAAAATC

## SEQ ID 3782

LRGRAGGFLPVNPADGPAKPDTRGHMADCLQYCLKI

## SEQ ID 3783

TTGCAGGTTTCAGATTTTAGACAATATTGTAAACAATCCGCCATATGCCCGCGCTGTGCGGTTTGGCGGGGCCGTCCGAGGATTAAACGGGCAGAAACCCGCTGCCCTTCCCTCAATT  
TCTTATATATCGCGTTCCATCAAAAGACGCATTGCTTTTCT

## SEQ ID 3784

LQVQIFRQYCKQSAICPRVSLAGPSAGLTGRNPPALPLNFLYLAFHQKTHCFS

## SEQ ID 3785

TTGTCTAAAAATCTGAACCTGCAACGCGAAATAAGGTAGAAATACGCCCGCTTATTTTACCGTCCAATCCCAATTTACCAAGGAAAAACGATGAGTACTTCAATTGAGTTACCGCGATCGCG  
GCGTCGGTATCGACGCGAGCGACCACTGGTCGAAAAAATCAACCGTTTGCCAAACGCCACCATGCGTCCGGAAGTATTGGGGGATTGGGCGGTTTGGCGCAATTGGTCGAAATCGGCAA  
AAAAATATCAAAACCCGATTGGTCAGCGGTACGCGACGGCTGGGTACCAAGCTCAAACTTGCCTTCGATTGGGACAAACAGATACGGTGGGCATCGACCTTGTTCGAATGAGTGTCAAC  
GATATTTTGGTTCAAGGAGCTGAACCATTTGTTTCTTGGATTATTTTGCCTGCGGTAAATTTGGATGTTCCGCGTGGCGACCGATGTCATCAAGGCATTGCCCAAGGTTCCGAAGAATCCG  
GCTGCGCCCTGATTGGCGGGGAAATGCGCAAAATGCCGGTATGTATCCCGTTGGTGAATACGATTGGCGGGTTTGGCGTGGCGTGGTGGAAAAAGAGAATGTCATTACCGGCTCAG  
CATCGCGCGCGGCGATGTGGTATTTGGGTTTGGCTTCCAACGGCGCACATTCAAACGGCTATTCCCTTATCCGTAAAAATCATCGAACGCGACAATCCGATCTGGATGCCGAGTTTGATAAT  
GGCAAACTTTACGTGAAGCCGTATTTGCGCGGACACGCTGTGTATGTGAAACCGGATTCTTGGCCGCTTTGGAAAAATTTACCATTAAGGTATGGCGCACATTACCGCGCGCGGCATTACCG  
AAAACTGCGCGCGCGCTGTGCTTAAACACCGTTGCCAAATCGATGCCGAATCGTGGGAATGGCCAAAGCTCTTCCAAATGGCTTCAAAAGGCGGCAATGTGGAACCCCAAGAAATGTA  
CCGACCTTTAACTGCGGCATCGGTATGTCGTCATCTGTCTGCCGAAGATGCCGATGCGGTTCCGTATCTGAGCGGGCAGGGCGAGACAGTGTACCGTTTGGGTTGCATCCGAGAG  
CGTCAAGGGAACGAGCATCAAAACCAAGTTGCC

## SEQ ID 3786

LSKNLNLQTRNKVEYAPLFYRPIPTIYQKTMSTSLSYRDAGVIGIDAGDLVEKIKPFAKTRMEVPLGDLGGFALVEIKKYQNPVLVSGTDGVTGLKLAFDWDKHDVTGIDLVAMSVN  
DILVQGAELPLFLDYFACGKLDVPRATDVIRGIAQCCEESGALIGGETAEMPGMYFVGEYDLGAFVGVVEKENVTGLSIGAGDVVLGLASNGHNSYSLIRKIHERNDPLDABFDN  
GKTLREAVIAPTRILYVKPILAALEKPTIKGMAHTGGGITTENVRVPLPKNTVAQIDAESWELPKLFQWLQAGNVETQEMRYTFCNGIGMVIVIAEADADAVRSFLSGQGETVYRLGCIRE  
RQGNHQQTQVA

## SEQ ID 3787

ATGCGGAAATGCCGTCTGAACAAATTCAGACGGCATTGATGCTTTGGAAGTCAGGCAACTTGGGTTTGATGCTCGTTCCCTTGACGCTCTCGGATCAACCCAAACGGTACACTGTCTCG  
CCCTGCCCGCTCAGGAA

## SEQ ID 3788

MRKRLKQIQAFDANKSGNLGLMLVPLTSLDATQTVHCLALPAQE

## SEQ ID 3789

ATGGTTTTTCAACCAACTACACTTTTTTGTAGTTCCTCATCAAGAACCAACCTTCATAATTACAATCATTTTTTTTGTGCAATACCAATAACG

## SEQ ID 3790

MVFSTQPTLFVSSHTNQNLHNYNHFFVQYQIT

## SEQ ID 3791

TTGTCCATATCGGCTTCTTAAAGGCTGTTTGGCAGATTCGGCAGCATTTGTATCGCGGCTGCAGTCAATTTCTGTCGCTCAAGCGCGCACTTTTCTTCACTTCGCGACGCGAGCGGCTG  
TTTTCGCGCGCAGGACAGCAGCGCCCGGCAACAGCGGCAACATTTCCGAACAGATGCCGACGACAAACGCGCCGAACATACGACAATCAGCGGCGAGATTGACACTCTGCCCCGGAAGAT  
AGGAAAAGTTAAGCGCATCCATATTAATGACGCGAAGCAGCAGGAAGAGCAGGATAATGATTTTGATGACGGTATAGATAAGTTTCATGTTTGTCCGTAAATAAAACCGCGCACGG  
ACAGCTTCGCACTCTGAACCAAGATTGGCT

## SEQ ID 3792

LSISAPLRLFGFSGSILYRRCQFLSAQARTFLHFRTOAAVFAAQGQPPQGGKHSEHDADKRAEQYDNQRQIDTLPRKIGKNGIHIHNDGKQBEQDNDFDGIDKPHVCSVNKNAAR  
TASHSEPLRL

## SEQ ID 3793

ATGCCGTCTGAATTTGTTTCAGACGGCATTTCGCGCATCTTCCAAACGCGTATCCGCAACACAGTTCTGCAAACTGATATTTTGGCCGGTATGGCGGCTAAACTTCTTCATCATATTTCGA  
TAATGCTA

## SEQ ID 3794

NPSEFVSDGISASSKRVSATQFCKLIFCFWRLKLLHHISIML

## SEQ ID 3795

TTGTTTATCTACATCGTATTCATCTTATTTTCCGAAATGTGAGCGTTTATGAAGCAATCCGTCCATAATAAAACAATTTTAAGTGTTTGTATTCATCTATGCTGTAAACGGCTTTT  
CCGCCCCCACCACCCCGCGA

## SEQ ID 3796

LFIPTSYSSYPFKCRFMKQSVHNRKTIISVLISSMSVTAFSAPHPPPR

## SEQ ID 3797

TTGCTCGCCTTGGCTACTATTGTACTGTCTGCGGCTCGCCGCTTGTCTGATTTTGTAAATCGCTATATTATTAAGCGAACTTCTTGGTTTTGTGTTGTTGCTTACGCTCGCT  
CCGA

## SEQ ID 3798

LPRLAVLFVLSAARRLVLFVNPLYLSELLGFLVRYGRSG

## SEQ ID 3799

ATGAAGATAACACTGCAAAATTAAGAAAGAGTACAGAAAGAACCGCTCCGTTCTTTTGTACCAGGAGTTACCGCCGCTTCTGCCGCGATATTGGGTATCCATCCGATTCCGCGG  
CACTGTTTACCGTAAATCCGACCGGTACCAACCATCGTTTGGCTTGGCTGCGGATGAGGTTTTCAGATGCCCGCGCGGCGCGGCGCAAGCTGTTTCGGCGTACCGCGTAAAGCGAG  
ACGCGGTGCGCGGCGGAGGAAAGCGGTGCTTCTCGGCATTCCGAACGCAACGGCGCGGCTATACCGTTGCCGAGGACGATGCCGAGCTGAAACGTGCCCCCTGCCGTCAAAAG  
AAATCATGCCGACGGTATTTGTTTATGCCGATAGCCCGGCGAGCGCGGCAAGTCGAGCGCGGCGGTTTACCCGTTGCCGATCAACCGTTCCAGGAATTTGCAGACCGTCCGAACC  
ACATTAAACGGCATGCGGAATTTTGAATCAGGCAAAACGCGCTTCCGGAATACAACGGAATCGATCGTAAACCTTTCCCGCGGTTGTTGAGGGAATGCGAATTTTCGATTAACTTCG  
CACACCGTCCCGGACGTAAATACTGCGGGATCGGTGTGAATT

## SEQ ID 3800

MKITHCKLKKVQKEPLRSFVPEVTARSAADILGIHPSAALFYRKIRTVTNHRLALAADEVFCEPAGPGASCFGVRRKRRRGRGAAGKAVVFGIPKRNGRAYTVAEDDAEPETLPPAVK  
KIMPDGIVYADSPSGSRGKSDAGGPTRCRINRSKEFADRNRHINGIGNFWQAKRALRKYNIDRKPFPLLRCEFRFNGTSPSRQLKILRDRCGI



## SEQ ID 3801

TTGTGCTCTCTGAATTTATAGAACGCCGAACGCTATTAAATCCGATGGTTATTGTGACGACTTTGTTTTTGTGTGTGTTTTGTGGTATTGGTTTTAACCGTGCCGGATCAGGTGCAGA  
TGTGGCTCGACCGGGGAAAGAGTCAATTTTACCGAGTTCAGCTGGTTTTATGTTTTAACGTTTTCCATTTTTTCGGTTTTTCGTGTACTCTCGGTGAGCGGTTGGGAAACATCAG  
GCTAGGACGGGATGAAGATGTCCCGAATTCGGCTTCTGTGTGGCTGGCGATCTGTGTGCGCCGGGATGGCGGTGGGCTGTATGTTTTTCGGCTGCGAGACCGGTGATGCAATAT  
TTTTCCGACATTACGGTGGCGCCCGGAAACACAGGACGAGCAGGCAATGCTGACACAGGTGTTCATTTGGGGCGTTACCGCTGGTGGGTGATCGGTACGATTGCATTGGCTTTGGCTT  
ATTTCCGTTTTCCGCTACAACTGCGCGCTTGCCTTGGCTTCTGTTTTTACCCCTGTGTAAGAAAAATTTCCGGAAGGTTCGGCGATGCCATTGATATTATGGGCTTGTCTACTTT  
TTTCGGCATCATCACCATTTGGGGTTCGGGGCTTCGCACTGGGCGCCGGATTGCGAGAAATGGGCTGGATTGCGGAAACAGCTTCGGCTGCGAGGTCTTGATTATCGCCCGCTTAATG  
TCCCTCGCCGCTGTTTCGGCAATATCCGGCGTGGGAAGGGCGTGAAGGTGTTGAGCGAGTTGAACCTGGGCTTCGCTTTTGTCTGTGTTTTTGGGCGCGGACCCCACTGTTT  
ACCTGTTGTGCGCATTCGCGGCAACATAGGGAATACCTCGGAAATCTGGTGGCGCTCAGTTTGAAGAACTTATGCGTACGAACGGGAACACAGCCGTGGTTGAATCTTGACCGGTGCT  
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GTTTTGTGTTTTACCGTCTTCGGCAATACGGCGATTGGCTGAATGACGGGGTTCGGGGGGAATGCTCGAAAGATGACCTCTCTCCGGAACGCTGCTTTTTAAATCTTTAATTAAC  
TCCCGCTGCGGAACTGACGAGCATCGTCAGCTGCTGGTCAATTCCTGTTTTTGTAACTTCTGCGGACTCCGGGATTATGTCCTGAACAAATATTACCTCTCGGGAACAAAGGCTTGAG  
CGCGCCACGGTGGCAGGCGGTATGTTGGGCGTGTGATGTCGCGTTGCGGTTTTGCTGATGCGCTCGGGCGGACTCGGCAACTCGAGTCTATGACCTGATGTTTCCCTCGCGTTT  
GCCCTGCTGATGCTGATAATGTGTTTACGCTGTGGAAAGGCTTGAGTGGGATAAGAAATATTTTGAGACCCGGGTCAACCTTACCAGTGTATTTTGAGCGGCGGCAAGTGAAGAGAC  
CGCTGGTGGGATAATGAGCGAGCAGCAGGAGGATATTTAAATTTCTCAACATACCGCATTCGCGGCTATGACGAGTTGCAACGGGAGCTTTCGGAAGAAATACCGCTTGAGCGGT  
CGCGGTGATAGATTTTTCATCAGGACGAGCCGCAATCGAGTTCGCTCATTCGGAAGAGACGATGCGCGATTATGATACGGGATTAGTCTGTCGGGCGAGGATGATCGACGAGTTG  
ATTAACGACGGCAAGCTGCCGATATCGGCGACGAGCACTTACAAACCTTACGCTTATTTTTTCGAGCGGCGGCTGGGTACGATGTCAGTATGAACAAGGACGAGCTGATTGCCG  
ACATTTTGAAGAACTACGAACGTTATTTGATGTTGTTGATGATGTCGCTCAGGAATGATGGCGACGAGCAGGTGGAATTCGCGAG

## SEQ ID 3802

LSLSEFIERTTSPNPMVILTTFFVCLVVLVLTVPDQVQMWLDRAKEVIFTEPSWFYVLTFSIFLGPLLILSVSLGNIRLGRDEVDPEFGFLSLMLAFLAAGHVGVLMPFGVAPRLMHHY  
PSDITVGAPEHQQALHHTVPHVGHANSVYGTIALALAYFGFRYKLPALRLSCFPLLEKI SGRFGDAIDIMALLATFFGIITTLGFGASQLGAGLQEMGWIENSFGVVLIIAAVH  
SLAVVSAISGVGKGVKVLSELNLGLAPLILFFVLAADPTVYLLSAPGDNI GNYLGNLRLSLKTYAYEREHKPFESWTVLYHAWWCSNAPFVGLFIARISKGRFTIREFVFGVLLIPGLFG  
VLWPTVPGNTAIWLDNGVAGGLEKMTSSPETLLFKFPNYLPLPELT/SIVSLVLSLFPVT SADSGIYVIANITSRDRGLSAPRQVAMWVMSAVAVLLMRSGGLGNLQSHLIVSLPF  
ALLMLIMCPSLWKLGLSADKKYFETRVNPTSVFTGCKWKLRLVIMSQTQEQDILKFKHTASPMHLELRELSEYGLSVRVDRKMFHQDEPAIEFVIRKETHRDFMYGLKSVGQDVSDQL  
INDGKLPRIHQITTKPYAYFPDGRVGYDVQYMKDELADILKNYERYIMLLDDVQGLMHEQVLEAB

## SEQ ID 3803

ATGAGGCGGTTCCCGCTCCGCAACCATAAAGGAAGTTTCATGAACCGGACTTATGCCAATTTCTACGAAATGCTCGCGCGCGCTGCCGCAAAACCGCAACGGCAGCGCAATGTTTCGACG  
GCAAGGAAAAAACCGCTTACCGCGCGCTCAAGCAGGAGCGCTCGCGCGCTATCTGCAAAATATCGCGCGTGAAGTTTCGGCGACACCGTTCGGCTGCGGCTTTCCAAATTCACAGAG  
ATTATATACCGCTTATTTCCGCGCTTCCGCCATCGCGCGGCTCGCGTACCGATGAACACATTTTGAAGAACAGCAATACCGGTATATCTGACGACTGCAAGCGCGCTTCTGTTT  
GCCTCGCGCGGCTGTCAGAAAGAAATGCGGGGCTGAAGCGCAACCGCGCTCGAAAAATCATTTGGACGGACAAAGCGCGCGCGGCAACCGCGGAAGGCGATGCTTTTTT  
AAAACGTGCGCGCTTCCCGGAAAAACCGGACTTGGCGCGCAACCCCGGATAAATGATTGGCACACATCATCTACACCTCCGGCAGCAGCGGCGCATCCAAAGGCGCGCTAATCAGTTA  
CGCCAACTGTTTCGCAACCTGAACGGCATCGAACGCTTTTAAATTTCAAACCGGACCGCTTATCGTTTCTGCGGATGTTCCACAGCTTCAAGCTGACGCTATGTCGTCTGCTG  
CGGATTTATATGGCGTTCGATATTTTGGTCAAAATCCGTTTTCCCTTTTCCAAAGCTTTTGAACAGGCGCTGCTCAACCGGCAACCGTGTTTTTTGGGCGTACCCGCGATTACACCG  
CGATGAGCAAGGCAAAATCCCTTGGTATTTTCAGATGCTTCAACCGCATCCCGCTGTTTATCAGCGCGCGCGCGCTTTGGCGGAACAAACCATCTTCGATTTTAAAGCAAGTTTCCCGG  
CGCCAAATGCTTGAAGGCTACGAGCTGAGCGAAGCTTCCCGCTGCTCGCGCTCAATACGCGGCAAGCGGCAAAAGCGCGGCGGCGATCCCGCTGCGGCTTTGGAAGCCAAAGCC  
GTCGATGAAGAAATGCTGCAAGTCCGCGCGCGCAAGTGGCGGAATGATGCTGAGGGGCGGTTGCGGTGATGCGGGGCTACCTCAATATGCTGCGCGCACCGATGAAGCAATCGTCAACG  
GCTGTTGAAAACGGGCGGATTTGTTTACCATAGCAGGACGGCTTATCTTTATCGTCGACCGCAAAAGAAATTTGATTATTTCCAAAGGTCAAAAGCTTATCCGCGCGAGATCGAAGA  
AGAAATCCCAAACTCGATGCCGTCGAAGCGCGCGCGCTCATCGCGTGAAGACCGTTATGCGGACGAGGAATGCTGCGCTTCCGTCCAATTTGAAGGAAGGTATGATTGTTGGCGGAGGAC  
GAAATCCGCGCGCACCTCGTACCGTGTGCGCAATTTCAAATCCCAACAGATCCACTTTAAAGACGGGCTGCGCGCAACGCTACGGGCAAGATTATGAACGGGCTCGAAGGAGC  
AGTTTGAAGGAACAAA

## SEQ ID 3804

MRAPAVRNHKGSPMNRNTYANFYEMLAACRKNNGTAVFDGKERTAYRALKQEAFAVAAYLQNIQVKGPDITVALAVNSNTEFITAYFAVSAIGAVAFPMNTFLKSEYAYILNDKARFLP  
ASAGLSKELAGLKAQTFPEKIITWTKSRPAGETAEGDAFFENVRFPPEKPDILGRQPRINDLAHIYTSOTGHPKALISYANLIFANLNGIERIFKISKDRFIVFLPMFHSPTLTAHVLL  
PIYMACSIIIVKSVFFSNVLKQALLKATVFLGPAITYAMSKAKIPWYRWFNRILRFISGGAPLABQPTLDFKAKFPRAKLLEGYGLSEASPVVAWNTPERQKARSVGIPLGLEAKA  
VDEELVEVPRGEVGLIVRGSSVMRGYLNMPAATDETVNGWLTGDFVTIDEDGFIFIVDRKDLIISKQNVYPREIIEEHLKDAVEAAAVIGVKDRYADEIVAFVQLKBEKMDLGED  
EIRRLHRTVLNFKIPKIHFKDGLPRNATGKVLKRVLKQFEGNK

## SEQ ID 3805

ATGTTTGGGACGGCGAACGCCCTCATTTGAAACAAATATGCGCTGTAAGACGGAAGCGGCGAGTTTATCATCTTTGCCCTTCAGACGGCATATCAACCGCGCTTTGCGCGCATGCGG  
GAGGTTTCGCGCGCTCTCTCTATGCTGAC

## SEQ ID 3806

HVADGERPHLRTICRLKTEGSLSSLPDGI SNAAPFAPHAGGSPSPFLCLT

## SEQ ID 3807

TTCCGATATCTGGCGGATGGGCAAGTATCAGATATGGAGATAAATTCAGCTGACGACCGCGCGCGCGGCTATTGACGTTGCTGTCGGCAGCGGATGGGTGGGGAACATTTTT  
TCGCGCATTTTCGATGATTTTCGCTGCCAAGCGGTTTGGTGGGTTTCGCGAGTCAGATTTTCGCTGGGATGCGGTGGAATGCCGTCTGAATTTTCGGTGTGCGCGAGATGAAGCGGGCGC  
GGGTGAGGAGCTGCTGTTCCATGCTCCATGCTTTTACGCTGATTTTCCAAAGCGCGGATGCTGTCGCGGAGGAAACCGGCTCGCATTAGGGCGGCGGCGAGGTGCGGTTTCGTA  
GAGGCTGCCCGCGCGGTTGGCGGGAAGCGGTTGGTCAGCGCGCGGCGGAGCGGCTGTACAGCTGCGCTGCTTCGGGATGGGGATGCTGTAAGATAGAGAC

## SEQ ID 3808

LRILAGMKYQILDDKFDVDHAAARVFDVAVGRRMGHEHFFAHFDDFACQGLVAFSGHFGADAVECRNLNFGCAADEAGAGEGLVFPFCVPTLVFSKGGDAVREBTGVAIQAQVGFV  
EAARAGGGKFPVGQAAGAAVHVACFGMGIVVKID

## SEQ ID 3809

TTGAAACTACGTTATTGGTATTGCACAAAAAATGATTGTAATTATGAAGGTTTTGGTTCGTATGGGAACATAACAAAAAGTGTAGGTGGGT

## SEQ ID 3810

LKRLYLVLHKKMIVIMKVLVRMGFNKKRLG

## SEQ ID 3811

ATGCCGTCCGACACGCTGCCCATCTTATCCGAAACGTCGAAATCGTTTAACTAACGCAATCTTGGTTACAGATGCGAAGCTGTCGCTGCGGCGTTTTTATTACGAGGCAACATGA  
AACTTATCATACCGTCATCAAAATCATTATCTGCTGCTTCTGCTGCTTCCGCTCATTAATATGGATGCGGTACCTTTTCTATCTTCGCGGCGAGATGTCATCTGCCGCTGAT  
TGTGTTATTGTTTCGCGCGGTTTGTGCTGCGCATGCTGTTGGAATGTTTCCCTGTTTCGGGCGGCTGCTGCTTTCGCGCGGAAACAGCGCGCTGCGTGGGAGTGAAGAAAGTGGC  
CGCTTGAGCGGACAGAAATGACTGACCGCGGATACAAATGCTCGCGAATCTGCCAACAGCGT

**SEQ ID 3812**

GEQ ID 3812  
MPSEHAAAFYPKPKCSFKLTQSWFRVRSCPCGVFTYGANMKLIYTVIKIIILLFLLAVINMDAVTFSYLPGQSVNLP LIJVLFGAFVVGIVFGHFAIFGRLLSLRGENSRLRAEVKXSA  
RLSGQKLTAPPIONAESAKQP

**SEQ ID 3813**

SEQ ID 3813  
ATGAACCCCAAACACTTCATCGCATTTTTCGCCCTGTTCGCCGCCACGCGAGGCAGAGCCCTGCCGTCGCCCTCCGTCAGCCCCGACACCGTTACCGTTTCCCGGTCGCCGCCCTACACGG  
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TACCGCGCGGCACTTCTTACCGAGCCCTGCGCAAAACGCTGCAAAAAAATCAGGGGCGACGGCGGCATAGGCTGGGTTTACCCCGCCAACGTCAAAGGGCAGCGCATGGCGGCCGTCGCGT  
CACAGCGGCAACTGGCAAAAGCTTACCAGCAGGAACAATACCGGAGATTTCGCCCTCGCGGCATCTCGCCCAACCGGACAGCGCGCGGCATGACCTGACCGCGTCTGACGGCAAAA  
CCGGCAACAGCGCGCTTTCCTGTTCGCAAAATCCGCTCGCGGAGATTTCGCCCTCGCGGCATCTCGCCCAACCGGACAGCGCGCGGCATGACCTGACCGCGTCTGACGGCAAAA  
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GACCGAAGTCCAACAGATGACGCGCGCGTCCGCCGTGAGGGGCGACGATGTTTGGCTTTGGCAAAACGCAATGGCGCGCATATGCAGCATGAAAAATGCGCTCAACCAAGGATGGGGC  
GCCAAGACGGCGTACACTTCTCCGCCCAAGGCTACCGCGCGCGCGCGGAAATGCTTCCGACAGCTCGCAAGAACTCGTCGCGCGCGCGCATCAGGCAA

**SEQ ID 3814**

SEQ ID 3814  
MNPKEHIAFSALEFAATQAEALFVASVSPDTPVTVSPSAPYTTDTNGLLLTDYGNAASPMMKKLSVAQSGEAFRLIQIGDSHTAGDFFTDALRRKLQKTWGGGIGWVYPANVKGQRMAAVR  
HSGNNQSFSTRNNWIGDFPLGGILAQTGSGGGMTLPASDGRTGKQFVSLFAKPLLAEQYTLTVNGNFTVSANGGGQVQLDTGAALPLAIQTMEPMDIGFINIENPAGGTTVSANGINGAQLTQW  
SKWRADRMNDLAQTGADLVILSYGTNEAFNNNIIDATTEQKWLDTVRQIRDSPAGLILIGAPESIKNTLVGCGTRPVLLTEVQCMQRKVARQGQTFMFSWQNMAGGICSMKNWLNQGWA  
AKDGVHFSAQGYRRAEMLADSLSELVRAAAIRQ

**SEQ ID 3815**

SEQ ID 3815

GTGGAAATACCGTCCGCCCCCCCTGTCCGATTATTGCGTGAATTGCGGCGGGCGCGACGAGTCTCTCGAGGCTGTGCGCAAGCATTTCGCCGCGCGCCGGTAGCCTTGGCGGGAGAAAGTGT  
ACGCCGCTCTTGTGGCCGCCACCATCTTGTTGAGCCAGTATTTTCATGCTGCATATGCGGCCCATTTGCGTTTGTCCAAAGACCAAAACATCGTCTGCCCTTGACGGGCGACGCGCGCTGCAATCT  
GTGGAATCTTGGTCAGAGGACGCGGCGCGTGCATACATACCCGAGCGTGTATTTTCAGGGAATTCGGCGCGCCGATGATGAGGATGCCGCGCGCGGCGCAGGCTGTGTCGGGATTTGGCGGAC  
GGTATCCAGCCATTTTGTTCGGTATCGGCAATGTGATGTTGTGTGTTGAAGGCTCTGTTGTTGCCCTAGGAAAGGATAACCAAATCGGCGCGGTTTGGGCAAGTCTGTTATACGGTGTG  
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CAGTGTGCGCGTGTGACGGACGCGCCCATGCGCTGCCCTTTGACGTTTGGCGGGGTAAACCCAGCCTATGCCCGCTGCGCCCATGTTTTCGAGGCGGTTTTCGCGAGGCGCTGCTGTAAGA  
AGTCCGCGCGCGTATGCGAGTCGCGGATTTGCAGGATGCGGAAGGCCCTCGCCCTGCTGTCGACGAGTGGATTTTTCACAAAGCGAGCGCGGGCGGTTTTCGCGGATTCGCGGTGAC  
CAGCCGCTTGTATGTCGTTGATAGGGGGCGGACGGGAAACGGTTAACGGTGTGCGGGCTGACGAGCAGCGGCGAGGCTCTGCTGCTGCGTGGCGGCGAAGAGGGCGGAAATTCGATGAAG  
TGTTCGGGTTTCATGCTGTGTACTGATGTTGCGTACTCGGTTCAAAACAGCATTTTTCATTAATTTTTCGCCAGCAGTATTTGTCTCTCGCGGTAAGTGTATGCCGCTCTTACT  
GGGG

**SEQ ID 3816**

SEQ ID 3816  
 VETPSAPPVRLLPDCGGADEFFEAVGKHFRRAPVALGGEVYAVFGGSLPEVPVFAHAYAAHVCLPRPKHRLPLTGDAPLHLLDFQGEDGARAAAYAEVRFQPGFGRADDEAGGGQVAVDLAD  
 GIQPFLLGIGNVDDVVVEGPGVAGKDNQIISAGLKVHVHVTGTFPLPGQLCAVDAAHRGNGNAAGGIFDVDEADVPRHFLGYGQQCRARIQYLPAAAVGGGVAVDQGQLFGBEORFGKQGN  
 ALPAGFAVRRGGQHAAAAGLGEDAAERISGTVPAGEALPVAAVTDGRHALPFDVGGVNPAYAAVAPCTLPQAFAGQGVGKEVAGNMRVADLQDAEGLAALCDGSEFFHPRRGGVAVVQG  
 QPVCIGVGGGRGNAGVGADGGDQGFCIRGGEQGGKCDVFGVHGCVLDGCVLGSKTFISIIISASSFCPSAVKCMPSLLR

**SEQ ID 3817**

SEQ ID 3817  
ATGCCAATTTTAAAGGGTTTGGACATGAAAAAATTTCTTTCCTCTTTCGCTCCATAGTGTCTGCCCTGATTGCCGTGTGGTTCAGCCAAAACCCCATCAACGCCTACTGGCAGCAGA  
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AACCGCGCGCAGCGCTCAAGACGCGCTTTCGCGAGATATGCGCGCTGAAGCCGCGCATCCGAAGCGCCCGCGCGCGCGGGAACAGATGAAACAAAGGCACCGAAGCCGCGCGCGT  
CGGGCGCGGCAAAAGTCTTTTTCGCGGAGATTCGTGATGCAAGGCGTTCGCGCTTTCGTGCAAAAAAGCCTGAAACAGCAATACGGCATCGAATCCGCCAACCTCCGCAAAACAGCA  
CGGGGCTTTCTTATCCCTCATCTTCGACTTGCCGGAAGACGATGGAAGAAACCTTGAAAAACATCCCGGAATCAGCTGCTCGGCTCTCTCTCGGGCCGACGACCCGCGGGGATTCC  
CGTCGGCAACACGCTACCTCAAATTCGCTTCCGACGAATCCGCGCAAGAATACCTGAACACCGCTCGACGATCCTTGAAGCCGCAACACGCAACGCAACGCAACGCAACGCAACG  
CCCTACATGAAAAAGTCAAGCTCGACGGTCAAGTGGCTGCTCGCAACAACTTTTCGGAACACTTGAAGGCAAAATCATCTGTATGCCACGCGCAAAACATCTGAGCGGCGGGAAG  
GCGCTACACCGATTCGCTCAACGCTCAACGGCAACCCGCTCGCTACCGCAGTAAGGACGGCATACACTTACCGCCGGAAGGACAAAAATGCTGCGGCAAAAAATATGAAAAAATCGT  
TTTGAACCGAGTACGCAACCATCAAGTACACAGCCA

**SEQ ID 3818**

SEQ ID 3818  
MPIIFKGLDMKNFSLFPASTILMSALIAVWFSQNPINAYWQOTYHRNSPLEFLAAYGWRRSGAALQENAYALSDGIKTFLSGETPPTAQDGGSDMHPPEAAASEAAPAGGTENWQGTAAAV  
RSGDKVFFAGDSLMQGVAPFFVQKSLKQQVGIESANLSKQSTGLSYSPFFDWPKTITETLKKHPEISVLAVFLGPNDPWDFVVGKRYLKFASDEWAQEYLKRVDRILLEAAHTRVQVVMGI  
PYMKVKVLDGQMRYLQKLLSEHLGKGIILIPTAQFLSGGKGKRYTDSVNVNKGPKVRYRSKDGIDHFAEGQKLLAEKIMEKIVPEPSTQPSSTQP

**SEQ ID 3819**

SEQ ID 3819

TTGTCCCAAGGATGGTTTATACGCCGCTGCCTGCTGCGAATTGCGCACTGTTTTTATCGCTCTCTCGCGGAATTTACTGGGGCTTTGCGAAATACCCGTCGCTCCAAAACCTGCTGCTTTTGG  
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CTTTGGGCTGGGGTGGCGCAATTGCGCCCTCGGATTACCGPTTTTGGGCTTTTCAAATATTTCGATTTTTTCCGTCGCGTGATGCACAATATGCGCGGAAAGGCGCGCAATCGACATCGT  
ATGCGCGCTGGGACTTTCTCATTTATACCTTCACGTCTGTCGCGCTATCTGTTTTTACTGCTTCCGCGCCCGCAGCGCGCGGTTTTTGGGTGGCAGCAGCTGCTGCTGCACCTAGATTTTTTC  
CCACCGTTACCTTCGCGCCGATTAATCCGCGCGCGCGCATGCAAAAGCAGCGGAGCGGCAACAGCGGGGTGACCTATGCGCAAAATCCGCGACCGCGACCGCGGTTGCGCCGTTCCGCGCCCGCCCT  
CGCGCGTTTCCCTGATTTTACTGGGCATTTGCCAAAATGGTGCGTTTGGCGGGGATACGGAACGCGGAAACTTGGGTGTCGCGCGGATTTTGAAATCCCAACCAATTCGACGGCTGGGGCGCGCTC  
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CGCGACCGCTATGCGGCTGAAATACCTTCGCGCGCTCTCTGTTGTTTACCTTTCATTCTGCTGCTGCTTAGCTTTTGTGCTCTTCAATACCGCAAAACCGGACGATCGAGCGCGAGTTT  
TCAGTCCCTCTCTTTGCGCAATGCGCGCGCTGGAACGCGCGCAACGGCGGATATGCTGCTGCTTGCCTCGTTTGATCTCTTGATGCTGCTCTACCTTACCTGCAACCGCGCTTTTGACGG  
CGCGGCTCAAAGGTTTGGAAAAAATCCCGATGTGGCTGTGTTTATCCAGATTTCCATCATCTGCTGCTGATATGCTGCTGCGCCCTTCGGGAGTACCCGGCTTTATTTATGCCAATTTT

SEQ ID 3820

SEQ ID 3820  
LSQGWFMPLLSVEFALFFIVFLPIYWGFAKYPVSQNLILLLAGMGWLYHISVPFAAIIIVLYSSCYWLLGELLRSDESTRRFWLGGCIAASITVLGFFKYDFFRPLIAQYAGKGGAILD  
MPLGLSYITFQSVAIVLYVCFRAPHAARPGWHELLLHLSFFPIVTSGPITRAAAFKSTDGEQAGALAQIRTRRPSRSPVRPALAVSLILLGIACKNWLAGLAIENWSPVFNPTQFDGMGVL



ATGCCGCTCTGAAGGGCGGGAGGGGCTTCAGACGGCATCGCTCGGTCAGGTTTCGGATATGGTGGTTCAAATTCAGGCAGACCCGCAAACCTGCCGCGCGCGTCAGCATATCCCGCAACGCCGA  
TGCAGGAAGATGCCGAGTATTGCGTAACC

MPSEGREGLQTASLGQVRIWVFKFRQTRKPAAAVSIPATPMQEMPEYCVT

GTGGGGATTGTCGTACGCACGCGGTGTTCTGGTCCATTACGGCTTCGCTGGCGGTAAGCATGCCCCCTGTGCGAAAAAGGAAATCAGGCATTGGGGCTGCTCAGACACGGGACCGGTATGG  
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CGCCTTCGGCAGCGTGAATACCGGTTCTTTAAGCAGCCTGCCCTGCTTTTGAAACGGAAAAAATGATGCTGCTGTATGCGGTAACGGTGC GGCGTATTACGGCGCACTTTTACCGCATAC  
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CCAAACATCTCGCGCGGATTTTGTGCGGCGCGGTGTGCTTATCGCCCTCTCTTCGGGGCTTTTTCGCTGCTTTGGCGCATTTTCTCGCCGCATTACGGGTTGTTGTTGTTATGTTGGGGAC  
GGCGATTGTGGTCTGTCAGCTTGGGGATGGTTGCCAAAGTTTGGATTTCGCCCTCCGATGCCGAGACCTTGCCAACTCGATTATTTCGGAGCTTTTACAACGTCGGTATAGCGCGCGCGCA  
CTGCTGGGACAT

VGIVLTHAVFWSTITASLAVRIAPVPGKGNQALGLLSTGTVMAMVAGIPIGRMVGQYLGWQASFLILIGLCSAAVMAVLAKSLPLPLSVNTGSSLSLPLILKKRKLMLLYAVTPVITAHTAY  
SYIEPFTVIQIGGFSARQVTVVPGLYGLAGFAASYLFGKWFPAKHPRAPLAGAVSLIALSSGLILPLAHFPAATYALVFVWGTATVVSGLMVAKVLDFASDAADLANSTSELYNVGIGGGA  
LLGH

TTGGCAATCGGCGCAATTATTTTTC AACACGCGCGGAATACATCCCCATCGCGCTTTTGAGCGACATCGGACGAAGCTTCGGCATGCGCGCGACCGAAACGGGTGTGATGATTACGTTTATG  
CGTGGATTGTGCGCGTGACTTCGCTGGCGCTGCCGCTGATGCTGCTGACGCGCAATTATGGAACGCGCGCGCTGCTGCTGGTCCGTGTTTTCGCTGTATTACTGTCAGCCACATCCTGTGC  
TTTGCCCTCGTGGCGTTTGTAAATCCTACTCGCAAGCGCGTGGGGATTGTGC

LAIGAFIFNTAEYIPIALLSDIGRSFGMAATETGVMITVYAHIVALTSLALPLMLLTRNYGTARPAAGPVCVLLSATSCRLPRGVLSYSQAAGLC

GTGTTCGGACGGCATACGGAGTATCGCATGTCGACAAATTTTACCAATACACCGCTCCTTTCCATTGAAAAATAACGGATTGGACACGGCATCGACAGAAAAACCGCCGCGCACTTGT  
CAAAACCTGTTTTCAGGGGTATCTTTACAACCTTCAAATTCAAACCGTTCAT

## VFGRHTEYALADNFTKYTAPFHLKNGGLDTASTEKPAHLSPCLQAYLYNLQIQTVH

[illegible]

GGCRFLPEHFPQFDLAVMGQQFVAYFGCRVAQFVVLLPAVEAVGGAALSGEGFVNQTAVGSDVQ\*GDVAVVVQELRLIAGMGKYQLDKDFVDHAAARVFDVAVGRRMGGEHFFAH  
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RRPALAHNLRLQCGLRMFVEEGEIGGAEDVFEKIQPHQRICRVLLCRRLYQRHNGVKARLGVCGKAAVFMVSADLPEPCGDGPGIEPVFFQTA\*PFFVFGFLPCPLPFAIALRL  
FFRPAQDFVBQILDFVPMNIEAV\*KSGITVETHAFGEQLPLFGRDRQGLSLPVVVLQAVFDIAQEAVGGKQGFVFRHNHNLGNFLQRLRAPQLQRAHLAAATHLENLGDKNFLADAA  
RAEFDVVRHAFDAADLAQVVAHRLIRAVIQIPAEHEGAHQRFDVVTRIRDYAFAERLAPFPAPLRNQILLQHGAQYQARATIRVRQPHIDAEHLVPGSNAVQQCNFLPDFGEKLL  
IPFPAPAVGVVFPIDENQIDVGRHVFVLLAARLAHHVAQLMRRFGITDORRAVHVPIIGVGEIQRGIDGKIGKQRNAGNFVQIADAVIAHNLHHITAIQLAQQLRFPFFLAFRADFV  
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ATGATAAATGACGAAAAATCTACTTTCAGATGTACTGAAACAAATATCAAGAACTAGGGTTTGATTGTGACAAAACCTATGATAATAGAGTTTTTTATAGGAGGTCTCTCAAAAAAATCTGCAAT  
CAATAGAAAGCCAACTCATTTCATTATCGGCAAGATTTTCAAATCAGTATTGAACAAGATGAATTCGGAGAAATGTGGACTTGTCTATTGTTCCGTCATATCGTCCCTCCCTTGAAAAACAT  
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**SEQ ID 3832**

MIIDEKSTSDVLKQYQELGFDLTKPMIIEFFIGGSQKNLQSIESQLISYRQDFQLSIEQDEFGEHMTCYCSVNIVPSPLENI LAIETTLFGLAQKND CNYEGFGSYGN

**SEQ ID 3833**

GTGTTGAAAATAAATCGCCGATTGCCAAGGCAACGATGCTCAACCAAGGTTTGTGCGAAGCGTTCATCTCAATTCTTATATGTGTCACCCCGCCAAAAGGGGGCGCATTTATGGTGAAT

**SEQ ID 3834**

VLKINAPIAKATMLNQLCBFISIPYMSHPAKRGRIMVN

**SEQ ID 3835**

SEQ ID 3835  
CTTCCTTAATTCACTTATCTTTCTGTCTGCGGACGGCAAAATCCAAATCAGGGGAAGCAGCCGCCTCCCGTTTCGGAGAAACACTCGGGACGCTGCTT

**SEQ ID 3836**

LLIH Y T F L V C R T A K S K S G G S S R L P F G E T L G T L L

**SEQ ID 3837**

SEQ ID 3837

TTGAAATCGTTCCATATGTTGAACATTGCCGCTCCCGATTGGGCAAGGTTGCCATTATGTGCGCAAGCATCCGTGCCGACCCGTTTCGCGGTTTGCCCAAGTTACAGCTCCGACTTACA  
ATAACGCCCGTCAGATTGCAGTACCACCAAGGAAAAATCGTGAACACCTCCTCCTCGACATCGGCGGCATGAGCTGCGGCGCTGCGTCAAAAGCGTTACCCGGATTTTAGAAGCGT  
AAAAGCGCTGCCAAGCGTCGAAGTCAGCTTGAATAACAAAAGTGCACCGTCGGATACGACCCGCGCAAAACCGACGCGGAAGCACTAATCGAAGCCGTAGAAGACGGCGGCTATGATGCG  
CGGTTGAAA

**SEQ ID 3838**

SEQ ID 3838  
LRIIVYVETLPFPDWARLPLCRKHPCTVSAFAQVHPTYNNAQILAVPTKGKIVETLLLDIGGMSGCGGCVKSVTRILESVKGVASVEVSLNKSATVGYDPAQTAABALI EAVEDGGYDA  
ALK

**SEQ ID 3839**

SEQ ID 3839  
ATGCCATCTGAAGCGGGGAGCGTGTTCAGACGGCATCGGGGAAACGCAAAGGCTTCAGACGGCATTTTGGCCGCTTTATTTCAACGCCGCATCA

**SEQ ID 3840**

MPSEGAERASDGIGETQRLQTAFLPLYFNAAS

**SEQ ID 3841**

SEQ ID 3841

TTGGTTAAACCTGCGGGCAATAGTGCTTCAGACAAACAAAATATGCCGAACAAAGAGAAAAAGCCGCTTTGCGCGCTGCAACGGAGAACGGTGTCCGGGGCGTGTCCGACATCAAAAATTCATATGATGATT

**SEQ ID 3842**

LVLKLAGNSAFROT KYAEQKEKSRLCALQRRTVCRA CPTSKIHM

**SEQ ID 3843**

SEQ ID 3843

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AAATGTGCGCTCGGAAGAAAAAGATATTTTGACCGTCGATGAATCATTCGGGAAGTGTGACATATATCATCTGTCACGGCAATTTGGTTCGGGGTGCCTCAGCGCAGTTAAAGACAAAATCTTT  
TCGATTTGCGGGAACCTGACCGAATACGGCATTGCTATATTTTCATACAATGTTTACCCTGGTTGGAAGCGGCAGGAGCAGTTGCGCGATATATGTCAGTTTTCGGCCGAGGGATGCGCT  
TTGGGAAGACCCCTTGAAGCAAGGACGCGGAAGAGCTTGATGCGATCAAGGCGCTGGCGGAAATTTTGGAAAACGACAAGGGCTTTGGGCGGCGGCAAACTTCGGCGATTCAAAAAATATT  
GAATCACAATACTATTATTGTTCGACACAAGATATATGAAATATTACAACGACCCGATTTACGTCTAACCGGTTTCATTGAATGGGCAAAACCGCCACCGGCTGGCGTATATCGGTGATACCGAT  
TTGCAATGTGCTCTTTGTATCTGTGAGGCGGACATACCGGGAGCGGATTCTGCGCATTTGGCAGGGGGTGATTATATGCCAAAGAATTTTACAGCGATATTTTATTCGACCGCCCAATTTCC  
ACCGTTTCGCTTTTATGCCGTGAGGAAGTCGGGATCTGTCAGCGCTGATGAGTCTGCTGCGCTCGAAGTGATAGAAAGTTTGAATTTTCGCCCCGGCAAGAGGGGAACAATCAACTTTGA  
TGAAAACGATACCTGCTTTTCGGGCATACCGGATGTGATGAAAAACCGGAGAGGGCTTTAAAACGGAAGATGTTGCGGAAAACTTTGCCCGCTGGAATTTCCGGCATTTGACCGCATG  
AAATCATATCCCAGCTTTTATTGCAAAACCATCTTCGGGGCTTTTCTGTTTCACTCAGACATGCAAGCGGGCAAAACCTTTTGTAGAACACAATAACCTATGCGCCGCGCTTTTACAACT  
ATGCGCGCCCTTTGTGGAACAACGCTGCGGAGGATTTGTCTGCTGTCCACCTGTACAAAGAAAGCGCCCTCATTCGATTCGATTCAGGGCATTTGTACATTTATGCGGCAATTGTGCGGCAATTGTGCGGCGC  
GATGACCAACACGAGGCATTGATTGAAACGGCTGCGCAAAATGTGAACAATCGTCAGCGCCACGCGCGACGGTTTGACATTCATCCGCTGCGCAAGTGATGTGGAAGAAATATTGCGCAGAC  
TTGGCAGACAGGCATTTTCTGTTTTCGGCGGAT

**SEQ ID 3844**

SEQ ID 3844  
LMYESKAFSQTAINALAEACARMMLKPTAAAKAKVLELGCSMGRNIITQALYTPDAEFVGIDLSGRQVAGQNAIIEKMGLNVRLSEEDKILTVDSEFGKFDYITVHGWSKRVPAVDKDKIF  
SICRNNLTVEYGIAYISYNNYVPGWKREQQLRDMQFAGRDALGEPLAERTKGLDAIKALAEILENDKGLGGGKLPAIQKILNHNNTYYAHEYMEIFNDPIYVNGPIEWANRHRLAYIGTD  
LHVSFVSMABETHREKRIKALAGGYIAKEFYSDILSDRQPHRSILCREEVGDTVRDESVAVEVIESLNFRPARGETINFDENDTLSSGIRDVMKTGEAFKTEDVAENLARRPGLLEFDRM  
KINSQILLQTLIGRFVSSSDNAGKPPFEDHKTYVPARFTNYAAAFVEHGAGAFVRPNRNVSTPSFGYGHLYIMRQLSRPTSKQALIEFVAENLIVSATPDGLTFHPHAEVYVEEILAD  
LADRHFLVSAD

**SEQ ID 3845**

SEQ ID 3845

ATGAACACAGACATTACCTTGCCCGATACGCGCCGATATCCCCAAAATCCGATTAAAAACCACTGCTGCTCAATGCTACCAAGTTGGCGCACAATTCGTCACAGGCTTGCGCGAACTTT  
CGTCGCGGACAGCTTCAAACCGAAATCAGGGGATGCTTGAGCAAAACCACTATATCAACCTTTCCCTCGCGCTGACGATGTGCGCCGATGCCGGAATTTATGCGCGCTGCTTTCCAGTGT  
GAA CGCGGATCTCGATTGCGAGAAAGAAGCGAAGTGCAGTGGTTGCGCCTGCCGTCGTCGTGTGTCGCGTGCAAGAAAGAACGGGCAATCGAGATGAAAGCTGCCGACGGAGGCATTG  
TTTGCTGCTGCAAAAATATCCGCACCTGCGCGGTTGACGCAAGAGACACAATGCTGCCCTTATCTTGTGCAATTCTCCGATTGTAGTTCGGGTGCGCGCGGATGAGTGGTGGGTGCCA  
AACAAAATACCGAAGCGGCGCGCAACACTTACGCGGTTTGCGCCCGCGCCCTTTGCTGTTGCGCGAAGGGCAGTCCGTCACGTCGTTTACGTGCTGGGTTTGGCAGCGGCAAAATTCA  
GGCGGCATTGGGCGAGAACCTTCTTTCAGGCAGGCTTGCCCTTAATGCAGGTATGCGCAGGAAAATCTTGCAATCGGAAGGCATTACGCTGTTTGCCTAACCTCCGCTTTCCCGGATACCCCGGG  
CGCGCGCTTTCAGACGGCAGCCACACGCGCAACGATATGGCGATGGATGTTTTTGCGGCAACCGCATACGCGCGTCAGGGTCGCGGCGCTGCGGCGTGGGTGCTGCGGCAAGG  
CGGGCGGACAGATTCTATTCCGATTATATGCGACCGACGGCGCTTTGAAGTCTGTCGCGAGGTGTTTTCGCGGACGCTTTCCTTTACCGATAAATATGCGCTCATCCAGCAGAAATTTCT  
CGACCTGATGGCAGAAATGCCGTGTAGAACACGTTTACCTGCTGCACAATCCCTTGGGCGAACAGGAAAACATCCGAGCTATGCGGAAGCGTTGAACCGGAAGGCGCAATCCGTTTTTC  
AGCGCA

SEQ ID 3846

SEQ ID 3846

MNQFTFLPDPTRPYQNPFIKNHILLNAYQLAHNSQASRKLLSSGQLQTEIRGMLEQNHYINLSLALMTSPDAGTYAALLSSVNAVLDCEKEGEVQWFPALPVVLVSGCKKERALEMKLPTRAL  
 FACIQNYPHLRALQTQETQWLPYLTVHSSDLSAVAPDEWWRAKQNTAAQAHLRRFAPRPLLLPEGQSVHVYVVLGFGSGKVQAALGQNTLLQAGLPLMQVQWQENLASEGITFLFANPLSPDTPA  
 RALSDGSHTRQRMAMDVFAANAIRAVRMQGRVGVVAAAKAGGQILFGFNATDGAFEVVQVQFCWQLSFTDNTIAVIQQNPLDLMAECRVEHVYLLHNPLGBQENIPSYARALKREGRNPPF  
 SA

SEQ ID 3847

SEQ ID 3847  
TATGATGCGTACGCTGCGTGGTCAAGCTGCGCGGATATTGGGACGGATGCTGCGGATAAAAAAACAGCGGCAATGCCGCCGTTTCCCGTTCAACCTCGCCAC

SEQ ID 3848

YHSNLRCLKPCPDRTDACR\*KNSGKCRFPFKPRH

**SEQ ID 3849**

ATGGGAATAAAAAATGAACAAATAATAATTTGTAAAAAATATAATACAGAAATATATCTGTTTCCGATGTTTCAAAAAATCGGTGTGTCTGAAAATGTCAACAGACAGGCCCTGTATCCGA  
TTCACGGGTAAAGCGACCTGCCAAAGGTGATCTAACGGTTGGTATATCTGGGCGGTGAAAACTCTCTCATGATAAAAAATTTTTCTGCCCTTGCATACGTTCCATTTCGAAATATG  
CGACCCGGAATCATCCCTTTTTGACACTCCGCCCGGTACCCTTTTTTAATTGGGAAAACGGTTATGAAGACGTATGTTTGTGAAATGCTATTAAATGATAAT

**SEQ ID 3850**

NR090807.1

MEQ ID 3850

MGIKNEQIIICKKYNTETYPVSDVSKIGVAENVKQTGLYPINGLRHRPKGDTNGWYTWAGENFSYDKNFPLPLHTFHLLQIWRFEIIPFLTLPPGYRFLIGENGYEDVWFDELLLN

**SEQ ID 3851**

GTGGAATGTCCTCTGCTGCTGCGGTGATGGGGGAGAAGGCACGTGATAGTCTATCCGACATTCTCTTGACCTAGAAGAAAAATGTCTCCAAGTCAGGACCTTTTGGACAAAAAGAAGTCATCGCGCTTACGTTTCAAAGAAACAACATAGCCCTATTTCGAAGTTGCTGATTGGTTGGTCTTGGAAAAATCCCGCTAGAGAAACGAAATCCATTACAAATCCAAACTCGTGGTATTGGAGATTGATTCGCCACCTCATTAGTCAAGAAATTAAGAAATCTATATTGGCGTTGGCGGTACGGCCGGTAATGATGGAGGTATTGGGATTCGCTGCTGGTTAGGTTATCAATTTTATGATGAGATGGAAAAATGCGCTTACCCGCTTGC GGCTCAATCTCTPACATAAACCCAGCTTCTGTTTCAATAGAAAAATTCGCTATGAAATTTCTGAAGATGTTTCACATTCGTAATTTTATGACAGATGTTGTGAGTCCCTATGTGGACACCAAGGTGGCGACCTATACGTTTGGCAAGCAAAAAGGGCTGGATTCTACTATGTTTGGAGCCGTAGATCAGGCAATACCAAGATTTTATTGAAAAAGTCCCCCTGCACAAATTAATAACTTAAAGGAGCAGGAGCTGGTGGAGGACATCGCTGGTGGTTTGTGTGCTTTTGCTCAGGCAAGTATGATATCTGGAATTTGACACCTGCCTGGACTCGATTGACCTTTGATTAAGAAA GTGTCAGATGTTGACTTGAGTTATGCTTGGTGGTGAAGAGACATAGACTGTTTGAAGTTTATGACGGAACCGCTATTTCGTGTAGCAAAAAGAACCCCTGTCGGAGTTCCGTGTCGCTATTTGCGCGCTTACGCTGAGATTTCGCTTACCATTTCGTTTGGAAATATCCAAGCTGCCTTTTCTATTTTTGGAGAAAAGTGAACTTTAGAAATGCCAGTCTTTATTTTGGA GCATACGGCTTCTAATATTGGATATTTATTAATAATATGCGCTAAGATT

**SEQ ID 3852**

SEQ ID 3692

VECLICPVGGGEGTVDAIRHSLDLEEKCLQVTGPFQGEVHRYFQKEQLALFEVADVLGKIPLEKRNPLQIQTRGIGELIRHLISQEIKEYTVGVGGTAGNDGGIGIAAGLGQTFYDE  
DGNALPACGGQSLLNPASVSTIENRYBIPEDVHIRILADVVSPLCGHQGATYTFGKGKGLDSTMFEAVDQAIQDFYEVKVPATLKLKGAGAGGGIAGGLCAPAQASTVSGTIDTCLDLIDPDK  
VSDVDLVIVGEGRLDRQSLAGKAPIGVAKRTFVGVPVVAICGSFAEDLPSLFFENIQAAFSILEKSEPLDSLKNASLYLEHTASNIGYLLNPKI

**SEQ ID 3853**

SEQ ID 3853

ATGTTTTCGCGAGGTTCCTTCCTATCTGCGGTACGATTAACCGGCGCGATGCCGCTGTGAAGGGTTTCGCGTTTCAGGCGGCATCCGCTTGGAACAGGGATGGGATATGAAAAAACCGAANAATCC  
TTTTCGTCTGCCTCGGCAACATCTGCCGTTTCGCCGATGGCGGAATATCATTTTCGCCGCCGCTGCCGCGGAAGCGGGCATTTCCCTTCGAAACCGGACAGCGCAGGGAATCTCGGGCTGGCAGCA  
CGCGCGAGGATATGCAACCGTGAAACCGCAAGATATTGAAAAAATCATCGGCATTGACGCTTCAGGCTTTACAGCGCGCAAAATCCGCCAAAGCGATTCGACGAGCTTTGACTCATCATCATCGCT  
ATGGACCGCAAGAAATTTCTCCGAATTTGAAAAAAATTTTCGCGAGGCGGCCGCGGAAAGCATTTTCAAGCTGACAGACCTGATACCGCGAAAGCGGATGACAGCGTCTCCGCGATCCGCGGTACA  
TGGGTGATTTGAAGCAACATACAGCGTTTCGGGATGTCAGGCTGTCCGGCATTATTGGAAAAGATTTCCCAA

**SEQ ID 3854**

SEQ ID 3854  
MFQVQLPYAVTINRPMPSERVSASGGIALEGQWDMKKPKILFVCLGNICRSPMAEYILRRRAAEAGIPELTDTSAGTSGWHDGEDMRETAKILKKYGDASGFTSRKIRQSDATAFYDIIA  
MDGNLSLELKEKTFGRRPKEKIFKLTDLIPESGYDHPDPWYMGDFESTYRLADAGCRALLKISK

**SEQ ID 3855**

SEQ ID 3855

TTGCGGATGACGCGTGTGGGCGATTATTGAAAAAGATTTCCAAATAAAGCAATTGAATACAAACACAATAATAAAACCGCGCTCTGTCGTATCGTGTGTTGCGAGGCATAAACAGGGAAT  
TTATGAAACAATAATTCAACAGAAAAATTATGCAACAGGCACGCAGAGGAGACTTGCAGGTAACCGCTTTGCGGCGACAGGTAATAGATATTGCTCTGCAGCAAAAGCGGCGTGAATTAAGC  
CTACAATGTTTGTGCAGATGACGCGCAGAGCAGAGCGTGTCTTGCCACCGCTACCGCTAACCGTGCCTGATTATTTGGCGGGATCAGGGCGGTTTACACAAATGGCGCGCGTCAAC  
GGCTATATTTTGCGCAGCCAGCGCAGACGAGTGCACAGCACTTGCACACACCGACGAAAGCGGACCGTCAATTTTGGTCTGCACGAATGCGCGCGCGCGGACG  
AGCAAAACCTTGCCACAGTGGGCGGCATCGCTGCAGGCGTGGCCGAAAGCGGTTTGGCGCTGAAAGAAGAACGTTGTTTAACTGGAATCTGTAAAAATGTGAGAAG

**SEQ ID 3856**

SEQ ID 3856  
LRHQAVGHYWKRPNKAIEYKHKYKTASCRIGRSDGINREFMKNTFNKQIKIEIQAARREDLQVTALREQVLDIVLQQSGVIKAYNVLSQMQQSGEGVLAPPTAYRALDFWADQGVHLHKVAAVN  
GYLLCSHAQHECNDCHDHEEARAHSAPILVCTEGCAADEQTLSEHWAAALRAGVAESGFALKEEHVVLPGICKKCK

**SEQ ID 3857**

SEQ ID 3857

ATGTGCAGAAGTGAIAAAAAACCAAGTCCACCTGATTTCAGGTTTTCTGGGAACAGGCAAAACACCACCGCGCTCAAAGCCCTGATGGCGCAIAAAGACCCGAACGAAAAATGGGTGATCATCG  
TCAACGAGTTCGCGCAAAATCGGCATTGACGCGCGGTATTGAGCGCAACAGGCATCCCTGTGGCAGAAATCGCCGGCGGCTGTTTATGCTGCACCGCCGCCCGCGCAAAATGGCGGTAAACGT  
GCAGAAATGCTGCGCGACGCCAAACCCGACCGCCTGATGATTGAGGCAAGCGGACTGGCGCAGCGCGCCAGCGTCATCGAGCAATGAAAGCAAAACCTCTGGACAGTCTTTTGGAAATC  
GGCGCGGCTCTTACCGTCGTGATCGCGGCAGTTCATCAATCCCGATTACGCGCAACAGGCGTGTGTATAAAGACCAAAATCGGCATTTCGCAGCTATTGGCGCCGAGCAAAACCGATTATP  
GCACCCCCGAAACAGCTTCGCCGAATTCATGACAAAGCGGCAAAACTGTTCACCACCAAAAGCTAAAGTGGTCGAAGTCCAAACGACCAACTTCGATATTCCTCGTAGT  
TGAAAAATCACGCTACCGCCTCAAAGCCCTGCCGGACAACACCATGGGCTTCAGTGCACAGTTTACATATTCGCGCGGACGGCATTCGAACGGGCAAAATATGACCAACTCTTCCCTCAAT  
GATTTGCCCAAAATGACCGAAGGACTGCTCGCGCCAAAGGCGGTGTTCCAAAGATTGGGGAAGCTGGGTGTGGCTCACTGGGTGGACGGGCACTGGGGCGCGCAACCAAGTGTCTTGGCGGC  
CGCATTCGCGTTTCAGCTGATTGCGCAAAATCGTTTGACGCGGATTTAATCGAACAAAACTTAAAGACGCATTGGAA

SEQ ID 3858

SEQ ID 3858

MSEVKKTKVHLISGFLTGKTTALKSLMAQKDPNEKWVIIVNEFGEIGIDGAVLSNDNGIPVARIAGGCLCCTAGPQGVTVQKMLRDAKPDRLMTASGLAHAASVIDELKAKPLDSLLEI  
GAVPTTVDPRQFINPDYAQQALYKDQIGICDVLAASTKDTLCTPEQLAEPHDKAAKLFPKAKVVEVQNAQLDQIQLDTPVVEKSRYLKALPDNTMGFQSQGTFPAGRDNGEKLTNFFN  
DLPKMTPEGLVRAKGVFQVLGTWVLLNWDGQGANQVSWRRDSRFELIAKSPDADLIEQKLKDALE

**SEQ ID 3859**

SEQ ID 3859

ATGAAACCAACAATTCAAACCGGTTTAAACCGCGCTGCTTTTGGCGGTTTCCCTGCGCTCATGGCGGCAACCCGCGTCTCGATGGAAACCGATATGGGCAATATCCGTTTGGTTTGTGACG  
AATCCAAAGCGCTCCAAACCGGTTGCCAATTTCTGCGCTATGCCCGAAAGGCTTTTACGACACACAGGATTTCACACCGGTCATCGCGCGCTTCGTCAATCAAGGCGACGGATTGACCGA  
GGACTTGTGTCAAAGCGCAACGATTAAGGCGGTTGCCAACGAATTCGGCAACGGCTTGAAAAACAACCGTTCCGGCACCATTCGCAATTGGCGCGGAGCGGACGCCGCCGATTCCGCGCGGCCCAA  
TTCTTTATCAATCTGGCGGACAACGGTTTCGCTCGACTACAAAACCGACAATACGGCTACACCGTTTTCGGACGGTAGAAGACCGGAATGGACACCGTTTCCAAATTTCCGCTCAAAA  
CCGCCACGCGCGGCTTTTCAACACCGTACCCGCTACGCGCGTCAAAATCCGTCGCGTTTGTGTCGGGCG

SEQ ID 3860

SEQ ID 3860  
MKPKFTVLITALLLAVSLPSMAATRVIMETDEMGNIRLVLDSEKASKTVANFVRYARKGFYDNTIFHRVIGGFVIQDGLTEDLVQATDKAVANESGNGLKNTVGTITAMARTAAPDASAAQ  
PFTNIADNGSLDYKNGOYGTVFGRVESGMDTVSKLARVKATATRGFYONVPVQPVKIREVVVGG

SEQ ID 3861

SEQ ID 3861

GTGTACTGCCCGACACAACACGCGACGGATTTTGACGGCGTACGGGTACGTTTGATATAAAGCCGCGCTGGCGGTTTGTACGCGGGCGAATTTTGAAACGGTGTCCATTTCGCTTTC  
ACCTCCGCGAAGAACCGGTGAGCGGATTTGTCGCTTTTGTAGTCGAGCGAACCGTTGTGCCCGAGATTGATAAAGAAATTGGCGGGCGGGCGGAATCGGGGGCTGCCGTCGCGCCATTGCGA  
TGGTGCCGACGGTGTGTTTCAAGCCGTGCGCGGATTCGTGGCAACGGCCTTATCGTGCCTTTTGCACCAAGTCTCCGTCGAATCCGTCGCCCTGGATGACGAAGCGCGGATGACGG  
GTGGAAAATCGTGTGTCGTAAGAAAGTTTTCGGCGCATAGCGCACGAATTGGCAACGGTTTGGAGCGTTTGGATTGTCGTCAAAACCAAACGGATATGCCCATTCGGTTTCCATCAGG  
ACGCGGGTTGCGCGCTAGACGCGCAGCGAAACCCGCAAAAGCACGCGGT

**SEQ ID 3862**

VLFPDNNATDFDGLGYGVYLKAAARGGFDAGDGPNGVHSAPYPAENGVAVLVSVPVVERTTVVRQIDKELGGGGIGGCCRPCHCDGADVFPQAVAGFVNGNLIGCLLHQVLQGSVALDDEAADDA  
VENRVVVKAFSGIAHEIENGFGGFGFVQNTDIAHIGFHODAGCRRHRROGNROKQRG

SEQ ID 3863

TTGTTGTCGGGCAGTAACACGCAGACAGACGTTTCAGACGGCGTCGCCGTTTTCCCAAAAAACGCCGTTTAAAGTAAAAAAATATTTTAAACAGACAGT

**SEQ ID 3864**

LLSGSNTQTDVQTASPVSQKTPFKVKKYFKTDS

SEQ ID 3865

ATGCGTCTGAAACCTTGCCCCGATATTCGGACGGATGCCTGCCGATAAAAAACAGCGGCAATGCCGCCGTTTCCCGTTCAAACCTCGCCACGCTCTTTTAAACAGCA

**SEQ ID 3866**

MPSETLPYSDGCLPIKKQRQMPFFVQTSPRSFKTA

**SEQ ID 3867**

ATGACGACAGCCCGTACCCGCGGTATTGCGCAGCGTTTTTTCACAGTCAAATGCCCGTCTCGCCTACCGCGAAGGCAAATGGCAGCCGACCGAATGGCAATCTTCCCAAGACCTTACCCCTTG  
CACCCGGCGCGCATGCCCTGCATTACGGCAGCGAATGCTTTGAAGGTTTGAAGGCCCTCCGTAGCGCAGACGGTAAATCGTGTCTGTTCGTCGCCAGCGCCAATATCGCGCGTATCGGCGA  
AAGTGGCGGACATTTTGCACTTGCBCGCGCCCCGAAACCCAAAGCTTATCTCGATGCTTTGGTGAACTGGTCAAACGTGCGCGCGACGAAATTCGCCGATGCGCTGCGCGCGCTGTACCTGCGC  
CCGACCTTAATCGGTACCGATCCCGTTATCGGCAAGGCGCGGTCTCTCTCCGAAACCGCCCTGCTGTATATTTTGGCTTCCCCCGTGGCGGACTATTTCAAAGTCGGCTCGCCCGTGAAAA  
TCTTGGTGGAAACCGAACACATCCGCTGCGCCCCGCATATGGGCGCGGTCAAATGCGCGGCAACTACGCTTCCGCCATGCACTGGTTGCTGAAGCGGAAAGCCGAATACGGCGCAAACTA  
AGTCTCTGTTCTGCCGGAACGGCGACGTTCAAGAAACCGCGCGCATCCAACCTTTATCTGATTAAACGGCGATGAAATCACTTACCAAACCTGTGACAGCAAGAAATCTCTCCGACGGCGTTACCGCG  
GATTCCGTGCTGACTGTGCGCCAAAGATTTGGCGTATACCGTCAGCGAACGTAAATTTACCGTTGACGAACTCAAGAGCTGTGGTGAAGAAACGGTGGCGGAAGCGATTTTGAACGCGCGCGCG  
CCGTCATCTCGCGCGGTACTTCTCTGTCATCGCGCGCAAGAAATCGAAGTGAAAAACCAAGAACCGGCTTATGCCATCCGTAAAGCGGATTACCGACATCCAGTACGGTTTGGCGGAAGA  
CAAATACCGCTGGCTGTGCGAAGTGTGC

**SEQ ID 3868**

MSRPVPAVFGSVFHSQMPVLAYREGKWQPTWEQSSQDLTLAPGAHALHYGSECFEGLKAFRQADGKIVLFRPTANTIAARMQASDILHLPRPETQAYLDALVELVKRAADEIPDAPAALYLR  
PFLILIGTFPIVIGKAGSPSEETALLYLASVPVGDIYFKVGSVPVKILVETEHIRCAPIHMGRCVKGCGNYASAMHMLLKAKAEYGANQVLFPCNGDVQETGASNFILINGDEITTKPLTDFLEHGVR  
DSVLTVAKDLGTVTSERNFTVDELKAAVENGAAAILGTAAVISPVTSFVIGGKEIEVKNQERGAIKAIKATIDIOYGLAEDKYGNLVEVC

**SEQ ID 3869**

[illegible]

**SEQ ID 3870**

MLPQTQPNPTQPNPTQPNPTQPNPSPLSDTAGANTEAITYTSDGITANSTQLEBQKKLFPACFDADGNFLIDRLQAEIAPQTDIGREFYEMNWLKGSYARLLRNLPEPTLISEOKTHNAKPE  
NAGSQNLLIRGDNLEVLKHLKNAYANSVKMIYIDPPYNTGSDGVQDDRKFTPAELALLANIDEDEAARIIDFTDKGSNSHSAMLTPMYPRLYIARELLKDDGVTFISIDNBEAAQLKLI  
CDEVGEGENFVAQLPWRKRTAKSDVPPGISQDYEWIFVPAKSCQFIAATKGKERRYIETDDPDRPWRTHDLTKQTTAAERPNSPFTMVDPTKGKYPANENATWRVTKDTFYDYINKGKI  
VFPDDYDFLINSNPMFYFQDDDKKAAGEDGKVAVSSRLPENGVLADAVAEYLAIFSRTLGPNLIMGTKEGTKEITDLPGSKIPFTPKPSPQLIKPLWISISSKNLGLDFFAGSGTTHA  
VMQLANDEGNRRYICVQLPEKTAKEKSPARKAGYPTFIDITKARIEKAAAKIRV

**SEQ ID 3871**

TTGCGCGCTTAACGATGAATTAAAGCGAAGAACAGCTGCGAAACGCTTCTGACCACCTGGACGCGTATGACGGGGCGGCACTGACCACGCGCGGTGTGAGCCTGTGCGGTTGGGCCAGTTATACGG  
CGTATCTGTGCGAAAAACGGCTGTATCTGCTTTAACAGAGGTTTTACTTCCGCGGATTGTCTGGCGTTTATCAAGAAGCTGGACGACGATGCGGATTTCAATCCCAACCGTGTGATTGTATT  
CGTAGCAATATGGCAGCGCGCATGCAAGCAGAACTCGACACGGCGGTTCGCGGTTATACCAATAAAAAAGAGATTGAGTTGAATGTGATTATCAGGGTGTG

SEQ ID 3872

1.PLNDELSEEOLOTLLTFTWLYDGAALITTPVEPVRLGSYTAYLCEKRLYLNNKGFTSADLLAFIKKLDDADFNPNRVIVFGSNMASAMQHELDQAVRGYTNKKEIBLNVIIRV

SEQ ID 3873

ATCGCGGGCGGTTTCGGCGGTTTGGGCGTGTTTGACGGGGCAACGCCAAATATCGGACGGCAGCAGAAATCCCGAACTTTTGTTTGCTGCAAAACAATACGCAAACAATATCTCGAAAG  
TGCAAAGCGAAACGGTATAGACGGCCGATTCCCCGACCGTTTCGGACGACCAAAATATCTTGAATATTTCCATGGAAACGGGCACGGGCAAAACCTATACCTACACACAAACCATGTTCGA  
CTGTCACCGTTGGCTGGGCGTGTTCAAATTATCGTGGTCTGTCGCACTTTGTCCATTAAAGCGGGAACACAGCAGTTTTTGCAAAGCAAGGCTTTGGCCAGACATTT

**SEQ ID 3874**

MRRAVSAILGVFDGATPKYRTADENPELLFAAKOYANNILKVQSONGIDGRFPDRSDDONILDISMETGTGKTYTYYTQTMFELHRWLGVPKFIVVVPFLSIKAGTQQFLQSKALARAF

SEQ ID 3875

GTGGTGGAAAGCGCGAAAAGAATAAGGCGAAAAAGTCCAATGCGCCCATACGATTGACGAATTTGTCAAAGCGGAAAAAAGGAAATTCATGTGCTGCTGATTAAACGCGGGCATGG  
 TTAATTCGTCGTCATGAACGATACGGGCGACAAGGCATTGAAGGATTTGTTTGACAATCCCGTTGATGCAATTGGCTGCCGTGCGCCCGTTTATGATTGTGGACGAACCGCATAAATTCOC  
 GACCCGAGATAGCGCGAAAACTGGGGCAATATCAAACGCTTAAACCGCAATATATTTTGGCTACGGTGCAACATTTAACGATGAAATATTAACAATTCGCTTTACCGTTTGAACGCGAGTA  
 GACGCGTTTAAACGACGGCTGCTCAAAGCGCTGCGCGTGTTTCAGGAAGAATTCAGGCGCGCATGGAATCGCGCGGTAAAACATGGTGTCGTCGCGACGGCAAGAACGGAATTTGAATTA  
 ACGAAAAGGACAAAAGCAGACGTTCAAATCGGCAAAAGGCGAAGATTTGGCGCAAAATCCATCCGGCTATTTCGGAATTGAAAATCGACAAAATGAATAAAACCGTGTGGTGTTAAGCAA  
 CGGCTTGGAGTTGAAAAACGGGTGCCGTCATCAACCTTATTCCTATTTCGCAACCGGTGCAGGATGCGATGATCGACGCGCGCGTTTCCGCAACATTTCAAGCTTGAACCGCGCTTTTGGCA  
 GAACGCGCGCCACAGCCCAAAATCAAGCCGCTGACGCTGTTTATTTAGCAGTATTCGCGGGCTACCGCAGCGCAACGAGCTTTACGCGACCTCGAAGAATATTTGAAAGTGGAGTTC  
 CGCGGAAGCGCGCACCGGCTCGAAAACCGGAGGACCGGCTTTTACCGGATTAACCTGCAAAAAGACGCTTGGACAGATGATTTCCGCTGCGACGCGCGCTATTTTCCAAAGACAATACAGA  
 CCGACGAGTATGAAATCGACGAGGAATCAATGAAATCCTGCACGATAAGGAAAACTGCTGCTTTTGGACAACCCGCGCGCTTTATTTTTCAAATGGACGCTGCGCGAAGGCTGGGAC



AATCCCAACGTTTTCCAGATTTCGAACTGCGTTCAGCGGCAGCAGCTTCCAAGCTGCAAGAGTCGGACGCGGCTGCGCTGCGCGTAAACGAGCTGATGGCGGGTGGCGGATG  
TACCGTACAACTGAAATTATTTGTCGATAGCAGCGAAAGAGCTTTGTGAAGCAGCTTGTGCGCGAAATCAACGACAATTTTTCAGGAAGAAATCCAAAAAGTTTACCGAAGAGCT  
GAAACAAAAAATATTTGCAAAATACCCGATATCAAAACCGCTGTTATGTAACCACTGTTTTAGAGCGCATCATGACGACAATGAAACTTTGCGGAAGAGCGGTATGACAAATTA  
AAAGCGCCTATCCCGAAGCTTTCCCAAGGTTTGGACAAAGGCAAGTCAGCAACGCCAAGAGCAGGGCAAGACACCATCATCATGCGCGAAGCGCAATATGAAGAACTCAAAGCCT  
TGTGGGAGCTGATTCACCAATAAGCCGTTTTGTCAGTACAAATCAAGATGAAGCGCAATTTGTCGATTATTTACCGCTTATTTGCGTGAAGACGCGCGCAAAATCCCGCAGGCGAT  
ATGACGCGCGTAAACGAGCTTATATCAACACGCGCTTATGCTTTCCCGCGCATAGACAGTATTGAAGATGAAGATTTATCGTTTCAACACAATGACTTACCGTGAGTTTCTGGAA  
AACTGGCACAACGCGCAAAATCCAGATCGAGCTTTGTCATCAGCGTTTTACCGCGTCCGCGCAGCACTGAACATTTGGGATTTTTGTAATATGACAGCATCGCCCAAAATCAAAACG  
GCTTCAACCGTTTTGCTTCATCATTTCCATATAATTCGAAGTTCAGCTGTTACCGCTTGTGCGGCAAGAAATCCATCCGACCAAAATTTACCAATAAGAGCGCAAAACCGCGCGGTGAA  
AAAGCAGATTTCGGCAGATTTGAAGATACGAGCAGCGCTGCGCGCGCTATCTCTCGCGGAGATTTTCTACGATTGCGATATAGAACATGAAATGTCGCGCAACCAACCAATGAA  
GGCGTAATCGTATTACCAAAATACCGAGAACTCCATCAAAATCCCTGTTGCGCGCGCGGCACTTTCGCGCGACTTTGCTTATATCGTGAAGCAAAAGCGCGGAGATTCTGAAC  
TTGTGATTGAAGCAAGGAGCTGACGGGCGGAAGATTTCGCAAAAGCGAAGAGCGGAAATCAACATGCGCAAAAGCTGTTGCGGAGATTTCGCAAGAAATCAAGGTGCTTCAA  
AAGCAGTTTGACGCGGAGAGATAGCGCACTGATCGGCAAAATATGCGCAGCGGCGGCTTCTGAAACGCGAC

## SEQ ID 3876

VVESAKNKGKSNAPITIEQPVKAENKKEIHVLLINAGNVNSSMNDTGDALKDLFDNPDVALAARVPMIVDEPHKPTRDSARTWGNIKRLKPYILRYGATTFNDEYVNLVRLTAV  
DAFNDGLVGRVVFQEMQGGMDAAVKLVSSDGKEAFELNEKDKQTFKLAKGEDLAQIHPAISDLKIDKMKNTVVVLSNGLKRTGAVINPYSYQTVQDAMQRAVAEHFKLERALLA  
ERAPQPKIKPLTLFFIDDIAGYRSGNELSGSLKDKFESWIRAEARLRKTESDPFYRYLQKTLDDVSACHGGYPSKDNITSDDRIBQENRILHDKELLSLNDPRPFIKSWTLRGGWD  
NPNVFIQIKLRSSGTTSKLQEVGRGLRPLVNELMARVDPVYKLVNYPVDSSEKDPVKQVGEINDNSPQREISKKFTEELQKILQYDPDIKPLVLVNLQPSDGLIDDNENPAEDGYDL  
KAAYPEAPFKGLDKGVSNKDEGKDTIIMREGKYEELKALWELJHKAVALQYKIKDBAEFVDFLFAVILRENAAKFPQAGICTAVNEAYINNGMLMSRRIDSTIEDDFIRFNTMYREFLE  
KLAQTAQIQMQLHQAQYFVRDELINQDFLNMQTLAQIKNGFNRLLHSHFHFELDYRLVSGKIHPTKTNKDGKPRVKKADLGRFEDTEHRAAGYLFGEIPYDSIEHENVANNQIE  
GVIVFTKIPRNSIKIPVAGGTYSPDFAYIVTKSGEILNFVIEAKGTGDAEDLRKSEERIKHAEKLFPAEISKEIKVVFQTFDGERIAELIQNMPAGHSENGH

## SEQ ID 3877

ATGATCGAGCGCGGCGACAAATCATGGTCTGCGCTCTCCGCGGCAAGACAGCTACGCGCTGTTAGACATCTCGCGCGCTCCAAGCCAGCGCGCGGATGATTGTAAGTGGTGGCG  
TCAATCTCGACCAAAACAGCGCGCTTCCCGAAGAGTATGCGCAGCTATCTCGAAGCATCGCGCTTCCCTACAAATCTGTAAGAGACACTTACTCCACCGTCAACCGCGTGT  
GGACGAAGGCAAAACGACTTGTGCTGTGCGCGCGCTGCGCGCGCGCATCTCTACCGCAGCGCAAGAAATTTGGGCTGCAACAAATCGCTTGGGACACACCGCGCAGCATCTCT  
GCCACCATGTTTTAATATGTTTTACGCGCGCAAACTCAAGGCAATGCGCGCAAGCTGTTAGCGGACAAACGCGCAACACATCGTCATCGCGCGCTGGCGTATGTAAGAAAGAAAGACT  
TAATCAAAATACGCCGAATTGAAACAGTTCCCATCATCCCGTCAACCTCTCGCGCTGCGCGCGCAACCTTACAACGCCAAGTATCGCGCGATGTCGCGGATTTGGGACAAACGCTTCC  
CGCGGATGCAATCGATGTTCTCGCGCTGCAAAACGCTGCTCTCCACCTTGCAGATCGCAACTCTTTGACTTTGCGCGATTTGGAACCGCTCAAAATCTGAAACCGCGCGGAT  
TTGGCTTTGACAGCGAAATAATGCCGCAACGCTTTTTCAGCGCGCAGCAAGAGATGAGAGCGAAATCAAAATCGAGCGCAAAAGCGCAACGCAAGTCAACATCTCGCGCAAC  
AGCGCAAACTCGCGCGCA

## SEQ ID 3878

MIKPGDKIMVCLSGGKDSYALLDILRLQASAPIDFELVAVNLDQKQPGFPPEEVLPTYLESIGVPYKIVEEDTYSVTKRVLDGKTTCSLCSRLRRGILYRTAKELGCTYKIALGHRDDIL  
ATMPLNMFYGGKLRAMPFKLVSDNGEHIVIRPLAYVKEKDLIKYAEKQFPPIPCNLCSQPNLQRVIGDMLRDWKRFPGRISMPSALQNVVPSHLATBELFDFAGLERGQNLKRGDD  
LAFDSEKMPERPSDGSSEDESEIKIIEPKAERKVINILANKPKTCGP

## SEQ ID 3879

AACCTCGCCACGCTCTTTTAAACAGCATAAGCCGCACTTTCTCCCGTGGGAATTTTTAAAAAACCATCACTCTTTACGATTTCATGCACTCTCTCACTGATTTCCTCGCATATTTCC  
ATTTTCAACGCTTATGCTGATTGCGCGCTTCAATCAATCCCTCGCTACTGCTTTTGTGCTTTTCCACACTACCCCAAAACCCATAATCATGCTTCAATCGTTTCAATAAATAA  
GGTCTGTTTCTGTCAGAAACAACGACAGTTTATAAATCTCGGAAACAAATGCGCTCTGACGCGCGGATAACGCTTCAGACGCGAT

## SEQ ID 3880

NLATLP\*NSISRTFLPCGIFPKRTITLYDFMQLLT\*FLRIHFQRLMLIAGFNQSLAYCFCCFSHTTPKTHNHVLQSFQINKVVSVKKQROFINCRKTKRLNAG\*RFRRH

## SEQ ID 3881

ATGATGAAACCTTACTGCCCTTTTTTGGCGTGGCGCGCTCAGCGGCAAGACCGCAAACTTCTGCAACGACAGCTTCCAACGACATCAATAATCTTCAGACCGGCGAGCGGTGTT  
ACGCGACTTACACAGCGCCAAAGGCGCGCTCATCGCAATATGATTGTCGTAACCGTGGAGACGATTGTCGCTGATTATGGCGCAAGATTGCTTGAAGCAACGGTCAAAACCGCTGCA  
GATGTTGTGTTGCGCGCAAGCCGTTTTTGAATCTCTGAAGATTACCGCGTGGCGCGGAATTGGCAGCATCGCGCAACCGCTTGGCGCGCAAGAACCGAGTCTCGCTTTACTCT  
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AAATCCGACGCGTTATCGGTGATGTCGCGCTACCAAGAAACCGCGCTGCGCGCGCATCTTCAACAGCACAATCATCGCGCGGTACACTTCAAAAAAGGTGCTACCGCGGACAGGA  
AATCATCGCGCGGCTCAGTATCGGGGCGAGTCAACCGCGCTTGGCGGTATTGTCGGAAATTCGCGAGCGCAAGCGCGCATCTGCTGACGCGCGAGCGCAAGAACCGCGCATCTGTA  
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AAACCAAAATGCGAGAA

## SEQ ID 3882

MKTKLLPFFGVARVSGEDQTFLLHGLSNDINNLTQACQATYNTPKGRVIANMIVNRRDGLLLIHAQDLLEATVKRIQNFVLRKAVFREILEDYAVGAELAAAEPLAAQEPSLAFTS  
ECVSDGICSVILHHRGILHIAPEALPPYDAAENANRLHEIRSGYPWICATKETAVAQMLAQHILIGVHFHKGCPYQGEILARAQYRGQVQRGLAVLSGNSAAEAGILLTADGERAGIV  
LDSVQSENFTALAVIKFSAQKELFVPPNGGIFRAVHLFPKTKNAE

## SEQ ID 3883

GTGTTATCGGATAGTGTGTTTACTCATTTTCTGTCATGCAAAACATGGAATTCGGTCAAGCGCAATGTTACCATATATCCCTTTATCGAAGGAAACCGATATGGATATCCGGTATTTCC  
GCACAACGCGCGCTATTCGGAAGCGGTTTGGCGGGCGGCTTGTATTTCTCTCCGCGATGGTTCCCGAAACCGTGAAGCGGCTGCCGAACAGACTGCCGACGCTGCTGCCCAACCGA  
CGCGTGGTGGCGGAATGCGGCTCGGACAAGGACACGTTTGGATGCGGTATCTACCTGCGGTATGCGGCAATGAAACCGGCTGCGGACGCTTGGGTTGCCCGCGC  
AGAAGCGCGCGCGCGCTGCGTGAAGCGCGCTCGCGCGTCCGAGTGGCGGTGCAAAATCAAAATACCGCGTGAAGAGAGACGCGGCACTGCA

## SEQ ID 3884

VLSDKCVYSFFVMQMEIGQAQCYHISPLSKETDMDIRYFGTTPRYSEAVCAGGLIFLSGVPEWGETAABQADVLAQTDKWLAECSGDKAEHLDAVITLMDGVDAEMNGVDAHVAAG  
RTPARACVEARLARPEWRVEIKITAVKRDAATA

## SEQ ID 3885

ATGAGTAACACACTTATCCGATAACACCTGCGGTACGCGTTTTGCGTGAAGAACGCGCATCGAATTTGAACCTTTTACCTATGCTATGAGGAACACCGCGCGCAGCGCGACTTTGCGCGSAC  
TGTTCGGCAAGACCAACTTGGTCAATTAACCAATGTTTTCAGAGATGAAACCGTGAAGGGCGGATGCTCTTGTATGACGCGCGCAACAGATTTCACCCGCAATCTGCGCGGCA  
TTTGGGTGCGGACACATCGGAACCGCGCGCTGCGCAGGCAACAGTGGACGCGGCTATCTGCTGCGCGGCAACACCGCGTTCGGCATCCGGCAAAATTTGGATATTTACGTCGAACAG  
TCGGTATGAGATTGGAACCACTATATCAATGGCGGAAACCGCGGTTCATTATCGGTATCCGCGCGGATGATTTAAATTTTGAACCGCAAAACCAATACGCGCGGCTT

## SEQ ID 3886

MSKHTYPTPAVRVLRNGIEFEPTTYAYEEHGGTAQFARLFKDEHLVLTIVLQDENGKPIVLMHGDQIISTRNLARHLGAKHI EPAAPQAQNKHTGYLVGGTTPFGIRTKLDIYVQ  
SYMDLETIYINGKRGFIIGIRPDELNINPKTIQAAV

## SEQ ID 3887

ATGGACAAAGATTGTATGCCGATTGGCGTGTGCCGCGAGCGGGGGCGGACGAAATCAACGCGCTACCGCAAGCTGGCGATGAAATACCATCCCGACCGCAATCCGGGCAATCTGC  
AGCGCGAAGAAAGTTTCAAGAAATCCAACGGGCTTACGATACGCTTTCCGACCTGTCAAAACGGAGCAATACGACGCGTCTTACAGCGGATGAGGAACGCGGGCGGAGGAAGAGGC  
ATTCCGCGCGGAACAGCGCGCGAGGAGAGTTTACGGCGAAGCAGATGCCCGCGAACAGCGGCTTACAGCGGAGTTTGAACGGCAGGCTTACGCTTCCGCCATGCTTACGAACCGGCTC  
GGCAGCGAAGCGGGCGCACTATATCTCCGCGCTACATCTGTTGGTGTGGTGCATATACAGTTACGCCATAGTGGCGGTGATTCTCGCTATATGAAACGGAAACAGTTTGG  
ACAGCATTTGCTATGCCGACATACCGAATACCTGATTAAACCTTTTGGGCGACATTTTGGCTTTATCTTTTGGGCGCGCTGACTGCCGCTTCCGCAATCGCGCTGCTGTTATTATTC  
AACGACCGCTGCTGATTCTACCGCATCATCGCGGCTTATCCGCTTCAACGACGCGAGGCGGCTTCCGCGGAGAAATGGATA

## SEQ ID 3888

MDKLYAVLGVSPQGADEIKRAYRKAMKYPDRNPGNLQAEKFKETQRAYDTLSLKRITQYDASFRHEERGRQEEAFRRBQARRBQFYGBQMRREQAFRRERERQASRSRHAYEPS  
GSGSGRNYLLAAYILFGLGAIQFMPFVGVILAYMKRNSLSDIVVAAHTEYLKTFWRFTWLYLLGALFARFAGIGVLVLIATFWYFYRIIAGFIRFNDGRAVAPKMI

## SEQ ID 3889

ATGGCTTACCTGTAAATCAGCATCGTTCAGCGTGTCCGTTTCCATTTTGTCTGAAATGGCAAGGAAGAAAAATCGACATCGCGAGCGGCTGCGCGTCAATATGTGGTCCGCGTCA  
TACTGACCTGTCGCTATTGAAGCGGATGTCGCGCAATATCGGTGCATTTTGGCGAGCTGGCGGCTGTTGGCGCTTTGGCGTGTCTGCGCTCCGATTGTGCTATTATGGGCAATC  
CGTAGAATCCCGGCTATCGTCAATCCGACGCGCGCAGCGTTTGTGCGCTGTTTACCGATTGTTGCCGCTTTGACGCTGTTTGGCGAAAACTCAGTGAAGGCAATCGATCGGACTG  
TGCCTCGCTTTTGGCGCATGTTCTGCTGCTTTTGAAGAGCGACAGCGCAAAAAATCAGGCGAGCGGTGGCGCGAGCGCTATTGCTGCTCGGTGTGGCGGGTTACGGCATTATCG  
ACATCTGTTTCAACAGCATGTCGCAAAAGCGGACGCGCATTTGCGGCAACCTGCTGTTGCAATTTGCGCTGGCGGTGTGCTGATGTTGCGCTGCTGTTTGGCAATCGGTGAGATGGG  
CGTTGAGAGCGTGGTGGCGGCATCTCTGGCGGCTTGAATTTTATGAACATCGTAACCTACATCACTGCGCACCAATGATGAAGACAGTCCACGCTGCTTTTGGCGGTATGAAAT  
ATCGGTGATGTTTATAGGACGCTTTCGGCGCATGTTCTTTAAGGAAAAATCAACACAATCAATACCGCAGGCAATGACTGCTATTATGCTCCATGCTGCTGCTGCTTCTATTGGA  
CAGAAGTTAAGGCATTGTTCCGCATA

## SEQ ID 3890

MAYLLISIVFSVSVSILKMKRKKIDIAQAVAVNVVAVILTVLVLKPDVGNIGALFPTWPLFAALGVLLPSVFMGKSVESAGIVKSDAAQRLSLFPLVIAALTLFGEKLSGLKILGL  
CLAFPAALFCLLWKSQSGKSGSAWRQALLLGVWAGYGIIDILFKQIAKSTAFAGNLLVAFALAGVLMFACLFAKSVWRVSVVGGILLGLNFMNIVYITTAHQMKDSEPLVPAHNM  
IGTVVLGLSGALFPKEKINTINAGIVLSLCSIACLFYWTEVKALFGL

## SEQ ID 3891

ATGATGTCGCGATTCTCCCAAACTAAGACCATATCTTAAGCCTTGCAGGTGCATTGTCGCGATTGGCTTTTGCAGACACCCGAAACATACCGAACAGCAGAAAGAACTGAATACCA  
TAGTGTCCATGCGAAACGCACTGCGGACCAAAAAGCGCGGACGCTGATTACAAAAACGCTCCAACGCTACGTCGCGAAGAAATACCTCGAACGCTACCGGCTCAATCCGCGG  
CGACGCTACTCAAGCGCTTAAACGGCTGTACAACATGAACACCGCAGCCGCGCGGCGGCTACGCGCCCAACATACGCGGTATCACCGCAAGGGCGCATCCGCTTACCATAGACGGC  
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AATCGGCGCTCGCGGTGCGATGTCATCGCACCATCGAACCTTCCGACATCATCCCCGAAGGAAGAACTGGGGAATTGAAGTCAAAACCGAGTTTTCGCGCAACACCGTGGCGCAGAA  
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ACCGCGCTGTTGTTGAGCAAGGCGATAGCGGACAGAAATCTCGGGCGGTAAAAAGCGCACTACTACGCGGCAACCGCGCTATCAAGCTACCTCAACACCCCTTACCGGTGCGGATGCTGTTACGACCATGATCTCTGA  
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CAATCATGCGCGGAAAAAGATATACTCTGCAATCTTCCGCGAGCTGTTGCCAAATATGCGCGCTGCTGTTCCGCGCGGCGAAGAAATCATGAACGCCACCGGACCAAAATCTCTG  
CTGCTGAAAAACAACTGTTATCTTCCGGAATACCAAAATCAGCTGCAATATATGGAACAACAAATCGGCTTCCGCGGAATCAACCCCTGATTAACGGCATGGATACCTGCTTTCGCGG  
AACAATCCTTAAACGAACTGTGTCAGCAGGACCGCGGCTAGGAGCAAAATCGACAGCAAACTACAAATCGGCTACGAATGGAAGCGCAAAACAAATGGATAGACCTTCAAGC  
CGATATGTTGGCGGTGAAGACGACAGTAACCGCATCAGAGCGCGCGGCTAGTCTGCGGCTCACTACGCTGCGGCTTGTATTGATGACGCTTGTGTTGTTGCAACATACGCAAAACCG  
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AGCTGCGCAGATACGATGAAGAACACCGTCCGATTAACGACCGCTGATACCGCGCTGATGGGCGATACGCGCGGCTACTACACCATCAGCGCGCGGATAAATATGTTGACCGGACAGCAACCAAT  
CGGCAAAATGATGAATCTGCGCGAACTGAAGCAAAAGCTGAATCAGGAACGCTACTACATCGAACATCCCGACCGCATCATGTTCCCGCGCGCGGCGGAGCTACCGAGCTGCTCGCGCAAC  
GTTTCAACCTCAGCAACCGCTCCGCTTTCGACAACTCAGCTCACCTTCCCGCGGCTTACGAGCGGAAACGTTGAAGAACCGACGATACCGGCAACCAATCGGATGATTGATGA  
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CGGTATTACGAATGGCGGATGAAGAGATATTGCCAACCAAAAGCGGATGTTGCGAGCTTTATGATCGCGATAGAGTGTGATGGCGAGTTGCAAGATATCAAGACCTTAAACCGCGTTT  
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ACAAGCTGATCGCGGCGGCGGCGGCGGAGGTATGCGCGCAACCGTAAACCTTACGCTGCGATGCGAGCGGCTTTCGCTTATGATGCTATGCGCGCTTACCGCATAGGGAAGCATATAGACTT  
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## SEQ ID 3892

MMSGFSPKPKRTILSLAGAFALAFADTPNNTQKELNTIVVHGRKSDQKQADDDVYKNSVNAVYVKEYLERYVQSGADVLKGLNGVYNNMPTTAGGATTPNIRIGITGKGRIPVTDG  
TEQTIDVMMNNYGVGDRNYLDPALFRSIAVEKSPALTRGVKSGVGAMSRITPEPDIPEGRNMGIEVKTETSGNTVAQRNDLRQLGRDYRLTSPIGATADGVSGMPDLVLTGTYGKSP  
TALLLDEGIADTKFSGGKSHNTFKDRQLMLSAFKTIDTDLAAYSHRQKNYAGKRGYQSYLANPIYGADACYDQYDPKSWREKIDILCKSSASLVPMAVLFRRPGEIIMNSHTDKIL  
LLKNWYLPDQKISLQYMDNKIFGEINPLITAWILGFAEQSLNEPVOQAPIGITKIDSKTYKIGYENKPNQNKWIDLQADMWRVKTDSNRHSGSGFPVGVITSDPDYDLWYCNIRKRP  
SPNLRGESCESAMTWAYGARSAREEVLRMIEDTPDKIARKLAEDENNRAITDRWMHGTGGYTTIPADKNVLDQTNQIGKMMNLAEKQKLNQERYIIEHPDRIIVPGARQRTDVRN  
GFNLNKLRLSDKLS/LFLAADYQRETFLEERTDTADSNDLNMFTGVLTFRMAALGGPQSAKKREWGANLVFDWPKTSRLNTQAGVRYQNYKNNI ELARQRAARNPWYQVGLSDSYVTGLM  
PYTELAEDEEDIANQKMLQLYDPRADQVAEYQDLNRRPFKEKNYDFDPHDTLVGQDTRFYAKSDGNFVQYADGNKNFDVLYLRRKQIIPMNAGKPDGKVIQTPMYRERVRNPPGKS  
GSYRRYIPGSHYITPGSVREMERMANENQIPSKEDNNQALEFNSDLNRTAWIRHQFGAEDRWMPQBRHWSPLAVSYDLADNHRLPARYARMSRPSLEIETATAGTGGGLYGS  
VAEYSLKPEKSTNWEVGYNFPAPFAKLROGDLRLFYSNKIKNQIDTSDNEDGMIQYDKAVSKGVQLSRSLDSGRFPASFGGTYRLKHMVCIDKGLIAFKFYLYLQVYLPCELEGGFGLSRF  
PQSLQPKYSLTLDVJGTRFFNEKLELMRAIHSKAEERNYDKLIADGAGQVYARNGKPYGHAATLTDAYARYRIKHIIDLPNFTVNLNRYLDPSNSTPVPFGRTTTFGKGRF

## SEQ ID 3893

ATGCCATCCGTAAGCGGATTACCGACATCCAGTACGGTTTGGCGGAAGACAATACGCGTGGCTGGTTCGAGTGTGCTGATGCTTTAAATAAAAAATCCGCTGTAACACCGCTTGGCGT  
TTCGAGCGGCAATTTCCGCTTCGGAACGTTTCCGCGCGCACTGCGAGCAAGTCGTTACAAAGCAATCGGTTAAACCAAGCGTCCGCAATTTCCCATCCCGCTGCCCAAGTGGCGCATTTTC



CCTGGAAATACGCTTCAAACGGCAACCGCCGCCGAAACCGGATCTCGGCACGGACGGCGCAGGATTTGAAAACGGCGGATTATCCCTCGGTGCTCAAGGCATTAATGCTGTAACCGCC  
GTCAACATAAGTATTTCCGCGGTAATGCCGAGCAGAGGTCCGACAGCAGGAAGCGCGGAGTATTCGCGACTTCTTCGATGTTAACGTTGCGGCGCAGCGGGTTGTGGCGCGGCGAGCTGT  
CCCAAGAGTTTCCGGAATCGCGGATGCCGAGCGCGGAGCGGTTTGTATCGGGCGCGGGAATGCGCTTTCAGCGGATGCCCTCTTACCAGACAGCGCGGTAAGCGGATGCCCTG  
CCTCAAGGCTCGCTTTTGGCATAACCATCAGCTTGTATTCGGAATCGCGGTACCGCGCCCAAGTAGCTAAGGGCGAGATGGCGGAGTTCTGCGCGCATCATCGGACGGCGCGCTTT  
TGCAATCGCGGACGGCTGTATCGGAAATTTCTGTGCGGTGTGAACGCTTCGCGGCTGATGCTGTCGAGGAAGTCCGCGCTCAAGGCTTCTTTCGCGCGAAGCGGATGGAATGCACC  
AAACCGTCAAGCCATCCCAATGTTTGGC

## SEQ ID 3894

MPSVRLPTSTVWRKTNTAGWSKADALNKKMPSETRLAFTAFSRSDRFRRTCSKSVQRQSVKTSVRISHPACRKSGLSLRIFKQTAARNRYSARTAHGFENGSLGAQGINAVTA  
VNI SDPAGNAGRQVQGGEGSIPDFPDGNVAAQRVVGGDVSGEPABIGDAGGGERPDRAGNAVADALFTGTGGGKADACLKAGFCHTHVIRNRAYRAQVAKGDDGGVPAHHRTGTF  
CQCGQAVCGNFVCGVERPAADAVEEVAAGQFFRREADGMHTVQAI PMPA

## SEQ ID 3895

ACCTCGCCGCGCGCTTGTTCAAATAGTGTCCAGTGAGAATAAACCGGCAATATTTCTTCATAAGTGTGGGCGAAGGAATATAACCGTCTTTGGCGGCATATACCTGACAAAT  
GATTCTATTTCTTCGGATAATCGAAATCCGCATAAATTTTTCACCTTCCCCAAAGGGCGGTAATTTCTTCCTTCTATGGAATACGTCATTAGGAGGATGTACAGCAATTTTGTAG  
GGGAATAACCCCTCGTTTCCGAGGCCAATCTTCAGAACAGCGCTTAAATTCAGAAATATGGATTATTTGGTAAAGATAGCTTGAACACCGGTTTCATCATGATCTGAAGCGCTCAATTT  
TCGGGCAATAAGCTGCCACATCAGCCCAACCAAGTATTTATTCATACCCCCACAGAAATATCTTCCAAAGAACGCGGACTTTTGTAGCGGTAAATCAAGGTTTCAAT

## SEQ ID 3896

TLPAVVQIVFVRI\*PGNIFISVGRNITVFGRIHPDK\*FYFRIIEIRINFFNPQRAVKFPLSMEYVI\*EDVQPIFRGITPRFRSQIF\*NRL\*FKNIGFIG\*R\*LEHAFIHI\*KRHF  
SGISCHISPTQVILIPPNILPRKADFLSG\*IKVH

## SEQ ID 3897

ATGGACTATAACCAACTGTTTATCTCACTTGCACAAATTTTGGAAACATCATGATATTAAGGATTTACTTGGACTTTAGGAAGAAATGTGAAGAACTTCCCGATTTCAGATTTC  
AAGTGATTCTTAATCATGAAGATGAGCCTTGGGTTTATGTCAGCTCTGGGATAGGTCATTTTAGGGCAGGAGTTTATATCATCAGCCCGTTTGAACACCTGAACATATTGAGACCTT  
GGCAATGCTGGCATCTCGAAGTATGCAATATCTGATCAATTTCAATTAGGGAAACCGTCAATATCGGTAGACCGTGGGTGAGCAATCATCTTCCGCGCATTTTCTGATTTCTCTGCT  
TATCTTATGGGCAAGAGTTGGAATATATGGAATATGTCGGAATTTTCTGGTTATTTGCCAATTACCAGACAGAAAGACTTTTCTGAACTACTTTCGGTAGAAGAAATGGAACGAAAT  
TTGATGAAGCGGTTATTGATTATTTAGATATAAATCTGCGAGTACTGTCGCGCAGGAGA

## SEQ ID 3898

MDYNQTVLSHLQKFKHHDIKGPTWTLGRIVEELPDFQVQVPIPNHEDEPMVYVSSGIGQFLGQEFFIISPFETPEHIETLAMLASASMHYPDQFLGKTVNIGRFWVEQSSFRHFLISLP  
YPYQGELEYMDNVRFPWLLPITQTERLFLNTHSVEELETKFDRAGIDYLDINRASTVWQAG

## SEQ ID 3899

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CAATAAATCAGTAACCATCTGATTGTGCGCTTAATTTTCATCGCGCGCGGCTGTCGAAATACAAAGATTGGAAGCGTTTCAATATTCCTTATACGCAATTTGGATATGGCGGCTCGTCCAA  
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CGGATGAAATTTGCAATTTCCGCGAGTTCAGAGCTGCGGCACATCGACCGCGCACTCCCTGCGGTGTATGTTCTCAACCTTCGACCGCGGATTATGACGAAATCAAGCCGGAACACCA  
AGACAACTCTGTCGACATCTGTCAGCGCGCGCGGTGGAAGTTACTTGGTTGGAACGATTTCGGCTGCAAGGGCGGTGTCGCGCAAGTCCGGAATACCGACGTTACTTCTGCTCAACCTG  
CCGGAATACTGCCCAACGGCGAGTCCGTCGCAATATCTGTTGACCAAGTTCGACGAAGCCCTCAACAAACGATAAAGACGCGGTTTAACTCTGCAATCATCGGCGAGCCAGCGGC  
CGACGATTACGAACGCTATACCGAAGCGGCGCAATTCACGCGGACATGCGATACCAACGAAATCGACAAATGCGCGCGCGCGCGGTTGGTTCACACTTACGCAATACGGTTTGT  
TGTGGATCAGTTTATCGCAAGGTTATCCGCAACTTGAAAACCGCGAGGATTGGAAGCGCGGTGTATTATGTTTCCGACACCGCGGAAAGTTTGGGCGAAACCGGATGTACCTGCGAC  
GCGCGCGCTTACGCCATCGCGCTTCCGACAGCGCATATCCGATGTTTATGTTGTTTCCAAAGGCTTCCGCAACCGGGGCGATAGATTTCCTTCAACAAACGCGCGG  
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## SEQ ID 3900

MLNNVLQTTAASARLITPGYVLTIVCLGLPALAYIAVKYRVWYKELLRLVLAASFLCALGLIAMQYQDYASFFRNKSVTHLIVPSNFIAGVSKYKDWKRSNIPYQLDMAVVQ  
NRPAAGLRRFVTVVGGTTTAAANGLNGYSRQTPFLAARGDEIVNFPQVRSCGTSTAHSLPCHPSTPDRDIDYDEIKAEHQDNLDDIVQAGVEVTHLENDGCKGVCGKVPNTDVTSLNL  
PEYCRNGECLDNLITLKFDALNKNDKDAVLLIHTIGSHGPTTYERYTEAEKPTPTCDTNEIDKCARATLVNTYDNTVLYVDQFIDKVIKLENRDDLESAAVYVSDHGESLGENGHYH  
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## SEQ ID 3901

ATGCCGACGGTATTGTTTATCCGATAGCCCGGCGAGCGCGGCAAGTCGACGCGCGCGGTTTACCGCTTGGCGCATCAACCGTTCCAAGGAATTTGCAGACCGTCGGAACACCATTA  
ACGGCATTTGGGAATTTTGGAAATCGCAAAACCGCGCTTGCAGAAATACACGGAATCGACCGCAACCTTTCCCGCGCTTCTTGAAGGATGGGAATTCGACTTAACCTCGGCACAC  
GTCCCGCGAGTAAAAATCTCGCGGATCGGTGGAAT

## SEQ ID 3902

MPDGIVYADSPGSRKSDAGGPTRCRINRSKEFADRRNHINGINFWNQAKRALRKVNGIDRKPPFPLKGEFRLNSGTPSRQLKILDRDCGI

## SEQ ID 3903

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## SEQ ID 3904

GLMAVYAGVDRLAHFQQAITHSITGAPQ

## SEQ ID 3905

ATGAAGTTATGGTGTCAAAATCAGGCTTTCAAACAACCTTTGAAAGGCGAACCATGAACAAGCCGTTTATCAGCAGCGCGAGTTGGCACTTTA

## SEQ ID 3906

NKLHCQNQAFKTTTFRQNHQAVYHAGAVGTL

## SEQ ID 3907

ATGACCGATATTTCACTCCATCCAAACGTTCTTCTGATGTCAAAATCCATAGCAAGAAACCAACCGGAAGTATGGTAAGGAATTTCTTTTTTCCCAAGGTTTCCGTTATCGGA  
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CAATATGGATTTTGGTTGGAATAATCAAAAAATCGGAACGTGATATTAATAATGAACCGAGCTGGAAGAAATGGTTTCAAGTGATTTGCTTTGGGAGTGCQAATTAATAAAT  
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## SEQ ID 3908

MTDIFTPSKRSFVMSKISHKTEKPEVLVRKFLPSQGFYRKNDKRYACKPDIVLPKYTKTVFTHGCFWHGSHCNKGHIKSNMDFWLEKITKNRERDINKNETELEKIGFKVIVVWCELEKN  
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## SEQ ID 3909

TTGTTTGTCTTCAGCGGCAAGATGTATCGGCTGTTCGCCAGAGGTCATATTAGTACGAATGCAATAATAATCTAATTAAGCTCATTATCAATATTGGTTGTAGATTGCATTGTG  
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## SEQ ID 3910

LFCLQRQDVSAVDRVHISTNANNLIKTHYQILVVDICQYIFPNI IALSSNKYKYHSNGRL

## SEQ ID 3911

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## SEQ ID 3912

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## SEQ ID 3913

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## SEQ ID 3914

VQTCIALRDFCFYFFQTASLEKGFHPMTHRLCLLFLPLCTVCLAAPSNDAADERRRLLEBGSRTQYQYRESWLDTEQARGEVEENDGYISIGSETYQVGDTAEELESATYHALNARQWHK  
VRQFAARYAKLPRHXPALIHLDALQKRDEGDFRAAGNSFQTALEAEPDNPRLLEAGRPYAEWNQKESAAAFKVLKTDIPAEATPIVENYLSLSELKRRRHHQGISLGYNSNVNQGN  
GINQCWELAGMCLMERLPLPPTDSTFSSYSATARTVPLKGNHGVQVRGLVNGRYTEKDKDSAAAMPDYGYRNGSLYAGIYADARSFSLPLPYEYDFDRNRHHTYRWAGADADWSRTLS  
PWRINSHAGAKKTYGGQSKTYFADFQYELGAGAEFSITLKSGLLVNFDARKAYPEKSSSKETATRLGAYRLFSGGTLYNAVLLYRRSLYDAASFVSDNKRDRKQYIMMAAGFPQ  
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## SEQ ID 3915

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## SEQ ID 3916

MAHFPNINYPYKGNMTVRIEHDLLGDREIPAEVYWGHTLRAIENFKISTQKISDVPQVRSIVMVKKATAQANGELGAVKPELAAAEKACDEVLLNRRCLDQFPSPDYVQGGATSVN  
MNTHEVIANLALAEALGYERGRYDIVNPMHVNASQSTNDAYPTGFRILAVYYSIGELLDKLTVLKNFAAKAEAFKIDVLKMGRTQLQDAVPMTAGQEFQSPQVLLLEKILNLDRTQLLEV  
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ITFAESQQLQINMEFVIAQCMFETISLLGNAVNLSKCVKGTIVNREICERYVFNISGLVLTNLPYIHRNGDLVGKICAQTKGVREVLVERGLLSEEBEINRLSPENLNPFL

## SEQ ID 3917

ATGAAAAATCATCTTCGCGCGCTCGCAGCGGACGCGTGGGCACTGCCCTCCGCCACTACAAAGTGGAGCAATATCACGCCAACGTCGCTTTCGCCATCGACCACTTCAACACCGCA  
CCAAGTCGCGCGTTTTTACGGTTCGACCGGTTCCGTGAGTTGATCAAGCAACACGCGCAAAATCGACATCACCATTCCCGTTCGCAACCTGCAAGCGGTTTCGCAACCCCTTCAC  
CGGCACTCGAAATCGCGCGCATCTTCGATGCGGCTCAATATCCGACATCCGCTTCTGTTTCCAGCAATTCACCTTCAACCGCAAAACCTTGTTCGCTGACGCGCAACCTGACCATG  
CGCGGCAAAACCGCCCGCTCAACTCAAGCGGAAATTCAGCTGCTACCAAGCGCGATGGCGGAAACCGAAGTTTGGCGGCGGACTTCAGCACCACCATGACGCGCAACCAATGG  
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## SEQ ID 3918

MKKIIFALAAAVGTASATYKVDYHANVRPAIDHNTSTNVGGFYGLTGSVEFDQAKRDKIDITIPVANLQSGSPPTGHLKSADIPDAQYPIRPFVSTKFPNFKKLVSVDGNLTM  
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## SEQ ID 3919

TTGAAAAATCGCCATCGGAAGATGCCGCGAGCAGGACGAACACTATACGGCCCGGATGAAATTTGCCATATCGTATGCGGCTGAAAAACGGGAAACGTTGTTTTTCGGTGGTTACTTTC  
CGGACTTCCCGCAAGCCCGCTGCGCGCAAAATATCTTTCGGGGGTTGTCTCCGCCATATCGGCTTACGGTTGGCAGGGCGGTTTGAAGAGAGGCAATTTGTCTGATTCGCAATCA

AGGCTTATTGTTTTCAGCTTCGATTGGATGTCGATGCGGACGTTTTTGGTCATACCGCGTTAACGAGGTAGTCCACGCCCATTTGGTGGGTGATGTTGGTGTGCTGAAGTCGCCGCC  
GCAAACTTCGGTTTCGCCCATCGGGCTTTGGTAGCAGTTGAATTTTCGGCTTTGAGTTGACGGGGCGGTTTTGCCCGCATGTCAGGTTCGCCGTCACGGAACAAGTTTTTTCGG  
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TAACA

## SEQ ID 3920

LKKCAIGMPQDDHYTGPDEIVHIVCRLKTGNVVPGRYFPDFPASPACRQNI FRRVVLRLHIGLRLAGRFDEGICADSHQGLLPCSFDLDDVDADVPHTGVNEVVHAPFGAVDGGAEVAA  
ANFGFRRLALVAEVEFFGFEDGGGFAAHGQVAVNGNKFPAVEVEFGNEADVRLLSGIEDVGGPQVAGEGLRTALQVGDGNGDVFVAFVCLIELDGTCTVKTADVAGVEVVDGETDVG  
VIVVHFGGGGADGCR CERGEDDFHDDNPLCGPVKAFILIT

## SEQ ID 3921

ATGGGGTTTCATGTTGCGGACTTGGTGGCGTTTTCGTACCAAAATATCGAATTTACCACAAAGTTGGAACAAGTTTACCTTCTCTGCTGTCTTCTGCTGAGCCCTTGTCTCCATCTGT  
TTGAGAACCCTCCATAATCGCTTTGACGATTATAACGTTCTGCGTTTTAGTTTGGTTGGACAATCATTTGAACCCAAACCCCTTCCGTTTCCGCTTATCGCCTT

## SEQ ID 3922

MGVHVADLVRFSPQISEFYHKLKDYVLLLPVLLPEPLHLFENLHNAFDDYNVLSVLVWLDNHYEPKPLFPFPPYRL

## SEQ ID 3923

CGAAAAGTCTTCCAAATGACGGCTGATTCCTCTTCAACAGTCGGATACCAATCTATGAAAATGCCGTCTGAACGGCAAAACGTCGGTTACAGCGCAT

## SEQ ID 3924

RKVFQMTADCLFNSRIPIYENAV\* TAKRAFRRH

## SEQ ID 3925

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CGATTTCCGCAACCTTTGGGACAGCTCGCCGCCACAACCGCTGCGCGCAAGTTACCATCGAAGAAGTCGGGAATACTGCCGCTTCTCTGTCGCGACCTGTGTCGCGCATTACC  
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## SEQ ID 3926

MGFLQGGKILITGMISERSIAYGLAKACREQGAELAFYTVVDKLEERVVRKMAELDELVFRCDVADDEINQVFDLKGHWGLDGLVHSGIFAPKEALSDFLDSISREAPNTAHEISA  
YSLPALAKAARPMRGRNSAIVALSYLGAVRAIPNYVMGMAKASLEAGIRFTAACLGKEGTRCNGISAGPIKTLAASGIADPGKLLGHVAHNPLRRNVITIEVGNTAFLSLSSGIT  
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## SEQ ID 3927

GTGTATCTTCATATTTTCGAGGGTAACATATCTGCTAATCTGGTACAGACCCAAAAACAAAGCAGGATAAACACCGCGTTTTTCATCCGCCCTGTTCGCCCGCGCGTTCGTCACACCGCC  
TGCAAAACCACCGTTTTACCGCGAGAAATGCCATAAATCCCGCTATGT

## SEQ ID 3928

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## SEQ ID 3929

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CACACCGTCCCGGACGCTAAAAATCTCCGGGATCGGTGTGAAT

## SEQ ID 3930

NKITHCKLKEVQKEPLRSFVPEVTARSADILGIHPDSALFYRKIRTVANHRLALADEVFEGPAGPGSGFCGRRKGRRGRAAGKAVVFGIPKRNGRAYTVAADDAEPETLLPAVKK  
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## SEQ ID 3931

TTGTGGCGGCAGATGAAAAACCGCTCAAAATCAACAGCGGCATTAAAGCAAGTTTTTGTTCATGAAACCGCTCTCTTTTTTAAGTATTGGGAATTAAGATAAAACAAACAACTTAT  
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## SEQ ID 3932

LSAADENALKINSIGIKASFLFMKTLFSLSIGELKIKQNLNDSISGGNYI

## SEQ ID 3933

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## SEQ ID 3934

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## SEQ ID 3935

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## SEQ ID 3936

LAGHYGTQGTASVQVGAQLIKGASTAVNGIP

## SEQ ID 3937

TTGTTCGCCGAACCGGCAACCGATTTCGCGTTGCCCTTCGTCGGCGGCTTTTTGGTTTCGATGTTGACGGAACCGGATACCGCGCTTCAGGATATGCCGTTTACGCGGTGGACGCG  
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CGCTCAGCGTGTGCTTTCCGCCCAACTCTCAACGGAAGCGTCTTTTTGGCTACGGCATCCAC

## SEQ ID 3938

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**SEQ ID 3939**

SEQ ID 3939  
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GCAAGGATATCCAAAACGCGCGGACGCGTTGTTTCGACGCGCCGACGCGCAAAATCAACCTGCTGCCCTTCTTGGAACTGGCAAAATACCGTCGGCGAAACCAATATGCTGACGTTTGAATGG  
GATCGCTTTGACAAATACC

**SEQ ID 3940**

SEQ ID 3940  
LARFGNIRAQGTFDLGQRFGENKAFGVRANGKLRHGDTPRHGYREDNKEFALNADYRGEKLRVTFDSIYAKRKINGGRARMQDIQAGGRLFDAPDGKINLLPSWAWQNTYGETNMLTFEN  
DAFDAT

**SEQ ID 3941**

SEQ ID 3941

GTGGTATTGGTTGGCAGCCATGCAAGTTTGGGTTGGGCTGCTGCGACCGCTTGTAACGCCAAACGGTTGGGGAATCAGCGTACCGGTAATAACGCGCTTTGGTTGTAGCCGATACCGCCGTA  
ATTTAGGTAATTGTCAAACGCATCCCAATTCAAACGTCAGCATATTGGTTTCGCCGACGGTATTTTGCCAGTTCCAGAAGCGCAGCGTTGATTTCGCCCTCGGGCGCGTCGAACAAGCGTC  
CGCGCGCGTTTTCGATATCTCGATACGCGCGCGCGCGCTTGATTTCGGTTTCGCGTAGATGGAGTCGAACGTCACGCGCAGTTTTTCGCCCGGATAATCGGCATT

SEQ ID 3942

SEQ ID 3942  
VVVVGSHAGFLAARTACTANGWGNQRTVITRFVVADTAGNLGIVKRIPFKRQHIGFADGILVPRRQQVDFAVGRVEQASAGVLDILHTRAAAVDFAPRVGDVERHAQPPFAATIGI

**SEQ ID 3943**

SEQ ID 3943

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**SEQ ID 3944**

SEQ ID 3944  
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ERNRGIEFNAYANLNLKTLRPTFGVMYTLQSSSNVYVTKTGVVERDTPPAKGLSLNGNSVPGKSYQDTPKQYAFPSYTLVDVGARYKTKLGNLTLVSSSVENL  
FNKNYWOVORGOFRSPAVVGLPRTYMLKAEIDF

SEQ ID 3945

SEQ ID 3945

GTGAAACCGCTGCGCAGACTGACAAACCTCCTTGGCCGCTGCGCCGTAGCGCGGGTCGCACTCATACAGCCGCGCTTCGCGCGGCAATTGGCGCAAGACCGGTTCATTACCGATAACACCC  
AACGGCAGCACTACGAACCCGGCGGCAATACCACTCTTTCGGCGCACCCGCGCGGCAAGCGTTCGACGCGACCGGCAAAATCAACGGTCATCCAAGCATATACCCACCAGATGGGCAACCT  
GCTCATCTCAACAGGCGCGCAATCCAAGGCAATCTGGTTACAGCTCGCTCGCTTTTCGGACACGGACACGAAGAACAGCCCCCTTCGACAACCAAGCGCGCGACAGCGCAAGCGAAGAAAA  
GGCAACGCTGACAGCGCTTACCGGTATCCGGCTCAACTGGGAAGGACACGAACATCATCCCGCGGATGCCGTACGACGCGCCGAGAGGGCGGCAATTACCCCAAACCTACGGCGGCACGAG  
ACGAATACACCTATCACGTCACAGGCAAGCGCCGCAATGATCAAACTCAATPCGACCGGACACCCGCAGCATCGGCGCAACGCAATTATTCGACAACCTACCAACCTCGGCGCAATTTCTCGGA  
CCGCGCGGATGAAGCCACAGAAAAATGTTCTGAGACCAATGCGAAGCTCGACCGCTGGGGGCAACAGCATGTAGGTTTGTCAACGGCGTCGCGCGCGGCGCTCAACCCCTTATTCGACGCG  
GGCGAAGGCTTGGGCATAGGCGACATATCTGACGGAACGCGCTATGCCATAGACAAGAGCGGATGCGCAACTGACCGCCCTTACCGCCGAGGGCAAAATTCGCCGCCATCGCGGGCTTGG  
CGAGCGCGCGGGCTTGAIAAAAAATCTGCGCGAAGCGCTTGACCGGTGGATCAAGAGAAAAACCCCAATGCGCGCGAAACCGTCGAAGCCCTGGTCAACGTCCTGCGCTTTGGCAAAATCA  
AAACCTGCAAGAAACCAACCAACCGGGGAAGGCTGCGGTTAGTGGGGATTTTCTAAATCTCAACCTGCTCCTTCACCGCAGCACTTGGTCAAAACGGCAGACGGCTCAAAAGCCATT  
GCCCATATTCGAAGCCGAGACCGGCTCCTTTCGAAGGACGAGGCAAGCGGAGAAACCGGATACAAACCCGTTACCGCCGATACGGCAATCCGTATCAAGAAACCGTTTACATTGAAGTT  
CAGACGGCATCGGCAACAGCAAAACCTGATTTCCAACCGCATCCACCCGTTTATTTCGACGCGCAATGGATTGAAGCGGAAGATTAAAGCGTCAAGAGCGCGGTGTTATTCGAAAGCGG  
CAAAACCCAAACCGTCCGCAACATCGTTGTCAAAACCAACCGCTCAAGCGCTACAATCTGCACGCTTGGCATTTGGCATACCTATCTGTTCGAAGGCGATAAGCGGAAACGGAAGGGGT  
TGGGTTTCATGATTGTTCAACCAACTAAACACGACAGCAAGTTTAATCGTCAACACGCAATTATGGAGGTTCTCAACAGATGGAGCAAGGGCTCAGGCAGCAAGACAGGCAGGAGAAG  
GTAAACCTTGTCAACTTGTGGTGAAGATTGATGATTTGGTACGAAAACCGCACCAAGTCCGCAACATGAACCCCAATTAGTAAACATTAATGATGAACATGTGTGTCACTTATGAGCA  
TGTGTCATCGAGCAACATGCCAGGGAAGCATAAAGGAATCAATGTTTAAACATGTCAAGGAAAGAGGTCGGCATGATGTCAAGATATTTCGAGAGAACGGCTAAAAAGCATGTGACTA

SEQ ID 3946

SEQ ID 3946  
VKPLRLRLTNLLAACAVAAVALIQPALAADLAQDPFITDFTQROHYEPGGKYHLFGDPRGVSVDRTGKINVIQDTHQMGNLLIQAAIQGNLGYTVRFSHGHCHEEHPFDNHAADSASEZK  
GNVDGDFTVYRLNWEGHEHPADAYDGPKGGNYKPKPGARDEYTHVNGTARSIKLNPTDTRSIQRLFDNYNNLGSNFSRDADEANRKMFEHNAKLDRWGNSEMFVNGVAAGALNPFISA  
GEALGIGDILYCTRYAIDKAAMRNIALPLPAEGKFAAIGLGSAAGEKNTREAVDRWIQENPNAESTVEALVNVLPFAKVKNLTKAAKPGKAASGDFSKSYTCSFHGSLTKVTADGYKAI  
AHTQAGDRVLSKDEASGETGYKPVYARYGNPYQBTVTYILEVSDGIGNSQTLISNRHPPFSYDGNKWKIAEDLKAGSRLLSESGKTQTVRNVIVVKPKPKLAYINLTVADWHYTVFKGDKAETEGV  
VQACDRCPPKLLKPKPERYNROTHYGGSDTGARAQAARQAGEBKPCPCGRIQIFGKTIAPSPQHEPPLVKHYHYEGHGHSMNADRAKHARESIRGTQCLTCRKEGAMMSRYSRQAKKRL

SEQ ID 3947

SEQ ID 3947

TTGTTTGAAAGTGATGAAAAACCTTTGATTTCAGTTTCGGCGAGTATTGCTCGGCGGTGCTTTGGGTACACCTTTATTATTTGGGTGTCAAAGCAGAAGAAAGTCTGACGCAGCAGCAAAAA  
TATTTCAGAAAAACGGGGCTTTTTCAGCCGTCGAATCGCACCAGTATGATCGAGGCTGGTTTACCTTCACGGAAACGACGGGTATCCGCTCTGAACCCGAGGTTGCTGCAATAATGCGCAGAAATA  
CCTGCCGGATAAATTGAAAAATAGTGTGTGGAACGCGGTTTACGCTGGTAAACCATATCAGCAACGCCCTCTTCGCGCGGGATTTCGGCACGCAGGCGGCACATTGAAACCGAGTTCAAATAC  
GCGCCTCGAAACCGAAAAAGTTTTGGAACGCTTTTTGGGAAACAAGTTTCGGGTTTTCCCTTGCCAAATACCGTTTATTTCACCGCAGCGGTAAAAATGGAAGTCAGTGTTCCCGCTTTTCGATT  
ATGAAGAAGTCGTGGGCATCAGCTGCATCGGTGGGAAGGCTGACGGGGGAAACGGTTTTATCAAAAAGGTTTCAAAGCTACCGCAACAGCTATAGTGCGCCCTTGTGTCAAATAACAGCTGGC  
AGCAAAAGCGCGATGCCGCGTTTGA AAAAGCGCATTTCGATTTCGGAACCTTCAGACGGCATCAATCCGCTTGCTTTGGGCAGCAGCAATCTGACTTTGAAAAATTTTCGCTCGAATGAAA  
GAGGCGTTCGATTACAACGTCAAATGAAACGAACTGGTCAACCTCGTTACCGATTTGAGATCGGCGCGTTTATCAATCCCAACGGCAGCATCGCAATCTCAAATCGAATCGGCAAGC  
TGGCTTTTTTCAACCAAGACCGGGGAATCGGGCGCGTTTTATCGACAGCGAAGGGCGGTTCCGTTTCGATACGTTGGTGTACCGGCGATGAAAAATCGCCCGCTGGACATTCATATCGCTGC  
CGAACACCTTCGATGCTTTCGCTTTAACCGTATTGAAACGCAAGTTTGCACAAATTTCTGCCAAAAAATGACTCGAGGAAAAATGATGTGGGGCGAAAAATCATGTTTAAAGGCATGAAGAAGGAATTGA  
TCCGGATTATTTACCCATGACCCGGTACTTAAATATCAAATTTTTTCGTTTCAACCTGTCTCGCAGGAAAAATGATGTGGGGCGAAAAATCATGTTTAAAGGCATGAAGAAGGAATTGA  
ACCAATTTGGGATGATGTTTAAAGAAACACGAGCGCAAAATCAGAAATGAGTATTCTCAAAAAATGTTGGAAGATTTCGCGGTAAAGTACGGCTGAGAAATATTTTCAAGTGTAAATGCCGAAGA  
TAGGGCGGAAGCGCAGGACGAGCATTGCCGATATTAAAGAAACATTGCGCCTGATGTTGACAGTACGGTCCAAAGTATGCGAAGGGAAAAATATCTTACTTTAGACGGTAAATCAGATTGAT  
ACGGTCATTTTCCCTTAAAAACAACGCCCTTGAAGTTAAACGGGAAAAACGCTGCAAAATGAAACCGGATCTCGATTTTTCGACGAGGAGATATGTTTTCGCGCACCGCGCAT



## SEQ ID 3948

LPFVMMKPLISVAALLGVALGTPYLVGKAEESLTQQQKILQKTGFLTVESHQYDRGWTSTETTVIRLKPPELLHNAQKYLNDNLKIVLEQPVTVLWNIHTEGPPAGGFGTQAHIEFEKY  
APETEKVLERFPFGKQVPSVLANVYVFNPGSGKMEVSPAFDYERLSGIRLHWEGLTGEBTVYQKFKSYRNSYDAPLFPKIKLADKGDAAFERAHFDSSETSDGINPLALGSSNLFLKFSLEWK  
EGVDYNNKLNELVNLVTDLQIGAFINPNSIAPSKIEVGKLAFTSTKGESGAFIDSEGRFRDFTLVYGDYKGPLDIHIAAEHLDSALTVLKRKPAQISAKMTEBQIRNDLIAAVKGD  
SGLFTHDVFLNLIKIFRFTLPQGIKIDVGGKIMFKGMKEDLNQLGLMLKKTETANIRMSIPQKMLDLAVSQAGNIFSVNAEDAEARASIASIDINETIRLMVDSTVQSMAREKYLTLGNDQID  
TVISLKNALKIKNGKTLQNEPDPDFDEGDMVSGQPH

## SEQ ID 3949

ATGGAATTCGGACGGGATAGGGGAACATTGAAATCCAGTTGAAATCTGTTATTGGAAGCATGGAGGAAAAATAAAGGCTGTATTTTAATA

## SEQ ID 3950

MEFRDRGTIEIQLKSVIGKHGGKIKGCILI

## SEQ ID 3951

ATGGCTTTAGTTGAATTGAAAGTGGCCGACATTGGCCGACACGAAAAATGTAGATATTATGCGCGTTGAAAGTGAAAGTGGCGACACCATCGCGGTGACGACACCCGTATTACCTTGGAAA  
CCGACAAAGCCGACGATGGAGCTGCTGCCGAAGTTGCGGCGGTGATCAAAGAAGTGAAAGTCAAAGTGGCGACAAATCTCCGAAGCGCGGTGATGTCGTCGTCGAAGCCGAAGGTGC  
GGCTGCCGCCCTTAAAGCCGACGAGCGGTGCCGCCCGCCGCGCAGGAAGCACCAGCTGCCGCTCTCTCCGCAAGCCGCGCAATTCGGCGGTGTCGCGATGCGGAGTACGACGTGGT  
GTATTGGCGCGGTGCCGCCGCTTACTCGCTGCAATTTGCCGCTGCGGATGAAGCTTGAAGTGCCTATCGTCGAGCGTTACAAAATTTTGGCGCGGTGTCCTGAACCTCGCGCTGTA  
TCCCTTCCAAAGCTTGTTCACAAATGCCGCGTTATCGACGAGTGGCGCACTTGGCTGCGCAACGGTATCAAATACCCCAAGCCGGAATCGACATCGATGCTTCGCGCTACAAAGA  
CGCGGTGTTTCCCGCTCACGCGGTGTTGGCAGGTATGGCGAAAAAGCCGTAAGATGGAGCTTATCCAAGCGCAGCGCAATTTCTGGATCTCCACCTTGAAGTGTGCTGACTGCC  
GGCAGCGGTACGAACAGCGACGCCCTACCGCGGAGAAAAATCGTTGCCCTTCAAAAATGTATCATTGCAGCAGCGCGCTAACCAAATGCTTTCATTCCTGAAGATCGCGCA  
TCATCGATTCCAGCGCGCATGCGCACTGAAAGAATACCGGCAAACTGCTGATTATCGCGCGCGGATATTATCGGCTCGAGATGGGTACGGTTTACAGCAGCGTGGGTTCGCGCTGGA  
TGTGGTTGAAATGATGAGCGCGCTGATGCAAGCGCGCAGACCGCGACTTGGTTAAAGTATGGCAAAAAACAAACGAATACCGTTTTCGAACATTTATGTCACACCAAAACCGTTGCACT  
GAGCCGAAAGAAGACGGCGTTTACGTTTACCTTTGAAGTGCAGTAAAGAGCCGCAACGTTACGATGCGGTACTGTCGCGCGAGCGCGTGGCGCTTAACGCAAACTCATCAGCG  
CAGAAAAAGCCGCTGTTGCCGTTTACCGATCGTGGCTTCATCGAAGTTGACAAACAAATGCGCACCACTACCGCACATCTACGCTATCGCGGATATCGTCGGTCAACCGATGTTGGCACA  
CAAGCGCTTACGAAGCGCACGTTGCCGCTGAAACCTGTGCCGCGCACAAAGCCTACTTCGACGCAAGCGTTATTCGCGCGTGTGCTACACTTCCCGCAAGTGGCATGGTGGTGAA  
ACCGAATTTGCTGCGCAAGCATCAGGCGCGCAAAATACCAAGCCAACTTCCCATGGCGCGTTCGCGTGTGCGATGCGCAACGCTTTCGCAACAGCGCTTACCAAGCTGATTTTCGATG  
CCGAAACCGCGCGCATCATCGCGCGCGCATTTGCTGCTCGAAGCGTGGCGCATGATCGCGCAAGTCTGCTTTCGCTATCGAATGGGCTGCGACGCGGACAGCATCGCGCAAAACCATCA  
CCGCAACCGCACTTGGCGCAATTCATCGGTATGCTGCGAAGTGGCTTGGGTGTATGTACCGACCTGCTCTCAAAAGAAAAA

## SEQ ID 3952

HALVELKVPDIGHENVDIIAIVENVGDITIAVDDTLITLETDKATMDVPAEAVGIVKEVKVKGDKISEGGILVVVEAEGAAAAFKAEEAFAEPAEAPAAQFPGAADAETDVI  
VLGGGPGGYSAFAAADEGLKVAIVERYKTLGGVCLNVGCI PSKALLHNAVIDEVRLHANGIKYKPELIDMLRAYKDGVSRLTGLLAGMAKSRKVDVIGDGGFLDPHLEVLTA  
GDAYEQAAPTGEKRIIVAFKNCIIAAGSRVTKLFFIPEDPRIIDSSGALALKEVPGKLLIIGGGIIGLENGTVYSTLGSRLDVVEHMDGLMGADRLVKVWQKNEYRFDINMVKTKVAV  
EPKEDGVYVTFEGANAPKEPQRYDAVLVAAGRAPNGKLSAERKAGVAVTDGRFIEVDKQMTNVPFHITAIIGDIVGQPMALHKAHVHEGHVAENACAGHKAYFDARVIPGVAYTSPEVAHVGE  
TELSAKASGRKIKTANFPMAASGRAIANGCNDGPKLIPDAETGRIIGGGIVGPNGGDMIGEVCLAIEMCGDAADIGKTIHPHPTLGESIGMAAEVALGVCTDLPQKKK

## SEQ ID 3953

GTGAAGATGCAGTTTACGCCCATCAAATGAAACAGATCTATATGACGGATGTTATATATCTACGACAACAGCAAGAAATTTGCCAAGAAATTTGCAACAGCTCCCGGCATCGAAATG  
GCTATATATATGTTTAAATAGAGATTTGTTTGGTCAATATCTATTTTGAATATCAGGTTGAACATCCAGAAACCCAGATGAGAAGGAAGTAACATCAGAGCTGAAGATTGTGCTG  
TATCTCTGAAGAGTGAATTTGCTAAGAGTGTATAGAAATTAAC

## SEQ ID 3954

VKNVAVAHQIETDLYDCYISTTTDKELAKKFPATSSGIENGYIYVLRDLFGQYSIFEYVEHPENPDEKEVITIRAECCGICEEVI IAKELIEIN

## SEQ ID 3955

GTGATGGTGTAAATTCAAACTTTAAATTAAATTAATTTATGGGAAATTTCTTATTATATAGAGGCATTAGTTGCCAACAGATGAGCAAAATTAATGGACAGT

## SEQ ID 3956

VHVLNSNFKLITYGKFLIYIEALVANKMSKIMDS

## SEQ ID 3957

ATGAGTATCTGAGAAATCAAAGTCCCGATATCGGCGGTACGAAAACTCGACATCATCGCGGTAGAAAGTTAAAGCGGGCGACACCATCGCGGTGACGACACCCGTATTACACTGGAAA  
CCGACAAAGCCGATGGATGTGCTGCCGATGCGCGCGGTGCTGTAAGAAGTAAAGTCAAAGTTCGCGGACAAATCTCCGAAGCGCGGTAAATTTGACCGTTGAAACCGGTGCGCG  
CGCTGCCGAAGCCGCCCGGCTGCTGCCGCCGGAAGCACAACCTGCACCCGCTGCCGCGAGCGGTGCAACCGTTCAAGTAGCCGTTCCCGATATCGCGCGCATACCGATGTAGATGTAATC  
CGCTTGAAATCAAAGTTCGGCAGCCGCTGCCGAAGCAGCAGCGCTGATTACTTTGGAACCCGATAAAGCGCAATGGACGTACCTTGTACCGCTGCGGTGCTGTTAAAGCGGTATCT  
TAAAGTCCGCGACAAAGTGTCCGAAGGCTTGCCTATTCGAAGTGAAGAACCGCGGCTTTCGCCGAGCAGCTCTCGCGCTGCGCTCAAGTGCACCCGCCCGCGCTGCTTACATC  
TGCGCACCCGCCCGGCTGCTTACATCTGCTGCGCTGCGCTGCCAAATCGATGAAGCGCTTTCGCCAAGCAGCAGCGCGTCTTCGCGCAGCAACCTGCGCGCGCAATTTGGGGTG  
GATTTGGGCAAGTCAAAGTAGCGGCTTGAAGGCGGTATCATGGAGACGACATCAAAGCCTTTGTGAAATCCGTAATGCAGGCGCGCGCGCAAACTGCGCGAGCGCGCGCATCT  
TGGCGCGCGGTGCTGACTTGTGCTGCGCTGCGCTTAAAGTGGACTTCTCCAAATTCGCGCAATGTGGAAGTTAAAGAAATTTGCCGCTTAAAGAAATCTCCCGTCAAACTGTCCGCAACT  
GGTGGTGAATCTCCTACGTTACCGTACACGAAGAAGCGGATATGACCGAATGGAAGAAATTCGCAACAGCTGAACAAAGAAATGGGAACGCGAAGCGGTGAACCTGTCGCCGTTGCGGTT  
ATCATCAAAGCCCTCGCTTCCGCGCTGAAAGCCTTCCCGCAATTCACCGCTTCTTGGACGCGCAACCTGCTGCTGAAAACTACTTCAACATCGGTTTTCGAGCGGATACGCGCAAG  
GCTTGGTTGTTCCCGTATCAAAGAGCTGGATCAAAGAGCTTGAACAAATCAGCCAGAAATTGACCGAATTTGTCAAAAAGCCCGGAGGCAAGCTCAAACCGCAAGAAATGCAAG  
CGCGTCTTTACATTTCCAGCTTTGGCGCGCATCGCGCGCAGGTTTTCACGCGGATTTGTAACGCTCCCGAAGTCTGCTTGGCGGTGTGCAAAATCCCAATCAAACCGGTTTGGAA  
GGCAAGAGTTTGGCGCGCGCTGATGTGCGCGGTGAGCGCTGCTTCGACACCGCGCTCATCGAGGTGCGCGCGGTATGCGCTTACCGCTATCTTGGCGAAGCTGTTGAAGACTTCC  
GCCGATTAACCTA

## SEQ ID 3958

MSIVEIKVPDIGHENVDIIAIVEKAGDTIAVDDTLITLETDKATMDVPAAGVVKVVKVKGDKISEGGVILTVETGAAAAEAPAAAAEAPAPAAAGGATVQVAVPDIGHETDVI  
AVEIKVGDTVAEDTLITLETDKATMDVPTAAGVVKVFLKVGDKVSEGSALIEVETAGSAAAAAPAAQAAAPAAVPTSAAPAAVPTSPASAAKIDEAFAKHAHGPSARKLARELV  
DLGQVKGSLKGRINGDDIKAFVKSVMQGAAPAAAGASLGGGLDLLPWPVDFSKFGNVEVKELSRKIKISQNLNRWVVIPIHVTVEADNTELEFRKQLNKEWREBKVLSPLAF  
IIRASVSALKAPFPNASLDGDLNLVKNYFNIGFAADTPNGLVVPVIRKVDVQKGLKQISQELFELSKAREBKLPQEMQGACTTSSLGIGGTGPTIPVNAPEVAILGVCKSQIKFVNN  
GKEFAPRLMCPISLSDHVRIDGAAGMRPTVFLANLLKDFRRTIL

## SEQ ID 3959

ATGTCACCCCAATACAGATGTTGACCTATCGAAACCAAGAGTGGCTGACGCGTTAAGTCCGCTCTCGAATATGAAGCGCGGCAACCGCGCAATACCTCTTGGAAAACTGCTCA  
AATACTGCGCGCAAAAGCGTACGTATGCCCCAGCGACGACCCCGTATTGTAATACCGTTTCGGTTGAAAAAGCAAGGCAATTCGCGCGGCAAAACATCGAACACCGCATTCG  
CGCATTCGTGCGCTGGAACCGCGCGCATCTGATTGCGCGCGCGCAAGAAAGATTGGAATGGGTGGGCACATCGCATCTTCCAACTGCGCGCAACATGACGAAGTGGTTTCAAC  
CACTTCTGGAAGCAAAAGGTGAAGTGAAGAGCGGATTTGGTCTTCTTCAAGGTACGTTGCCCCGGCATCTATGACGCGCATTCGTCGAAGCGCTGACGGAAGACCGACTGA

ACAACCTCCGCCAAGAAGTGGACGGACACGGTCTGCCTTCCATATCCACACCCCACTCTTGGCCGACTTCTGGCAGTTCCGCAACGATTCATGGGCTTGGGCCCATCATGGCGATTATCAGGCGCGTTCCTGAAATCATCTGGAATCATCGCGCTTGGCAAAACCCAAAGGCCGTAAGATFATGGTGTTCCTGCGCGCAGCGCGAAATGGACGAACCCGAATCCCAAGGTGCAATCGCGCTGGCGGCATCGCGAAGGCTTGGACACCTGATTTTTCGTATCATGCAACCTGCAACCGCTTGGACGGTCCGGTGGCGGCAACGGCAAAATCATCCAAGATATGGAAGGCAACTTTGCCGTGTCGCTGGATGTGTCGTCAAAGTCAITTTGGGGCGCGCGTTGGGACCGCCTCTTGGCGAAGACAAAGACGGTATCTTGGCGCAACGTATGGAAGAATGTTTGGACGGCGACTACCAATTTACAAATCCAAAGACGGCGGTATGTGCGCGAACACTTCTTCAATACGCCCGAACTGAAAGCATTTGGTGGCGATATGACCGATGAGCAACTCTGGGCATTGAACCGCGCGCGGCACGATCCTCAAAAAGTGTACAAACGCTTACGACCGCGCAGCGAACCATGCCGACGGCAAACTTACCCTTATCTTGGCGAAAACCATTAAGGTATACGGTATGGCCGACTCCGGCGACGCTCAGAACGTTGGCCACCAAGCGCAAAAATATGGACAAAGCGTCCCTGAARCAATTCGCCGACCGCTTTGCATCTCCGTTTACCGGACCAACAAATGGAAGCGGCATCTGCCTTACAGTACTTTGCCCGCATACGGAAGAATACAAAATACCTGCACGCGCCGATGTTTGGCGCGCTACTCTGCCCGCAACCAACGACGAGGAAGTATTGGAAGTGCCCGAGCTGTGGGCATTTCGACGCACAACTCAANTCCCGGTAAGCCGAGTGTCTGCACACGATGCAATTCGTCCGCATGTCTGTGCCACTTTGCTGAAAGACAAAAAATTCGGCAACCGCTCGTACCTATCTGTTCCCGACGAAAGCCTATCTTTCGGCATGGTGAAGTATGTTCCGCGCAATATACCGTATTTGGAATCCCAAGGCCAACAAATACACGCGCTCAAGACAAAGACCACTGATGTTCTATAAGAATCCGTTGACGGTCAAAATCTGCAAGAAGGTATTAAACGAACCGGGCGGATGECGCACTGGAATTCGGGCTGCGACCACTACGCGCAACAGCGACTCTCGCGATGATCCGTTCTACATCTACTACTCCATGTTTCGGTTTC CAACGTATCGGCGACTTTGGCTTTGGCGGGCGGGCGATATGCACGGCGCGCGCTTCTGCTGCGGCGGTACTGCGCGCTACGACGCTGAACGCTGACCAAGCTGACCAACGAAGCGGCCACA GCCACATCCAGCGCGACTGATTCGGAATCTGCGTATCTTATGACCCGACCTTCCAAATCAAGAAGTGGCCGCTCATCGTACAAAGACGCTTGGCGGATGTTATGCGCAATAAATGAAGACGCTGTT CTACTACATCTACCCCTGATGAACGAGAACTACACCCATCCCGATATGTCGGAAGGTGCGGAACAGCACTCTGAAGGATGATGATCTGCTGAAGCGCGCGGCAAGGCCGACAAGAAGTCA CAATTGATGGGTTCCGGTAGCAATTTGCAASAAGTGTATGCGCGTGGCGAGCTGCTGAAGAAAGCGACTTTCGGCGTGAAGCGGACATCTGGTCTTGGCCGCTCTTCAACCTGCTGCACCGG CACGCGATCGAAACGAAAGCTTCAACGCGCTGCATTCGCGTGAAGCTGAAAAGTGCCCTTTCGTTACTTCCCACTGCAAGTTCATGACGGTTCGGGTATTCGCCGCTACCGACTATATCGG CATGTCGACCGGCTATCCGCGGTACATCCCGAACGACTACCATGTCTTGGGCATGACGGTTTTCGGCGCTTCGACACCGCGCGCAACCTGCGCGCTCTTCTTGAAGTGGACCGCTAC AACGTTGCCGTGGCAGCATTTGGCGCATTTGGCGGAACAAAGCAAGTCAGCAAGAAACCGTTCAACAAGCCATTGAGAAATACGGCATCAAGCCGATTCAGCCCCTAGCTGGAAGCG

**SEQ ID 3960**

EQ ID 3960  
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 HPFKACGECSEBGLVFPQGHVAPGIIYARAFYBGRLETFEQLNNPQREVGDHGLSPYHPHLLPDFWQFPPTVSMGLGPTIMAIYQARFLKYLESRGLAKTKGRKRVWFCFGDGEWMDPESESQALIA  
 LAAREGLBNLTFVINCNTQLRLDGPVRGNGKI IQELBGNFAGAGWNVVKVITGRRWRDLAKDKGILQRMEECLDGDYQYTKSKDGAYVREHFFNTPELKAIVADMTDEQLWALNRGGHD  
 POKVYNYADRAANHADGKPTVILAKITKYGGMGASGEGQVNAHQAKMKMDKSLKQFDRDRPITVPTEDEQIESGLDPLYLTPADPTEEYKYLHARRDALGGYLPQRKPTQEVLEVPELSAFDAQ  
 LKSSGEREFSTTMAFVRIILSLDKKKIGKRVVPIVPDESRTFGMBGMFRQYGIWNPKGQQYTPQDKDLMPFKESVDGQILQELBNPAGAMDWIAAATSYANSDFAMI PPYIYYSMPGF  
 QRI GD LAWAAGDMHARGFLGGTAGRTTLNNEGLOHEDGHSHIQADLI PNCVSYDITQYFEVAVITQDGLARMYANNEDVPPYITL INENYTHPDMPGAEQDILKGHYLLKAGCKGDKKY  
 QLMGSGTILQEVIAGAEILLKADFGVEADIWSCP FNLLHHRDAIETERFNRLHPLEAEKVPVFTSQLQGHDPVIAATDYIRSYADRIIRATIPNDYHVLGTGFCGRSDSRANLRFPFEVDKY  
 NVVAALAAALAEQGVSKETVQQAIEKYGIKADSAPSWKR

**SEQ ID 3961**

SEQ ID 3961

TCGCGCCAAATGCGCTTCAACATCTTTGACCAACGCCGGGCGCTTTGTATATCAATCCGCTGACACTTGGACGCGGTCGTGCCAAGCGGATTTTCTCTGCGCGGTCCCGGCTTCCATA  
ATGCGCGCTACGCGGATAATCGCAATGCGCGCTGTATGTGTTCCGCCAGTTTPTTCAGCACCCGGTGTCTTTTTCGCGCACGGGAAACCGCTCAAAACCGCCCTGCTGCCTGCGAGCG  
AGCGGCTGCGAGGCTGTGATTGTGCGATGTTGGTGTGGTAGCGATGATGCCGTCCATTTCGAGCGATTTGACAGCAGCGGGCGATGTCTTCGATTGTGTCTTACCAATCGGGGGCGAT  
TTTGACGGCTAGCGGGATATATTTCGCGTGGGCGCGCAAGCTGCGCCTGTGTGTTTTCAGGGCTTCGAGCAATGCGCCCAATTGCGCGCGGCTTCGCGCGCGCGAGGTTTGTGTG  
TTGGGCGAGGAAATGTGACGGTAAATGTAGCTTGGCTGCGCGTAGGCTTTTTCGAGGCAGATTAAATACATATCCGCGCGCTTTGATGAGGCGTAAACCGGTTTTCGCGATGTGTGATG  
CCAATACGCCCTTGATATTGCTTTTTCATATTCGCTATCATCGCTCGATGCTGTGTTGTAAACCCATTTCGCTGATGATGCTTGGTGTTCTGGGAACGCGGAAGAGCGCGGCTG  
CGGCTTGCCGGGCTGCGGGTGGCGTACCAATCGGCTGCGATTTCGAGAGGCGGCAAAACGAGCGCGCCCAAGCGTCGATGTATTACCGTTTGTGTCGAGACCTGCGGCAAGCCGACAGG  
TTGGGCAAAATCCATACCCATCGCTTTTATAGGTTTGGTACGGTTGTGCGGTTACGGGAATCAGGCCCAATTTATAAACCGGTGTGAGAGCGCTGAGCGGTGAAGTGGTGGGCTTTTTCGGCAT  
CGAGTCAAAACAGGATGCGCGGGGCAAGTGGATACATGACAGGGCTTTCTGCTTCAGATGGAAATGCCGCCATTTTAAACGAAATCCGCGCAAAACATACGGCACAC

**SEQ ID 3962**

SEQ ID 3962

SRQCLQTFDFDQRRFAVYQSAVHLDDGGRQAQDFLCRVPAFHNAAYADNRQCAVYVFRQFFQHPVAFFAHGKTAQTAALLACERMAAEA\*FVDGGVGSDDAVHFDGDDAGDVFDFLCFTQIGGD  
FDG\*RDIFAVGGGKLRLLPVFGFPECAQFAAALQRAEVFGVGRGNVDGNVACVRVGFPEAD\*IIIGVLDGGRNEVFADVAQYALIFAFNTIAYHRVDAVVKVTHSVDDALVFGNAEEARL

**SEQ ID 3963**

[illegible]

**SEQ ID 3964**

SEQ ID 3964  
MPSEERRCGIKVPPPPCIDSGAEKDICLPPARFRNAGIRQACGAADGRAFFVHNSTFVPVTAMPSEBQYRQASRNISNQGNTMSLQNIETAFENRADIPTPTTVAPEVKEAVLETIRQLDSGX  
LRVAERLGVGGEKVNENAKKAVLLSFRIQDNEVLNDGVNKYFDKVPKTFADWSEDEFKNAGFRAPVPGAVARRGSGFVARNVLA MPSYVNI GAVYDEGAMVDTWATVGSQAQIGKNVHLSGGV  
GIGGVLEPLQAAPTILEDNCFIGARSEIVEGAIVEGGSVISMGVFIGQSTKIFDRTTGETIYQGRVPAGSVVWSSGLPSKDGSHSLYCAVIVKRVDQAQTRAKTSVNE LLRGI

**SEQ ID 3965**

SEQ ID 3965  
TTGTTTCCGGTTTGATTTAGAAATTTTCGTTTTGCTTATTATTTTTCACAAACGAAATAAAGGGGTGGCTACACCTCCCTCCGATTAAACACTCAACA

**SEQ ID 3966**

LFRFDLKFVFAYYFSQTKIKGLATPSLPKHS

SEQ ID 3967

SEQ ID 3967  
ATGTTTCAAAAAATTATAAAGCTTTGGAAGCAAGGGAACCTTGAAAAAAATGTTTCGGTCTGCTCCGCACGAAATCCTATCAGCAATCGGGTCTGCTGGCAAATAACCATGCTTTTAA  
AAGCAGGTTTATACTGAAGTTGGCGTTTGGTAAGGACAGGCTTTT

SEQ ID 3968

SEQ ID 3900

MFSKNYKSLGSKGLEKKCSVC SARNPISNRVCWQITMLLKAGFILKLAPGKDRSF

SEQ ID 3969

SEQ ID 3969  
GTGGGATATCGAATCGTTATGTCCTCTGTCGGCAATTTTCCTATTGCAGAAAATCTATACACAAGCTTTGTGGACAACCGTGTGATAAGCCACGGCTTGTGT

SEQ ID 3970

VG Y R I V M S L S A I F L L O K I Y T Q A L W T T V L I S H G L C



## SEQ ID 3971

TTGGAGGTGGTGC AAAACCTGCTTTTTTCGGTTTACAATCTGCACCGATTACTTTTGAATCTGCCTGTTTGGAAAAATACTTTTATGAAAGCCACCAATCTTTATCTCTACTTTAA  
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CTATGATGCCATGTATGACGCTCACTGCCGCACTTTTACCGCTTCGGGTTTGGCGTTCCGCGCGCTGCGCGCAGACACCGCGCAGCATCGCGGTACGGGTTCCGACAGTTTCAAGTGTG  
CGGAAAGCGCGGAGATGTGATGTCATACGCGACACTTCCGATTCGCGCGCAATATCGAGTTGGCACCGGACTTGGCGCTTAAAGGTGAAGCTGCCGCGCTCAGGCTGTGTGACCA  
AAGTACATACCAACCGTCAAAACCAATTGAGTCTTTGGTTGAATTCCTGAATTTCCGGTTGAACAAACCTCAATCCATCGTGTGTAAGGCGAAACGAAGCGCACTCGTCTACT  
GCTGTGCGTGGCGACCATGAGTTTAACGACATCAAGCGAGAAAACTGGCGCGCTAAAATCGCCACTGACTATGGCAAGCCCTGCCGCGATTGTGTAACAATTCGCGCAACCGCGGT  
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GCGCGCAATATACCAAGCTATGAACGTCAGCTTCTCGACAAATACGGCAATTCGCAATCATGAAATGGGCTGTACGCGCATCGGCACTACCGCGCTGTTGCCCGCGCATCGAG  
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CCGAATTGCTGCGCGGCGGCGGATGTCTGCGGACGCGGCGGAGCGAGCGAGCGGCTATGCTGAAAGATTCGAGCTTCTCGGTATCCGCGACCGCATGCTCATCGCGACCGCGC  
CTTGAAGAAGCAATGTCGAATACGCGCAACCGCGCGGCAACGAAGCGCAGGCGAGTTCATCGGAGAAATTTGTGCGGTGTAAACGCTTCAATTAATGCG

## SEQ ID 3972

LEVGAKEPAFFALQAPDLLNLNLFVWKNFTMKASQFFISTLKEAPAEAAAFASHKLMIRAGLIKANASGLYTWPMGLRLVLRKVENVREEMARAGSVELLMFVVPVPAELMQESGRNEFYGKE  
LLRLKDRHERDFCMGPTCEEVADIIVRKEINSYKQLPKNFYHIQTKRDEVPRFVGMREAFVMDAYSFHADYASIQATYDAMDAHCRIFTRIGLAFRPVADTGSIGGTSHEPQVL  
AESGEDIAYSDTSDYANIELAPTLPLKGERAAQAVLTKVHTPNVKTIESLVEFINIPEVQTLKSIVVEGENEGELVLLLRGDHFNIDIKAEKLAGVKSPLTHASPAALVEPFGANGG  
SLGPFVGTGKVVADFATEKGADWVIGANEDDYHTGTFNFRDAEPEFVDLRNVVEGDESPDQGRKLKLARGIEVGHVFLRGKTYQAMNVSFLDNWKGSIQINEMGYGIGITRVVAAATB  
QNNDEKGIWTKAMAPFEVVI VPMNYKSDTVREADRIYAEKLAAGADVLLDDRERAGVLLNDSLELGIPIRIVIGDRALKENVEYAEERRGNEAQAIVAGTIVARVTASLNA

## SEQ ID 3973

TTGGGGGAAAGTGAAGTGGCTTCAGTATTTTGAAGGAGAGCAGTCGAGGTGCGCAATTTTCTGTATCGGCAGGAATATGCGGCACATGTGGAAGAGTTAAAAACGAAATACCTT  
CAGAACCTGTGTGTTTATGAAGCCGTGAGCAGCATTTTGAACAGCGCGGTACAATCTTCTGCGCGGAGTTTCAAGTGGATGTGAGTTTGAAGTGGCACTAGTGTGCTGATFGCGCG  
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CTGAAGGCGAAAGGCTTACGCGCATTTCTGCGTGGTGTGCGATTTTTCGCGCGGCGAGACAGAAATCGGCAATCAAGATAAGGTTGTTTTCATTAACAAACCGCGCATTTGAACACGCGC  
GGGAGACTGGTTGATGATTTACCGATTTCGGAAATTTTACACAACTGGCGCGGATACGTTTGGGGAAGGGGATTGTTGTTTACCGGAACGCTTCCGCGTGGCGCAATCGG  
TCCGGGGGCAATTTGGCATTGGAGCTGGACGCTTGGTGGCGCTCTTTCACGATAGGGGT

## SEQ ID 3974

LGSEVASVFLGEAEVGNIFCIGRNYAAHVELKNRIPSEPVVPMKPSGSIILSGGTTLLPEFSRDVQFCELVLLIGRSDGTGBGEDILGCVAGYGVGLDLTARDIQCRILKAQGLFW  
LKAQGRHSACVDFAAADRI GNQDKVLFSLKQNVLRQGETGLMIYPIREILHLKLAADYGLRGDLVFTGTGPGVGAIGAGDNIALKELDLVCASTPTIGC

## SEQ ID 3975

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CAAGTTTGAACCGCGGCTGAACCGCGAGGTTCATCTCCCGCTCTATTGGGTTGACGAACGGCTGTGCTCCGCTCTGTGCGGAAAGCCCTGCTTTCGGAAGCAGAGGTCTTGGGCAAAAAACG  
AAATCGTGCTCGACCAAGTGGCGCGCAAGCATCTGTCAGCGTTTCTCGAGGCGCGCGCGGCAAGTTTTCACCGCGCGTGAAGGT

## SEQ ID 3976

MHKIPKGTALAFDFGEARI GVAQGDARLGLSHPLATVTTGSSNDEKFAATAKLVQEWQPRYFVVLGVHADGTREHMTLSRKFGRLNRFNLVYVWDERLSVSCAESLLSEAQVLGKRR  
KSVLDQVAQAAILHGFLEGGPABCFNREG

## SEQ ID 3977

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CTTGAACAGCTTGGCGATTGCGCGCAATTTTTCATCTGTTGCTGCCCGCGTACGCTGCGCAGCGGATGGGACAGCCCAATTCGCGCATGCCCTGCGCCAGCGCGATGCGCGCTTCGCG  
GAAGTCGAATGCGCATGCGCTTCTTTTGAATTTTATGATGCGCGCTTCCGCAAAAGCGCGAGCGGTTCGATGCGCGGATTTGGCGAATGCGCGCGGCTAACGGTGTTCGTTAGGGAT  
GTCGAACAGGATGTGTCGTCGCGCGGAACGGTCAGCCAGCATTTGTCGCGCAAGTTTCGCGTTCGAGCTGCCCTTGTCTCCAGCTCGAATAGCCTATGC

## SEQ ID 3978

VQDGLRRLVHRFAFFAQDLCFRKQAFGTGROPPFVNPIDGIEPAVQPAKSLARQVRHFMFRAVGMHGQSDDKITRLPFLNQLGDCREFFIVAAAGNGGQRMGPQFRIALRHADARFA  
EVEQCRSFVWFMHGRLEPKTGAGRCRVWRMRNRVRRGCTGCVRRRERSATHCRQVRVRAALCSSSNSLC

## SEQ ID 3979

ATGAACCTGTCCAACCACTTCTGCTCGCCATGCCCCGATATGGAAGACGCGTTTTTTCACAAATCGTCTCTATATCTGCAACACAGATGAAGACGCGCGACTCGGTATCGCCATCAACA  
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CCACTCCGATCGGCACTGGCAAGCAGCATCGCGCTTTCAGACGCGCATCGCGCTGACCTTCTCCGCGATGTGCTGAAACAAATTTACCGCAAGCGCGGTTCGCAAAAGCTTATC  
AGCATAGGCTATTTCGAGCTGGAGCAAGGGCAGCTCGAAGCGCAATTCGCGCAATCGTGGCTGACCGTTCCGCGCGACCAACATCTCTTCGATCTCCCTACGAACACCGCTTACG  
CCGCGCATTCGCAAACTCGCATCGACCGCTCGCGCTGTTTTTCGGGAGCGCGCATGCA

## SEQ ID 3980

MNLSNHLVAMPDMEDAFFSQSVVYICKHDEGALGIAINKPSPTIMDIFSATGKNIPMRMHDSVMHGGFVQVERGYVHTPIGNWQSSIGVSDGIALTSSRDVLENLISREBAGVDKALI  
SIGYSSWSKQLERELADNANLTFVPADEHILFDIPYEHRYAAFAKLGIDPLALFSGAGHA

## SEQ ID 3981

ATGAAAACCTGCTCTCTCTCATCCCTCTGACTACCGCTGCGGCGACATGACCGCGCATACCGCGCCACGCGCGCGCAACGCTTTGCGCGTGAACAGGAATCGTTCGCGCATCGT  
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GCTACGAATCCCAATACCAAGCAATACGCGCTTGGATGGGACCTTACAGCTGCGGCAAAACCGTCAAAGCTTCAGACCGCTGATGTTGATTTCTCGACATCACCCCTACGCGG  
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## SEQ ID 3982

MKTLLLLLPLVLTACGTLTGIPAHGGGKRFPAVEQELVAASSRAAVKEMDLSALKGRKAALYVSVMGDQSGNISGGYRISDALIRGGYTHNPDSATRYSPAYDPTATTKSDALSQVTTST  
SLINAPAAAL/KNNNGKRGERSAGLSVNGTGDYRNELTANPRDVSFLTNLIQTVPYLRGIEVPPYADTDVFTVDVFGTVRSRTELHLYNAETLKAQTKLEYFAVDRDSRKLLIAPKTA  
AYESQYQBYALMNGPYSVGKTVKASDRLMVDSDITPYGDTTAQNRDPFKQNNKPNPDVGNVIRRRKGG

## SEQ ID 3983

GTGCGCCCTCCAAACAAAGCAAACCTGCCGCCCTCCGGAACCGGGATTCACCGTAAGGAATTTTGATGAACAGACTGCTACTGCTGCTGCGCCCGCTCCGCCGACTGCGCTGCG  
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CCGATAAAAAATCCGACAAACGC

## SEQ ID 3984

VRPSQSKPCLRPENGSTDKETLMNRLLLLSAVLPACGSGETDKIGRASTVFNMLGNDRDIEVEGFDPDVQGVACYISYAKKGLKEMVNLLEEDASDASVSCVQTASSISFDETAVR  
KPKEVFKRGTFAPKSRQIVRYDYFKKAFAYLVSDKIVQSGPNLSAVSCFSGIPQTDGVQADTSKLLAGACIIISNPIKNPDR

## SEQ ID 3985

GTGTCGGAACACAATATCCGTTGCAGCAFTGAAATATGCCGACAATATAAGGCTGTTTGAGCCGATTGCAAGTATCCGCGCAAGAAGGTGCAAGATTGGGCAACCGCATTTTCAGAC  
GCATAAC

## SEQ ID 3986

VSEHNIRCSIENMHPNIRLFEPIASIRAKVKQDWANGIFRRHN

## SEQ ID 3987

GTGACGCTTCAGTATTATCCAACTTTTCCGAAGGTGCAACCATCGGCTACAAAACCCCTTCGCTTGCCCTGATGCTGCTTTTTTCCAGCCCCCGCTTGCCGCCCGACGCGCGCACACA  
ACCGTTCCCCCGAAGTGAAGAAACAGGCGAAGCAAAAAGAACAGCCCGAAGCGCGGGAAGGCAAAAAGCAAAAAGGCAAAAATGCCGAGTGAAGATAAAAAACAGGCGCGCAAGA  
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## SEQ ID 3988

VQPSVLSNFSEGRTHRYKPLLLALMLVFPSTPAVAHDAHNRSAEVKQAKNKKEQPEAAEGKKEKGNAAVKDKKTGKKAKEFKKTAKNKRKAKEATSRQARKRGREGDKSKAEHK  
KAHGKPVSGSKENAKTQFENKQKKGAKGQGNPRKGGAKBKDTVSANKKARS DNKGAVKRDKKHTEENKAKTDSDELKA AVAAATNDVENKALLKQSEGMLLHVSNLSKQLQREIRIQ  
ERIRQERIRQARGLNASVNRKQREAWDKPQKLNTELNRKTEVAATKAQISRFVSGNYKNSRPNALFLKNAEPGQKNRFLRYTRYVNASNREVVLDLEKQKALAVQEQKINRELARK  
KIQANVQSILKKQGVTDAAEYTESRRQNAKISKDARKLLEQKGNBQQLNKLKLSNLEKKAEBHRIQDAERAKRLABAKLAAAEKARKEAQQKABARRAEMSNLTAEDRNIQAPSVMGISG  
DGFSRMQRLKKFVGVGPTGLFGQNRSGGDNVKGVPYSTPATVESIAPGTVSVADELGYGVVVIDHGENYISYAGLSREISAGKGYTVAAGSKIGTSGSLPDGEEGLYLQIRYRGQVL  
NPSGNIR

## SEQ ID 3989

TTGCGGTTTCCCTACCTGTGTTTTCGCGTTTTCGGAATCAAGAGAGAAAGTTAAAGAAGAAATGTGCAAACTGTTTTTAAGAAATCGCACTTTATACTTTGGGTGCAATCAGCGCGCT  
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## SEQ ID 3990

LPPAVVFPVSGFWKSRKVEKBCRNLPKRSHFILWVQSAAMP

## SEQ ID 3991

GTGTCGACACGCTCGCGCTCGCGGCTTTCAAAAGTACGTTCTTATCTTTTACTTCGACATCGGGAACAATCCCTGTCGCTGAATGGAACGCTGTTGCGGCTGTAATACAGGGCGGTC  
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TCCAACACACGCGCTTGAGCGGTTTTCCTTTATTTTCCCTTACAGCTCTTTTCGCGCGGATTGAGCGTTTCGACCGCTCCGCTCTTGAAGTGGACACGCGGATATAGCCGTAATCGG  
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GACTCGTTATCCCGCGCTCTCTCGCGCGCAAAACCTTCACCGCAGACTTACGGCGACGCGCGCTGATGCAACCAAGTATAAAGTCCGATTTTCTTAAAAACAGGTTTCGACATTT  
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ATCTGCGCTTTCGTAGCGGGCAGCTTCCGTTTTCAAACGGTTCAGCTCGGTAFTGAGTTTGTGGAATTTGTGCCAACGCTCGCGCTGTTTGCGGTTGACGGGAAGCAAGGTTGCCGGCGCCT  
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**SEQ ID 3992**

VSDQVRLAAFKSTPLIFYPFDIGNPNCLNGTVVRRVIQGGRQLDRAAVGQRNQSLNRFTTEALRQLDDDRAPVVLQCGADNLRGRSGRTGIDQYRRNHRNRPQLGRNTRQRVAHTVHILGNGFYHAYVAVASIGADDDRFRQRRRHRADRAQKPAAGVVAQIQHQPLERFSFIFLYQLFCGGIDAPDRFLLELRHADIAVIFGQVMDADHFNFNNGQVDDYRLVGIFARQQRQSNLRLTLRPHFPHRFADRHTARRNITIDFNEIAAFHLRPPGRVLRNRRNHFDKTVLPDPHQAAPKAAAGLLYLGTFTVFIHPGMRIGTQHTHLTRTKQKQIGGFVMTVCLNLTNVRHLRDTGLHRQDFWIPVLLGGKTLHRQTYGHAADCTQKICQDIPRRNFRHSSLTSLDPQKPEWGTGKGLGHTAHIGITICKEPVSATRSVPARRVQLHSTITLYLQVPLFPVVRQKPARADFAQSCDRITLAGNGFAQTGIDADVVLAVTDHDFAVAVQLVRIAYRSRRNAPNRCRRSGIEHAFPNIAAAPVLPEKPGRHTVNRFPQTSLHAASTVGTADTHNRRRLDVPVFGGQVGHFTRSRSPLLRRRFFSGPFGCRQPGFSQPSFCFRILNAVGFPPFLQIAQELVQLLLVPFLFQQFSGIPGDFGILSAAPRLPRRIGYTLFPQOGLHVCINFLQTKGLIVDFLLLYRQSLLLFFQILNFPFIGGVYITRITQKAVPLTRFGVPFQEQGNRIRPAVIFPVRVETGNLFRSGDFRFTQVLQIEFLFVPSFALLFAVDGSKCVAARLTOTLLADTFLADTLFLKLFEGEIDMRKHQSPALFBQGFVFDIGGSGNGRQPGFQVIGFGFGLIFKVFFVPLPHCFVGLVGTGFTICRNSVPRLLAARLIALSPSCFVFLVFRKLCPVFFGSGHGLACLFFVRLRLFIIPASFARRLPGCRLLLCFPAVFGGFFFLPCLPAACFLPHCGILAFVFFPFRFLRQVFFFLVFLRLLPHFGTGVVCRVGGNGGRKNEHCKQKXGKGFVHGSGKGVG

**SEQ ID 3993**

TTGGGTGCAATCAGCGCGGTGGCCGTAAAGTCTGGCGGTGCAGGGTTTTCGCCGCCGAGAAGGACGGCGGGGATAACGAAGTCTCTGCGGTGCAATCCATCCGTACGATGGCGGAGGTTTACG  
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**SEQ ID 3994**

LGAISGVAVSLAVQGFABEKDGRDNEVLPQSIRTMAEVYQGQIKANYTHDKPDADLPEGAKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKVVSPIEDTPAERAEV  
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 GVSAAPLPESEAVVSTKGRDGKDMVLKAVPEDYVYMGGDPLAGIPAEIKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSPFGKSVQTLIPLNSGSAVKLTALTYTPNDRSIQ  
 AOGIVPDVEVKDKERTYTESREADLVGHIGNLGGEDVNSETLAVPLEKDADKPAAKEKGGKKKDEKLSRRRIPNPAKDQDLRKALDLVKSPEQWQKSLGLAAKPVSNKDKDKK

**SEQ ID 3995**

ATGTCAAACATCGAACCAAGTTAAGAAAAATTATGTGCAACAACCTGGGGCTAAACGAAGCCGACGTGAAAAACGAATCTTCCTCCAAGACGACTGGGGCGGGATTCTTTGGATACCG  
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SEQ ID 3996

MSNTEOQVKKI IAEOLGVNEADVKNESFODDLGADSLDTVELVMALEEAFGCEI PDEDAEKI TTVQLAIDYINAHNG

SEQ ID 3997

TTGTTCTTGGTATTGGGATCTCGTAGCGCGGGCTTTTAGGGGCAATCAGCAGTTTCCGGCTGTCGCGGTCGACGGCGAAATATTCAGAGCTTGGTTTGGGCTTTAAGGGTTTCGGCGTTGTAG  
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GGGATGAGGAGCAGCAGGTTTTCATCGCAGGTTGTTGTTGTTGTTGAACCGTTGAGTGTAAATGGAATTTAAGGGTTTGTAAACGAAAGGGGTGGAATAFGCCGTCGAAACGGCAGGG  
CGGGCTTCAAGCAGCATGTTTTCCTTGGGCTGAC

**SEQ ID 3998**

LFLVLGFGVGGGFRGNQQFPAVAVDGEIPELGLGFKGFGVVEVQFGTAADGAEYVDGYEYVGVGFGRYDFDAAQVEDGLDEVGBGNVAGVGEQGFVAVVARAVDQSGGAFAPASVVFQ  
GGGGGVQKRCGSGYAGERVCGGGGSGVIGGVAVSGGAVVVVAAAYQCVDGVASAAYVARTLVAHNGDVKGGFASFGQGGVHFFDGGAGRCGDEFLFDGKAFAPAAVGGYAGQCAAGGEY  
GDREEGFGHGRVCFVLNGFELCKWILRVCKRGKWKRLNGRAGFOTALFLHLY

SEQ ID 3999

ATGGACGGAAATCTGCCGCTCTGAACGGCTCGAGCGCTTGCACGCACATTGCCGGCCCGAGGTCGGATCCGCCCTATGCCGATGTGGACAAATCCGCAATCCGTTTTCGGTTATCCCTCGA  
TA

SEQ ID 4000

MDGNLPSERLERLHAHCRPEVGSAYADVDKIRNPFSGYPLI

SEQ ID 4001

FTGACGATCGGCTCGAAGGATTTCAGACGGCATATTATGTTTGAAGGACAGGTTATGAGCGGATTTTTACCGGAATTTGAACCGTGGCGCATTTATAGTGGATTAAACAAAAATCAGGA  
CAAGGCGACGAAGCCGCGACAGATCAAAA

SEQ ID 4002

LTMPSERISDGILCLKGOVMSDFLPEFEPCGIYSGLTKIRTRRRRSREOYK

SEQ ID 4003

ATGGAAGTATTCGCGATACCCAAATTCGCCCTTCAAACCTCCACCAACCCCTCCGCCCGCAGCGCGACCAAGCCACCGCCATTGCGGGGCTGATCGAAGGGCTTTTCAGACGGCCTTGCTTACT  
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CGTGTCCGAGCTACACCGTCTTCCCGTCCAGCCACTACGTTACCCCGCGGACACCGTATTCGCGCGCTGCGAATCCATCAAGAAGAATTCGCGGAACGCATCGAANTTTTCGCTCGCG  
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CATGAAGCGCGCTGCGACGAAACCGAAGCGCGCGGAAACAGATTAAATTCAACGAAGACAGCGTATTCGTGCGCGACGAGATTAAAAACAGGTCAAGACATCATCGACGCGCGT  
TACCACGAAGAAGCAGTGGCAAGGCCGTAGACAAGGCAAAACAAAGTCAAAGTCGCGCAAAATCCACAAGGAAGAGCGGATTAAAGAAATCGCAAACTGGAAGAAAGCCATGCGAGC  
AGGCGCGTAGGATTACAGTTTGAAGAAGCTGCTGTGTGAGGGATAGGATTAGCAATATTAAGAGAATTTGTTGTTTGGGGCGAG

**SEQ ID 4004**

MEVIRYFNSFFKLHQFPFAGDQPTAIALGLIEGLSDGLAYQLTGLVSGKTYTMANVIAQSGRPALIMAHNKTLLAQLYAEHREFFPENAVEFYVSYDDYYQPEAYVPSRDLFIKDSAI  
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RVGRYTVFPPSHVTPRDFVLRACESIKEELRERIEFFAREQRPVEQRIEQRTRFDLEMLYEMGFCKGIENYSRHSFGKKSEPPPTLMDYLPDNAMEFIDESHVITVTQIGMYKGDASR  
KQNLVDVGFRLPSARDNRLKFEHEFEKVMPTVFSATPAKYEEHAGQVVEQVVRPTGLVDPQTIRPVATQVDDLMSEINDRIQKGERVLVTT/LKRMAEQLTDYVSELGKVRVILHSD  
IDTVERVEIIRDLRLGLFDVLVGINLLREGLDIEVSLVAI LDADKEGFLRSHRSLQITIGRAARNVNGVAILYADKIDTSMKAAVDETERRREKQIKFNEEHGIVPQIKKQVKDIDGV  
YHEEDSGKRRQGNKVKVGEIHNEEDAIKELAKLEKAMQQAARDLQPEAAVLDRISNIKENLLPGAE

**SEQ ID 4005**

GTGCGCACACGCTATGTATTACAGGCTGCGATTACTATTTCAAAATCACTCCGCCCAACAAACAANTCTCTTTAATATGCTAATCTCTCAACACAGAGCTTCTTCAAACTG

**SEQ ID 4006**

VAHTLCIQAAITISKSLRPKQQLLFNIANPIPHSSFFKL

**SEQ ID 4007**

ATGCCCTCGTTTCCCGCGCACTTTACCCCGCTGACCGCTGCTGCTGTGTGGCTGTACCGCTTTCTCCGCCCGCACACGGCAATCACACCCATTTGGGGCTATACCGGACACGACTCTC  
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GCTCTCTTCCATCTGGAACGCTATGCGGATGACCGCAGGAAAGTGAACCTCAACCAACCGTTTCGAGCGCATCCACCTACTGCCGAAACGGTTGAAATACTACCGCTTTCGGGTTGCGT  
GACCACGCGCGCTGACAGAGGGCGTATCATGTTGTGTGTGAAACTTATGACCACATCGACCAACGCAAGCGGAAAAATTCACCGCGCGCTCGTTTCGGAACAAACCGCCCGTA  
CAGCCTCTGAATGCACGCTGTATTGAA

**SEQ ID 4008**

MPRPRTLRLTAVLLACATFASAAAHGNHHTWGYTGHDSPESWGNLSEKFLCSTGKNQSPVNITETVSGKLPAIKVNYKPSMVDVENGHTIQVNYPEGNTLTVNGRTYTLKQFPHV  
PSENQIKGRTPMEARFVHLDENKQPLVLAVLYEAGKTNGRLSSIWNVEMTAGVKLNQPFDASTLLPKRLKYRFAGSLTTPPCTEGVSWLVLKTYDHIQDAQAEKPTRAVGSENNRPV  
QPLNARVVIE

**SEQ ID 4009**

TTGAATCGGATTCAAATATCTTTGTTCGGCTATTAATATTTTCCCGATAAAGGTAGCCATGCCTCATGGTTATCCAAATAAGCAGGACTTATAGAAAA

**SEQ ID 4010**

LNRIQISLLRLIFFRKIVAMPHGYPNKAGLIEK

**SEQ ID 4011**

ATGACATATTTAAAGTAATAGCAATTAGTATAGTTTATACATTTTATTATGCAAAATTAATCTTAAATGTTAGAAAAAGGATTGATTCTTAGTAGAAAAATAGATAAATATTACC  
AGCAATATGGATCTTACCAATAAATTTGATTTTATATCAACTAAACATGATTTTACCAGTGAATCATTTGTGATTTTGGGATAAAAAATTCGAGGATATGTAATTTGTACTTCGT  
AAGAAATGATAAGACTTACTATTTTATGTCATGGGTTTCTCATCGAAATACTATTTTTCATCTCACAATAAATAAAGAAATTCAAATTCAAATAAATATGAT

**SEQ ID 4012**

MTYLVIAISIVLYILLQINLKMLEKRIDFLVENIDKYYQYGSYPNDFPISKTFDFTESYCDFWKNLAGYGNCFVKNDKDYTLVLMGFSSKILPSENKIKFNSNKYD

**SEQ ID 4013**

TTGGGACTTGTATTCAACCGGATCGGATAACAGACCGCGGATAAAAAATGCCGTCTGAAGCATGTTTCTTACAGACGGCATCTTTCAAGATAAAGCAGCGGGCGATGTTTCAATAC  
AAGTTTGAACAATGGTTTGAACGGCAAAACCGGTATACCGCACGCATCTTGTAGGTTTAACTGCACATCGGTTTTAAAGTTTATTCGCGCCGCGAGA

**SEQ ID 4014**

LGLGIQTDRIIDRIKKRLKHVCLQTAFFQDKAAGDVSIQVLKQWFERQKRVYTARILVGFNLHIGFKVYSARR

**SEQ ID 4015**

AACATCGAACAAAGTTAAGAAAAATATGCTGAACAACTGGCGTAAACGAAGCCGAGCTGAAAAACGAATCTTCCTTCCAAGACGACTTGGGCGCGGATCTTTGGATACCGTGGAGT  
TGGTTATGGCTTGGAAAGAGCCTTCGGCTGCGAAATCCCGACGAAGATGCCGAAAAAATCAACACCGTCCAAGTGGCTATCGACTACATCAATGCCCAACAGGCTAACCGGTGCTGCG  
CCGACACAACAGCCTCTGCTGCACCGCGCAA

**SEQ ID 4016**

NIEQVKKIIAEQLGVNEADVKNESFPQDDLGAADSLDTVELVMALEAFGEIPDEDAEKITTVQLAIDYINAHNG\*FVVARENSLOCTAQ

**SEQ ID 4017**

ATGAAGATAACACTGCAAAATTAAGAAAGAGTACAGAAAGAACCGCTCGGTCTTTTGTACCGGAAGTTACCGCCGCTTCTGCGCGCGATTTTGGGTATCATCCGATTCGCGG  
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ACATTAAACGGCATTTGGAACTTCGGAATTCAGGCAAAACGCGCTTTCGCAAAATACACGGAATTCGATCGTAAACCTTTCCCGCGGTGTTTGGAGGAATTCGGAATTTACCTTAACTCCG  
CACACCGCCCGCGAGCTAAAAATCTGCGGGATCGGTGTTGGAAT

**SEQ ID 4018**

MKITHCKLKEVQKEPLRSPVFEVTARSAADILGIHPSAALFYRKIRTVTNHRLLAADEVFERPAGPGGSCFGRRKRRRGRGAAGKAVVFGIPKRNGRAYTVAEDDAEPETLPAPVK  
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**SEQ ID 4019**

TTGTTAGACTACATTCCTGCTATATTTTTAATCCGGTTCTGAAAAATCAAGGAAAAACAGATGGATGCTTTTACCCGTGCATGGTATGCGCTCGAACGCCAFTATCAGGATACGTGCCACATCC  
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CGGAGCGCTATTTCGCTTCGGTCGCGCCGCTGAGTTTTCGCGGTGATGGTTGCGGTTGGCGGGCGCGGTTTCCGCGAACTGCTAGCGGGGGCGCACGCGATGGACAGCCATTTTTCACACGCG  
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GGCA

**SEQ ID 4020**

LLDYITLLYFNPVLKNQKQMDAFTRAWYALERHYQDTCIILLRDFAEPDRFERMHERLDGMLFOYSKNRFGEDTLQLLCRLAETADLEGKMRALRTGAKVNGSEGRAALHTALRLPDGA  
 DAVYADGRDVLPEIRRELNRALKFAHSLDDGLYQGITGKRIADFVHIGIGSSDLGPAHCQALEPFRRQISVHFVSNADPACLDEVLCLRLNPEPTMPCVASKSFTPTETLLNABAVKAHYR  
 GAGFSESETAHHFCVASDAETQCSFGFIAAGBVPFAMYDVWGGRYSVSWPUGLVPMVAVGGARPRELLAGAHAMDSHFHTTTPRRNIPVLMALIAVWYNNPQHADQOTAVPYSHNLRLLPAW  
 LNQLDMESLGRKSRASDGPAACTGTGIVFGVBVCNQAHYFQLLHQHQLTICPDFIVMTAQGAEDGRSRFTVANAQAGABALMGKRTLDPEARBLADLPEABERZLAPHKEFPGNRPSNS  
 LLDRLITPCNLGMLMAAYEHKTFVQGAJMVNVPNDQGVGEYKQLAKTITIGELGEGTSHVDASTEGFIMAFVRECRLLQAGAA

SEQ ID 4021

ATGACAGACACCCCGAAAAACCAACACCAACGACCTGCCGGCGGACACTCCGCGAGCATCCGAGTTTCGTCCTCCGCAAAAGCCACATGACCCGCCGACAGCAACGCGCCATCGATACCTTATGGGACAGCTTCGGCATCGACTACCAAGCAACACCGCCGATCTTGATGCCGCTTTCGGAAGCAGCGGACCTAAAACTCTCGAAATAGGCTTCGGTATGGGAATGGCAAGCGCAGAAATCGCCCGCGCTGCCCGAAACCGCATTTCTCGGCATCGACGTACACGGCCCCGGCGTAGGCAACCTGCTCAAACCTCATCAACGAAACCAATTGGAAACATCCCGCTGATGCGGCACGATCGCGTAGAAGTTGTCGAAATAATGCTGCAAGACGGCTGCTCGACGGCATCCACATATTCTTCCCGACCGGTGGCAGCAAAAAAGCCACCACAAACGCGCTGTGATACAAGCCCCCTGTATGCCAAACTACTGCTGCCAAATCTCAAACCGCGGCTATATCCACATCGCGCAGACTGGGAAGAAATATGCACAGCAGATGCTTGAAGTCTGCTGACAGCCTTCGACAACTCGCAAAATACGGCGCAGACTACGCCCCCATTCCGGACTACCGCCCGGAACAACAATTTCGAAGCGCGCGGCAAGACGCTCTCGGACAGCGGCTTTGGGACTTCGTATCAAAACGATCGGA

SEQ ID 4022

MTDTTPENQTPNDLPAGHSRSIRSFLVLRQSHMTAAQORADITLWDSFGIDYQATPADLDRFGSSRPKILEIGFCMGZSAEIAARRLPETDFLAI DVHGPVGNLKLINZHNLENIRVRRH  
DAVEVVENMLQDGLSDGIHIFPPDFWHKKRHHKRRLIQAPPIAKLLPKLTKGGYIHLATDWEZYAOQLVLSSFDNLONTAADYAPTPDYRPETPKFEARGKRLGHGVWDLVFKRIG

**SEQ ID 4023**

ATGTATTATCTTCGACAGAGGCACAGCCGCCGACTACAAACAAAGCCCGCAATGGTTTGAAACAAGCCACTCGCAAAAAACAGTATGGCGTTCACAACTCGCCTGCATCCATTACAGCG  
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**SEQ ID 4024**

MYYPGQGTAA~~DYNKARKW~~FEQATSQKNSMAFYNLACIH~~YSGHGV~~KPD

SEQ ID 4025

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SEQ ID 4026

MKGTSAKNNPHGQYLLAQYCRHGTTPPDFETAHLLYRKAAQGLPEAHWQLGLQYRFGQTKADTAQAVNHLRAAQQGYIIPAYTPIABLILPTAPDEAVYRFGQAAQENDPDAHAALADI  
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SEQ ID 4027

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CGGCACGCCCGCGGATTTTGAACCGCGCACCTGCTCTACCGCAAAGCGCGGCACAAGGCTTGCCGGAAGCACATTTGGCAACTCGGGCTGCAATACCGTTTTCGGACAAGGGACGAAAGCC  
ACACCGGCACAGGCGGCAATCATTTTTCGCCGCCGCCGCGCAACAAGGATACATTTCCCGCTTACACCCCGCTTGCCGGAATCATCTTACCTACCGCTCCCGATGAAGCCGTTTACCGGTTCC  
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SEQ ID 4028

MTRQNGKRSIDMNNPDFLYRQALERLSQKQYTYNFTVEVRRLLTEASADHPAAAFELAKLHMNANSPHQDREGQGMENLRIAAEQGHFYARYNLAYIQELEGAPPFTLLPLYRPLAEAGLPEAQ  
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SEQ ID 4029

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GATGTCGTGTGATTGACCGCGGTGAAGGCGCAATCGCGGTATCGCCGTATCGGTATGGGAAGAACTCGGGCTGCACATCCCTTTAGTCGGTATTGCCAAAGCCCGGACGCAAGACCGCGCA  
TGGAAGAACTCATACTGCTCTTTCAGCGGCAACTCTTCCGCTGCTCTCTATAGCCGGCTTGCATTTATTGCAAAACGATACCGGATGAATPACACCGCTTTGCGATCAGCGGCCACCG  
TAAAAAACCGCGACAAGACGCGGTTACCTGCTCTCTCGGCGACATTCGCCGTGTATGCGACAAAACGCGCCGCAAGCCCTGCTTACCGCTTCGCGGCACTGCGCGGCGTGATTGCCGCCAGC  
CGCGAGGACTTGAAAAAAGTGAAGGCATCAGCAAGGCATTGGCGGAACCAATTATTAATCATCTGCAT

**SEQ ID 4030**

SEQ ID 4030  
MPSEAVQIMDNWTEHRSPEQFDIPLFLKLNPKLPGVYRFFDEGGNVLYVGKAVNLKRRVSGYFQKNDHSPRIALMVQKVRIETTITRSEAEALILENNFKALSPKYNILPRDDKSYFY  
LMLSGHQYQPMAYYRGTLKNPNQYFGYPYNSNAVRDSIQVLQKVFMRLTCEDSVFHEHRDRCCLLYQIKRCTAPCVGHISEEDYCDSVRQAATFIANGKTDELTRTLQHKMQTAANLQFEEA  
ARYRDIQIALGIIQSNOFIDSKNPNPNNDIDLIALAVSDGLVCVHVMSIRGRHVGDKSFFPDTKNDPEPNGQDYAEAFVAHQYLGKSKPDIISNFPVPDALKEALBGEHGKMQFVTKT  
IGERKVLWKMAEQNAQMAITQRHLQSQNQHERIDELAKILGMNSDGINRLECFDIISHTQGEATIASCVVYDQNIQPSQYRRYNTTTAKPGIDYAAAMREVLITRRYKGIQEAENGESVKWP  
DVVLIDGGKGQIGVAVSVWEELGLHILPLVGLAKGPERKAGMEELILPFTGELFRLPNPSPALHLLQTVRDESHRFAITGHRKKRDKARVTSLSGDIPIGVGSKRRQALLTRFGGLRGVLAAS  
REDLEKVEGISKALAEITYNLH

**SEQ ID 4031**

SEQ ID 4031

GTGTTGGGACATGTTTTCCTTTGCTGTGTCAGATTTTCGGATTCTACCCGAATTATCGGCGGTTTGAGAAATTTTGACCATACCGCGCTTCAGACGGCATCCCGCAGCCTTGACTGCC  
GTCTGAACATCAAAACCGGAAATCAAACCTATGTCACAAACAAAAATCCGTTTCCAATCGAGGGGATGACCTGTCAAGCATGTGCTGTCGCGCATTGAAAAAGTGTGTAACAAAAAGATTTTGT  
CGAATCGGCGGGAGTGAACATTTGCCAGTGTAGGAAGCGCAGGTTTACGTTTGTACGGCAGAAAACTCGGTTGCCGACATTGCCAAAATCATTGAGAAAAACCGGTTACGGCGCGAAGGAAAA  
ACGGAAGATACATTTGCCCAACGACTGAAGCAGACACCATATTGTCGCTGCGGTTGTGGCTTTTGTGACCATCAATATCCCGTTCCTTATCGGTATGTTAGGATGATGCTAAAAAGGGCTGA  
ATTGGACACGCGACGATGATGATGATTTCCGCGCTGTATGGCAGTTTGTACTGGCAAGCATAGTCAACTTTGGCTGGCAATCCCGTTTACAAAAAGCGCGTGGGCAAGCATTAAGGGCGGGCT  
TGGGAATATGGACGTACTCGTTTACCATCGGCACGCTGTCGATTACCTGTATTCCGTTTATATGCTGTTTTCAGTTTCGCATGCGGCGCACGSGTATGGCGCATGTGTATTTTGAAGCGGCG  
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ACGGCGAATGGAACAACTGCCCATCGACCAAGTGCACAAATCGGCACCTTATCCGCACCAACCCAGCGCAACGCATGCTGCCAGCGGCAATGTCGGAAGCGGCGAGCGGTTGGGCGGACGA  
AAGCCACCTTACCGCGCAATCCAATCCGGAAGAGAAAAAGCGGGCGGCAAGTGTTCGGCGGCGCGGATGTGACCAACCGTGGCGGATGACGAGCGGCGGATGAAAGCGGCGGCGTATTGTGCCA  
CTGCTCGCGCATGATGAACCGCTCTCTTGAAGCACAAGGCATGAAGCACCAGTATGGCGGCTGCGACTGTGACACGCGGTTGCCGTTTGTGGTATGCTGCCGTCGCGCTCGGTCTGGCGACCCCTGCCGCGATATGTT  
CTTTTATCGTTGCTTGGCTGATTAAAGGCGGATTTGGCGGCTGCGACTGTGACACGCGGTTGCCGTTTGTGGTATGCTGCCGTCGCGCTCGGTCTGGCGACCCCTGCCGCGATATGTT  
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GAAGCCATAGGCGGCTGAAAAAACACAATATCGATGCTATATTATGAGCGGGCATACCAAAGTACGCTGCAATACGTCGCGCAACCGAATTTGGCGG  
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GAAAGGCGGTCGGGACGTTGCGGAAACACCGCGCTCGCGCACGCTGATGACGATTCGGTCAATCAGCTCGCGGATCGCTGCTGATATCGCAGGCAACGTTGGAAAAACATCAAGCAAAAC  
CTATTTTTCGCTCTCTCTACAAATATATTGGGCATTCCGCTCGCGCGCTCGGCTTTTAAATCCCGTCATACGAGCGCGGCAATGCGGCGCAAGCTCGGTTTCGGTATTGGGCAATGCC  
TGCCTCTGAAATGGGTAAAAATCGAT

**SEQ ID 4032**

SEQ ID 4032

VLHGCFSAVSSFRILPELSARLRNFDTGVQTASRSLDCRLNIKTGIKLMQQKIRPQIBGMTQCAASRIEKVLNKKDFVESAGVNFASEAQVTFDGSKTSVADIAKIIKKTGYGAKKE  
TETDLPQRAEHHTGWRLMLLLTINIPFLIGVMMLKGLNWRTRDHMI PPVWQFVLASIVQLWLAI PPYKSAWASTKGGGLANDMDLVPTIGTVSYILSVYMLFFSSHAHGMHVYFEG  
VMVIGFVSLGKFLHRTKSSLSLGLLLKLTPTQVNWQRNGEWKQLPIDQVQIGDLIRTNHGERIAADGIIIESGSGWADESHLTGESNPEEKKAGGKVLGALALMTGSSVYRAAQLGSQT  
LLGDMNALSEAQGSKAPIARVADKAAAVPPTVVGIALITFIVAWLIGDWTVALMHAVAVLVIACPCALGLATPAALMVGMKGVKHEGTFPKDAAMEEAAHVDAVVLDKTGTLTBGRP  
QVAAYVYPVDSGDFEDALYRIAAAVQGNAAHPLARIATVSAQAQGLEIPAAQNAQTTVVGAGITAEVEGVGLVKSGLKAEFAELTFPKPSDGVWEIASAVTVSVNGKPIGAPALSDALKADTA  
RAIGRLKKNHINISGDNQSTVEYVAKQLGIAHAFGNMSPCDKAAEVQKLKAAAGKTVMVVGDGINDAPALAAANVSFAMKGGADVAETHASATLTMQHSVNQLADALLISQATLENIKQN  
LFFAFFNYNLGIPLAALGFLNFPVIAGAAMAASSVSVLGNALRLKRVWKID

**SEQ ID 4033**

SEQ ID 4033

ATGCGCAAACTGTTTGAACCCCTGCCGCCAAATTACAGACGGCATCTGCACGACAGCCGCATATGCCCCCATATTCGCACAACCAACAGCGAGGTTATCATGAGTCAGAGAAGAGTAGTCATTA  
CAGGCTTTAGGTTCAGGTTTCCCTCTTCGCGAACACTTGC CGCAGAGGCTTGGGACAACTGCTGCGCCGGCAAAGCGGCATCGCGCGGATTAACCCGCTTTGAGCCATTCGGAATCAACAGCGC  
TGTGCGCGGCGAAGTCGCGGGTTTGCGACATCGGACAATACATCAGCGCGAAGAAGCGCGCGGATGGAGCTGTGTTACATCCACTACGGCATTCGCCCGCGCATTTGCAGGCGATTCGCCGATTGC  
GGTTTGGACGATGTGGA AAAACCTCGACAAAGACCGCATCGCGGTGAACATCGTTCCGCGCATTCGGCGGACTGCCCAGCATCAGAGCCACCGCAAAGCCGTAATCGAAGCGCGCGCGCGCA  
AAATCAACCCCTTTCTTTATCCCGGTTTCGTGATCACTGGATTTCGGGACAGCTTACCATTCTCAAAGGCTATCCGCGCGCGGCAATCGGATGGTTCCTCCGCTGTACCAACCGCGCGCGCA  
CGCCATTCGGCGATTCGCCCGCAGCTACTCAATAATCAGCGACCGGCACATGTTTTCGCGCGCGCGGCAAGCGCAATCAGCACTTTGGGCGTGGCGGTTCCTGCGATGAAGAGCCCTC  
TCCACCGCGAAGCAGCAGCCCGCACCCCTTCCTCGGTCGTGGGACAAAGGCGCGCAGCGGCTTCGTATCCTGGCGAAGCGCGCGGCAATTGGTGTGGAAGAAATAGAACACGCGCAAAAAC  
CGGCGCGGAAAATCTACGCGCAAAATCGTCGGCTTCGGCATGAGTTCGGATCTTACCATATCAACGCGCGCAACGAAGAAGGCCCGCCCTTGGCGTTACCCGCGCGCTCAAGAGTGTGCGG  
CATCAATCCCGAAGACGTGGATTACGTCAAGCGCGACGGCAGCTCCACCCCTTTGGGCGGATGCCAACGAACAAACCGCTCAAACGCGGTTTCGGCGAAGACAGCGCTGCAAAAAGTCTCATC  
AGCTCGACCAATCCATGACCGGCCACCTGCTCGGCGCGCGCGCGCGTGTGAGCGCTGTACAGCATTTTGGCGATACACAGCGCAAAATCCCGCGCACCTCAACATTTTGAACAAG  
ACGTTGAAGCGCGCTCGCATTTGGACTACTCGCGCAACGAAGCGCGCAGCGGAAATCGACGTTGCCATTTCCTCAACTCTCTCGGCTTCGCGCGCAACCAACGCTACGCTGGTCTTCAACG  
CTTCAAAAGGC

SEQ ID 4034

SEQ ID 4034  
 MANCLNPCRKLQTASARQPHMPPIPTTNSEVINSQRRVVITGLQVSPVGNATAEAWNDLLAGKSGIGAITRFDASDINSRVAGEVRGFDIGQYISAKEARRMDVFTHYGIAAALQAIADS  
 GLDDVENLDDKRIGVNISSGIGGLPSIEATGKAVIEGGARKINPFPIPSGLINLISHVITILKGYRGPSTGVMVSACTTGAAHTGDSARLIKYGADIMVAGGAEGAISTLGVGGFAAMKAL  
 STRNDPATASRPWDKGRDGVIEGAGILVLEELHAKRGAKIYAETVGFPMSSDAYHITAPNEBGPALAVTRALKDAGINPEDVDVYNAGTSTPLGDANETKALKRAFGHEHACKTVI  
 SSTKSMTHGLLGAGGVEAVYSILAIHDKGIPPTINIFQDVEAGCDLDYCANEARDAEIDVALNSNPGFGGTNGTLVFRKFKG



## SEQ ID 4035

GTGTTTATCTTCATATTTTCGAGGGTAACATATCTGCTAATCTGTACAGACCTTGTCTTATCGTTTGAATGCTGCACCGATGTTAACGATAATCTGTGTTTACGGAAAAATCAAAT  
TGCAGAGTTTGAAGAGCGCGCGGGATTCAATATTGTAAGCAGGATTGGATTTTTCTCGCGGGCGGCTTCGTGGCGACGCTTTTGAACAATTTTACGGGCAAAAGCTGACGGAAGA  
AGAAGTGTGGAAAACTGGTAAAGAACAGATGCGCGCGTCTGTGAGGATATGCGCGCATATGCGCGGATTGGGTTTGAAGCGAAAGGCTATGCCCTGCTCTTTCGAACAGCTCGCG  
CAGTTGAAAAATCCCGTCACTGTATCTGAAATACCGCAAGACGACCATTTTTCGTTATGCGCGGAGTGGCAATACGTTTTCGTTGCCGACCGCTCGCGGGTCACTGTTTCGA  
TGAGCAGGGCGCAGTTTGGAGGCTTGGCAACCCGTCAGGGAATTTGGCAGGCAAAATTTTGGCGTCTGCCGAAAAAGCGGAGCGGATTTCAAATAAATGTTTTCACACATCA  
TCCCAAGCGGACAGGAGTTTGCAGTCGACAGGTAATAATGTCGCTGCTAT

## SEQ ID 4036

VCVLHISRVTYLLIWRPLSYRLNAPMFNDNPVYKIKLQSWKARRDFNIVKQDLDFSCGAASVATLLNNFYGQKI/TEEEVLEKLGKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLA  
QLKIPVIVLYKRYKDDHFSVLRGVDGNTVLLADPSPGHVMSRAQFLBAMQTRGNLAKGLAVVFKAEALSNKLFTHHFKRQTEFAVGQVQKWRAY

## SEQ ID 4037

TTGCAGGATATTGTTGCGGGTCAAATGCCGCGGAGGGTATAGTAATTAAACAAAACCGGTACGCGGTTGCCCGCCCCGCTCAAAGAGAACGATTCC

## SEQ ID 4038

LQDIVAGQMPAGGYSKLTGTALPRPGSKRTIP

## SEQ ID 4039

ATGTCCCAACCCGCAAACTGATTATTTGGGTTCCGCGCCCGCGGATACACCGCGCGCTATGCGGCACGTGCCAATTTAAACCCCGTCATTATTACAGTATCGCGCAAGCGGGC  
AACTGATGACAACGACTGAAGTGGCAACTGGCTGCGGATGCGGACGCGGTGCAAGGCGCGAATTGATGCGCGGTTTCGCGCCACGCGCAACGTTTCGGAACGGAATCATTTTGA  
CCAAATCAACGCGCTGATCTGCAAAAACGCGCTTCGCACCTCAAAGGCGATATGGCGGAGTACACTTGCAGTGCCTGATTGTGCGCCACGCGCGCTCGCCCAATACCTTGGTTGCGG  
AGTGAGGAAGCGTTTGCAGGGAAGCGCTTTCGCGCTGCGCCACCTGCGCAGGTTTCTCTACAAAAATCAAGATGTTGCGGTAGTGGCGCGGCAATACGCGAGTTGAGGAGGCACTCT  
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GGAAGCAACCTGCAAGAGTACTGGCGACGATCGGGCGGTAATGGCGCAATTATTAATAACCAACGCGGTTCTGATCAACAAATGCGCGTACGCGGATCTTATCGCCATCGGCGAC  
AAGCGCAATACGATATTTCGAAAGGCGAGTTGAAATGACGAGCGCGGTACCTGAAACAAAGGCGGCGCGGCAATATGCGGTGCAACCAATATGCAAGCGGATGCGCGCGG  
GCGAGTAAAGACCATACCTACCGTCAGGCAATTACACGCGCGCTCCGCGCTGTCAGCGCGCTTTGGACGCGAAGCGTTGCGTGGCGAGCCAAACATF

## SEQ ID 4040

MSQHRKLIILGSGPAGYTAAYAAANLNPVITGIAQGGQLMTTTEVDNWPADADGVQGPMLARFLAHERFGEIIPDQINAVDLQKRPALKGDMGEYTCDALIVATGASAKYLGLP  
SEEAFAKGVSACATCDGFFPKNQDVAVVGGGNTAVEEALYLANLAKTATVTLHRRSEFRAEKIMIDKLMKRVEEGKIILKLESNLQEVLDGDRGVNGALLKNNDSQDQIAVSGIFIAIGH  
KPNTDIPKQLEMDRAGYLTGTGADNVGATNIEGVAAAGDVKDHTYRQAITSAAGSCQAALDAERWLGSONI

## SEQ ID 4041

ATGCGTCATTACAGATCGTGTATTATCGTTTCATCTGATCAAGCGAGCAAGTCCCGCTATGGTTGAACGTTACAAAACCATGATTACCGAGGCAACGGAAGATTACCGTTTGGAAAG  
ATTGGGGCGCCGCCAAGTGGCTTACCGGATTAACAAATCCATAAAGCACATTATGTTTGTATGAACATGAAACCACTCCCGAAGTTGTTGGGGAGTTGGAAACCGCGTTCCGTTTCAA  
TGATCGGATATTGCGTCATCTGACCATCAAAACCAACGCGGTTACCGAAGCTCCCGTATGCTGGCGCGGAAAAGGCTAAGAACTGTTGGTGGCGCGGCTGAAGAAGCGGCTGCC  
CAA

## SEQ ID 4042

MRHYEIVFIHVPDQSEBQVPMVERYKMTI TEANGRIHRLDWRRLQLAYPINKIKAHYVLMNIETTEPVVGELETAPRPNDAVLRLHITIKTHAVTEASPMLGGEKAKNLLVGAEEAAA  
Q

## SEQ ID 4043

TTGGGCGAGCGCTTCTTCAGCGCGCGGACCAACAGGTTCTTAGCCTTTTCGCGCGCCAGCATAGGGGAGGCTTCGGTAACGGCGTGTGTTGTTTGTGTTGATGGTCAGATGACGCAATACCGCA  
TCATTGAAACGGAACGCGGTTTCCAACTCCCAACAACCTTCGGGAGTGGTTTCGATGTTTCATCAAAACATAATGCTTTATGGAATTTGTTAATCGGGTAAGCAGTTGGCGCGCGGCC  
AATCTTCCAAACGCGTAATCTTACCGTTTTCGCTCGGTAATCATGTTTGTAAACGTTTCAACCATAGCGGCACTTGTCTCGCTTTGATCAGGATGAACGATAAACAGCATCTCGTAATGAGC  
CATGTTATCTCTTATGATGTTGTAAGAAACAGCTTCTGCCATGCGAAAGCAGAAGCGAAGGTTCAAATAGCAGGCATTATATTGGGTTTTCGCGCAAGCAATCAAGGATTTGGTACGAAAAA  
CTTGCAATTCGCGCAAAATTTTCGTTTTCAGACGCGATTCAAATGTTTGGCTGCCAGCCACGTTCCGCGTCCAAAGCGCC

## SEQ ID 4044

LGSRFPSSRADQVLISLFAAQHRRGGFGNGVFGDGMQYRI IETERGQFLPNFNGSGDFVHQNIMCFMDFVNRVSQLAAAPIPQTVNLTVCLGNHGFVTFNHSHILLALIRMDKHDLVHT  
HVISLMMVKTAFCBAKAGKVQIAGIILGADGKIDLVKRTCPKISVSDGIQMFVLPSSRSASKAA

## SEQ ID 4045

TTGGGATTCATAATCTTGTTCGCTTGGCGCGCTGATTGAAAGGCTTTCCCTATTTCGATATACGCTGCCGGAATCCCTGTTTATGATATTATTTAAAGCAGCAATCGTGCGCAGGAGG  
AAAATGGGCGCAATGCTTGTCCAATTGGAATCCCGCGCGGATTTTGGGTAGGCGGCGAAGAGTGGCAGTATCGGCAAGGCGACTGCCCAACAGTCAAGGTTTATTAGCTCAAAA  
AAGCAGAGCTTCCCTGATGCCGATGCTCAGGATACAAAATATTAAGAAATATAAGGT

## SEQ ID 4046

LGFTNLVSLAALIEKAFPIRYTPAGIPVLDIILKHESWQENGQQLVQLBIPARILGRQAGEWQYRQGDCAITVEGFLAQKSRRLMPLRLIQNIKEYKG

## SEQ ID 4047

ATGGCTCGTCAATCATTAACGATGAAAAATCTCGCGTTTCAGCGCTGAAAAATCCAGAAGTCGATTACAAACAAGTTGATTGCTGAAAGACTTTATCTCTGAAAACGGTAAAAATCA  
TTCTGCCGCTACAGGAACGAAGGCAATTTACCAACGCCAATTTGGCTGTTGCCGTAAAAACGCGCGCTTCTTGGCACTCTGCTTATACCGACCAACACAAA

## SEQ ID 4048

MARQSPKRRKFCRPTAEKIQEVDYKQVLLKDFISENGKIIIPARITGTAFYQRLAVAVKRAFLALLPYTDQHK

## SEQ ID 4049

ATGAAAGAGTTTGAAGCAGCGCGCGCGGAATTTGAAGCAAAACAGGCGGAATTTTGGCAGATGCCGAGCGCTCAGGAAAACTGGACGGTCAACCGTTACCGTTGCACAGAAAGCGG  
GTGTGAGCGCGCGCTGTTGCGTTCCGTTACCAATGCCGACATGCTGCCGCAATCGTTGCTGCCGCGCATCGAAGCGGTGAAGCAAAATGACGCTGCCGCAACGCTCTCTGAAAGCGGT  
TGGAGAGTACGAAGTGAAGTGGCTTTACACACTGATGCCGTTGCTAAATTAATCTGTTGCCGCTATGCCGCGAGCCGAG

## SEQ ID 4050

MKEPEARAELEKQAEILADARARQEKLDQTVFVAQKAGVDGRFLGSVTNADIAAAIIVAAGIEAVKANVRLNPLKAVGTYEVEVALHTDAVAKITVAVIAAAB

## SEQ ID 4051

ATGCCGCTGAAACCCGCGGATTATCAGAATGTGGTTTCAGACGCGATTGTTTGTGTTTCCGTATATTCTGCAAAAATCGGACGCGTTGTTTATTATTGCTGAGGCTTTGCGAGAA  
TGGTTGT

## SEQ ID 4052

MSEFLPIIRMFQTAFLVFSVSAKIGTVVFFLPEVFAEMVC

## SEQ ID 4053

ATGCATCAAAATTCGTTAAACAAACATTTCTGCAAGACCTCAGGCAATAAAAACAACCGTCCCGATTTCGAGAATATACGGAACAAACAAATGCCGTCTGAAACCAATTCG  
ATAATCGGCAGGGTTTCAGACGGCATCTGATAATTTCAATTACTCGGCTGCGGCA

## SEQ ID 4054

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## SEQ ID 4055

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TCAATAAATAATACACAGGAACCGCCATGACAGAAATCCATCACCCGCGACAGTATGCAATACGATGTGCTGATGTCGGCGCAGGCCCGTCCGGGTGTCCGCCGCCATCAAACTCAAGCA  
GCTTCCGCAACAGAAAGCGCGCGAAATCAGCGTTTTCGCTGGTGGAGAGGGTTTCGGAGGCGGGGCGCATTCGCTGGCGGGCGCGGTTATCGATCCGATTGCGCTGAATGAGCTGATCC  
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ACATCGTCAGCTTAGGCGAAGTCTGCGCTGTTGCGGAGCAGCGGAAATATGCGCGTGGAAATCTATCCGGGCTTTGCGCGCGCGAAGTCTGTATACGAAGACGGCTCGGTCAA  
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TCCAAAGCAATCATCGAAGCTTTCCAACTCGACCAAAACAGCCAGCGCAAACTTACGCTTGGGCGATCAAGAAAGTTTGGGAAGTGCCTGTAACAGCATCAGCCGGTTTGGTGGTGC  
ATAGCGCAGGCTGCGCGTGCAGCAAAACCTACGCGCGTGGCTTTATTTACCATTTTCGACGACAACAAAGTCGCGCTCGGCTTCGCTGCTGGTTTGGACTATCAAAACCGTATCTGTC  
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TGCTGAACAATTCGCAACAGATGATAGACGTAACATATAAAGAAATACGCTCTCCGCAACGCGCTATTGTCGCGCGCGCTATATGAATATCATGAAGAAACGCACTCGCGCTGCA  
AATCAACGCGCAAACTCGCTGCACTGCAAAACCTCGCACATCAAGACCGGACGCAAAACATCACTGGATTGCGCGGCAAGCGCAAGCGGCAAGTATACGCGCGGATG

## SEQ ID 4056

MVACLKFRQRSSNRKHGFRPLLYLVITCSRCIITDLPNNKYTGAMTESITRDSMQYDVVIVGAGPSGLSAAIKLKQLABQNGREISVCVVERKSEAGHSLAGAVIDPIALNELIP  
DWKEKAPLRTVTQDKVLPLTEKAPNLPTPNFNDHNGYIVSLGEVVRWLABQENMGVEIYPGFAAEVLVHEDGSVKGATGMDGVKDGPTDSFQPMELNARQTLFAEGCRGSL  
SKQIIEFQLDQNSQPTTYGLGKEVVEPSEQHGPLVVSAGWPLDSKTYGGAIFYHFDNKNVAVGVVGLDYQNPYLSPFEEFQRFKTHPEIRKTFEGGRRIAYGARSILBGLQSLP  
KLSFGGVLIGDAAGFLNMPRIKGIHTSMKSAMLAABAVPPLLENFEEVESDGGKEAGNYQKLFQSWLYQELYAARNVRPSFKWGVYLSGLTYGIDQIMPRGKAPWTLKEHGRDNEQLK  
KAAVCKPIDYKPKDGLVTFDLRLSVFLANLAHEENQPDHLVANNPQTMIDVNYKEYASPETRYCPAGVYIEENGSPRLQINAANCVCKTCIDKDPQNTIWTICPEGASGPNYGM

## SEQ ID 4057

ATGAAAACCGCGACATCCCGCTGCGGGCGGCAACCGGACAGAAATCGGATGCGATTATACCTTATTTAGCGGCTGTCCGGCATTTATGCGCACACAATAAATCTGCAAGATATGTT  
CGCGGTCAAAATGCGCGCGGAGGTA

## SEQ ID 4058

MKTADIPPAGGRDRICDYYTLFRRLSGIYAHTINLAGYCCGSNAGRRV

## SEQ ID 4059

TTGTATGCCGTCATTATGCGGAAATACCGTTTGGGAGCAGTCGCATCGCATGAGTCGGCAGGCGAGCGATGCGCGGATGCTTCGGCGGTGAAGCGAGGAAATCGGCAGTTTGA  
AAAAGGCAATGGAATTCGCGAGTGGTGTGATTGGGTGTTGAAAGCA

## SEQ ID 4060

LYAGHYGNTVWEAVASHVGATAGDAMPSPGVKAGSAVWKKAMESAGRCRLGGERQ

## SEQ ID 4061

GTGCGCCGACTTATTGCTTTTACCACCCAAATCGACACCTACCTCGGNTCCATTGCTTTTTCCAAATCGCGATTTCCTTGCTTCACGCGCGAAGGCATCGCGCATCGCTGCGG  
TGCGAGTCCATCGCATCGGACTGCTCCCAACCGTATTTCGCGCA

## SEQ ID 4062

VRPTCLSPNRLPADSIAFFQYADFPAPTPEGIGASPAVPTPCDASQTVFPP

## SEQ ID 4063

ATGTGCATTTGGGACATATCTTAATCTGCTTGGCGTAGGCAGTGCAGGCTTTTATTTGCCGCTGTTTCGCTGTAGGCGCGGTACGCTGATTGTCCTGTCTTTTATGGGTGCTTG  
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GCGGTTCACTTTCCGCTCCCTTCTTAATCCACTGCGGCTTCCCGCGCATAAAGCCATCGGCACATCATCGGCTTGGCTGGCGGATGCACTCTCCGCGCAATATCGTATCTGCTCAA  
CGGTGCAATATTCAGGATTGCGGAAAGGTCGCTGGGCTTCTTTACCTGCGCGCGCTGCGGCTCTCAGCGCGCAACCATGCTTTGCCCCGCTCGGTGCAAAACCGCGCAAAA  
CTTCTCTGCAAACTCAAAGAACTCTTCGCGATATGTTGCTTTTGTATGCGGAAAAATGCTGTACAACTGCTT

## SEQ ID 4064

MWHWDIILILLVAGSAGFIAGLFGVGGTFLIVPVVLWVLDLQGLAQHPYAQHLAVGTSPFVAVMPTAFSSMLQKHKKQAVDWTIPAMMPGMPGVFAGALSAYIIPAGLIQIFILFLTA  
VAFKTLHTGRQTASRPLPLGLTAVSTLFGAMSSWVGIGGSLVSPFLHCGFPAHKAIGTSSGLAWPIALSGAISLVNGLNLAGLPEGSLGLFLYLPVAVLSAATIAFAPLGVKTAHK  
LSSAKLKESFGIMLLLAGKMLNLL

## SEQ ID 4065

ATGCAAGGACGTTATGAAACCGCGCATCGCGGTATTCATCTCTATGTTGCTGGACGGTATGACGCGGCGGTGGCGCGGCTGACCAACAGCAAGCGCGTTCGGGAGCAGCTCGACA  
GOCTTCCGACATGGTCAGCTTCGGGTTGCCCCCGCGCTTATGCTTACCAAAATGCGAGCTTTGGCAGTTTCGGCAAAATCGGTTATTCGCTGCTTCTATCTAGCGCTGCGCGCGCT  
ACGCTTCGCGTGTTCACACGCTCATCGGCAAGGTGGACAAACGCTGGTTATCGCGGTACCCAGTCCGACTGCGCGCGCTGATTGTCGGGCTGATTGGGTCAACCAACAGCGTGGAA  
AAATTCGCGCGCTTCACTGGTGGGATAGGATCACACTGTTTCCGCGCTGTCGATGATTGTCAAATCCCTTTTGGAGTTTAAAGAAATCAACATCCGAGCAAGTCCCTTTG  
TGGAAATGCTGCTGCTGCTTACTGCTGCTTCTGCTCACTTGGGAACCGTGCCTGCTCTTTCTGCTTCTTCTCGGATACAGCTGCTCGGCTACATTTAGCGGCGACGCGGATTTG  
GAAAAATACAGAAAGCGGAT

## SEQ ID 4066

MHGRIYTAIAVFIISMLDGMGRVARLTNSQSAFGEQLDSLADNVSPGAPALIAKWLQWFGKIGYVAFIYCACAALRLALFNTLIGKVDKRWFIGVPSPTAAALIVGLIWNHNSVB  
KPPAVHWWALGSLTIFAGLSMIVQIPFWSFKEINIRRVQVPVGMILLAVILLVITWEPSSLVILFLPLGYSLSGYIMAARRFWKKYRKAD

## SEQ ID 4067

TTGCCCGCAATGCCCTCTGAAACACAGGCTTGGCGCTAAGCGCGCAATATGAGGATTTCGCGCTGCCGAAACCGGTTTGTACAAACCGGCGAG

## SEQ ID 4068

LPAMPSENGLPLRRQYEDLRNRFPATTRQ

**SEQ ID 4069**

TTGTTTTCAGACGGCATTGCGGGCAACCTTTGCGGGCGGGCAAAAACCTTGTCCTATAATTTATCCCGCTTCAAAATCAGCATACGGTCGGAAATGCAAAAAATATCTTTCAATTTGTTGA  
AACCTACAAACTCCCTGAAAAATAGGGAAATACCGCCCCGGTTTGAACGGGCGCGCATATTCCGATGCCCTCCCTCCGATACCTTCGGCAAGCGCAGAAATGCCCGGCAACAATATCCA  
TCCGGCAAAATCCGAAACAACACACCCGGTGGCAGGCAGAGTCAAAACGCCCGCAAAAGCATCCGCCATCAGAAAAACAACCGCCTCCGAGGGCTTCATCTTAAAGGGCGTATTGTTGCA

**SEQ ID 4070**

LFSDGIAGNLCGGRKTLSYNLSRFKISIRSEMOKISFNLLKPTNSLKIGKYRPGNGAPHIPMPSLYRLPASAEMPGNNIHPAKSETTHPVAGRVKPPRKASAIRKTNRLRGLHPKGRIVR

**SEQ ID 4071**

ATGATGAAAAGAGATCTGGCAGTATCGGCATATGCCGTGATGACTCGGGCGGCACAGGCTCCGATACTTACGGCTATCTCGCCGTTTGGCAGAATCCGAGGATGCAACAGATGTTTTGC  
AGGTTAAACCAACAAAAGAGATTTCGGCGAAAAGCGAAGCGTTTGCCGAGTTGGAAGCCTTTTGCAAAGGTCAGGACACGCTTGCGGGCATTCGGAAGACGACGCGACCGGATGCGCGTC  
GGTCGTGTCGTGAACAATACCTGTCTCGCTGGCATACCCGAAAGCCTTGGCGCGATCGCGGTTGAAAACCGCGTCGTGATTACTTCTCCGCGTTTACGAGCGTTCATCAGGTCGCA  
CTCAACCACTGCATAAAAAATACGGCGCACAGGGACAATCGGGCTTGAAAACAGTGTATTGCACGTCATCTCTTATTACGGCGGGGCTGTTCGCTCCTTAATCCAACACCTGAAA

**SEQ ID 4072**

MMKKILAVSALCLTAAQAADFTYGLAVHQNPQDANDVLQVTKEDSAKSEAFAELEAFCKGQDTLAGIAEPTGCRSVVSLNNTVCVSLAYPKALGAMRVENAVVITSFRFTSVBQVA  
LNCCKIKKYGAQCGCGLFTVYCTSSSYGGAVRSLIOHLE

**SEQ ID 4073**

ATGCTTACATTTTCAAGTAAATCCAAACAGAAATGCCGCTCTGAACGTTGAAGCCAAAGGTCAGACGGCATTTTTTGTTCATAGGTTCAAACGGGGCAGGTTCGAACAACTGCCCCATTCCCTT  
AFTCC

**SEQ ID 4074**

MLTFSSKSKQKRLNVEAKVQTAFVIGSNGAGSNNCPYPYS

SEQ ID 4075

TTGAACCGATTGAAAGAAGATGGTATGAACCAACTGAAACTTGCCGTTTCCGGCGCGCAGATTTTATTGTGGCATTCCGGCGCAATGGTGCTGGTTCCTCCGTGCTGACCGGCTGTAATCCGG  
CTCTTCGCGCTTTTGGGCGCAGGCTTGGGAACGCTGCTGTPCCAAATCAACACCAACGCAAGTACCGATTTTTCTCGGTTCTTCGTTTGGCTTTATACGGCGCGATATATCTACTCCGGTCGG  
CGAATGGGGGGCTGCCCTCCACCATGTGTCGGGCTGTGTGCGCCGCGCTTTATGTATTTGTGTGTTCGCCGCGCTAGCTCCGTTGGCGCGGACTGGCGCGGATACAAACACTCTGCCGCCGGCT  
GTCACCGGCCCTTGTCATCATTCGCTCATCGGTCTGTGTTGCGCGTGGCGGCAAGCAGCATGSCAAATGGGTGAGTCACGGCAACAGGCTACAGCTATACCGGATTCGCTGATCTTTTCGG  
TTCTTACCTTTTGGCGTTATGCGGCATTCGTATCTGCTTTTCCGACGAGGATGATGAAGCTGATTTCCCATCTTGATCGGTGTGCGTCCAGGTTATGTTTGTGGCATGTCTGATGGGATGGTGGGA  
CACGACAAGCATTGCACACGCGCCCTGGTTTCGCCGTTTCCCATTTTGAACAGCCCTCAGGTCAACTGGCAGGCGGCACTGTTTATGCTGCCCGGTTCGCCGTGCGCCCCGCATCGAACACATC  
GGCGGCATCATGGCAATCGGCAATGTAAACGGGAAAAGACTACACAAAAGACCCGGGCTTGGACAAAACCTTTGCGGGCGACGGCTTGGCGGTGCGTTTGGGGTCTGATCGGCGGCCCGC  
CGGTTACAACTTACGGCGAAGTAACGGGTGCGGTGATGATTACCAAAAACAGCAACCCCGTCAATCATGACTTTGGGCGGGCGTTTTCGCGGTCTGATAGGGGTTTTCGGCAAAATCAATGC  
GTTTTTGGCTTCCATTCCGATGCCCGTGATGGCGGGCATTTATGCTGCTGCTGTTCGGCACGATTGCTTCTTTAGGCATCAAAAACCTTGATTGATGCCAAAGTCGATTTGATGCTGCCGAAA  
AACTCGGTCATCGTACAGCTCGGTATGACCACGGGCATTCGGCGGTATGACATCTCAAAATGGGCAGTTCACGCTTTGTGCGCGTGGGCTTGTGCGCGCTACTCGCCATGTGTGTGAACAGCC  
TGCTTGGCATGATCCGAAAGTATCC

**SEQ ID 4076**

LNRLKEDGMNQLKLAIVSGAQILFVAFGAMVLVPLLTGLNPAALLAGLGLTLLFQITTKRVKVPILFGSSFAPIAPITYSVGEWGLPSTMFGFLAAGFMYFVFAALIRWGLAAVHKLLFPFV  
VTGPVIMVIGLSVAVAASSMAMQADGKQVIDYDTSLLSGFTFAVTAIVSVFGSRMKLIPILIGVASGYVLALLMGLVDTTSTIAHAPFWAFVPHFETPQVNWQAALFMLPVAVAPATEHT  
GGIMAIGNVTGKDYTKDPLGDKTLAGDGLGVCVAGLIGGPPVITYGEVTFGAMVITKNSNPVIMTAAVFAVCMAPFGKFNALASIPMPVMGGIMLLFGTIASLGIKTLLIDAKVDLHLPK  
NLVIVSSVLTGTGIGMTLKLGSFSFVGVGLCAVLAIVLNSLLPDPKES

**SEQ ID 4077**

ATGGAGTATAATCCGACACTTTCATATTCAATCCGCAAGCCGTCOCGAACCCTTATTTCAGACGGCATTTTCCGGTAATACGGCATGACAGAAAATCCCA

SEQ ID 4078

MEYNPTLSIFNPQAVPNPYFRRHFPVIRHDRKIP

**SEQ ID 4079**

TTGTCGGCTTTCTGTGTCGTGCGGACGTGGGGACGGGCTCCCGCCCTGCCTTTTGCTGTTTTTTATGGGATTTTCTGTCAATGCCGTATTACCGGAAAATGCCGTCTGAAATAAGGG  
TTCGGGACGGCTTCGGGATTGAATAATGGAAAGTGTGGGATTATACTCCATTCTCCCGCTTTCATCTCGCAACAGACAGACGTTGCCCTTCAGACGGCATATCTTGGCCGACGTATGTAT  
TTTTACGACGCCCTTCGGCAAACAGTA

**SEQ ID 4080**

LSAFLLRADVGDGLPALPFAVFLWDFSVMPYYRKMPSERVRDGLRIEYGKCRIILHFSRFHPATDRRCLSDGISLPDVCIFTQPLGKPV

SEQ ID 4081

ATGGGTTTGGCGGCAACCCGTGATTTTGGCGGATTTCCTCGATCAGTTTCGATATGGCGGATCCGCTCTGGTCGCACAGTTTACCAGGTTGTGGAAGATGCCGCCAATTGGGGCGGACTGTTCCGCGGTATGTTGGCGATGTGCGGCTATTATCTTTTCGGCTGGTCGTTCTGGTGGTGGAATAGCGGCTGCCCTGGCTCGTGCGTATAAAAAATTTCGCTGCACAGCAAAACAGACGGGAAACGAGGCAATACACCAACAAAATCGCTGCCGCCGCGCTGTTTGTCTGACGGCTTTCAGCCCCGCTCTGGAGTATTTTGTGCTGGGCGGAAAATATGCCGACTCCTGCCTGTGCGGACAGGGCGGTATGGTCGGCATACGTTGCGGCGAGGTTTGCCTGGCTGGTGGGAAATCGGGCAGCCCTGATATTCCTGGTTGTTCTGCTGTTTGTGCTGCTTGCCTGCTGGTGCAGATTTCATGGCTGGAATTTTGTGAACGGTGGCGGCGAGGTTTCAAACCGCTTATCCGCGAAGTGTATGCTTTGAGAAAACGCCGCCGAATACCAAACAGCGGTGTGATACCCAAATACACGCGCATGTGTGTAAGAAGCAAAAACATCTACTGCCAAACCGTGTCTTGGCCGAAGGCAGCAGCAGCAACGCCAATTCGCTCGGGTTTCCGTTGCGCGCGCGCTAAATATCAACCTTCGCTGTTTGAAGACAAAGAAGTACAGCAGAACGGCGAATACCAACAGCTACATTGAACCTATTTCGGGATTCCCGACAGCGAGCCGGTCAGCATCAATCCCGCCGAATTGGAGCGCACTGCCGAATATCGAATGCCAAGTTCGAGAACTTCCGAGAACTTCCGCGATATCGCGGACATCCGGCCCCGTCATCACGCGCTACGAAATCGAACCCGGCGCAAGGTGTCAAAGGCAGCCCAATTGTTGCCCTGTGCAAGAGATTGGCAGCGCTATATGTCGCTGCAATCCGTGCGTATCGTGCBAACCAATTGCGGGCAAAAACAGATGGGCATTCGAGTTGCCAACGCACAAAGCCCAAGACGTGATGTTGAGCGAAATCTTGTCCTCGCCCGTATTTCGCGAAGCCAAATCAAAGCTGACCGTCGCGCTGGGCAAAAGACATCGCCGGTACGCCCGCTGTCGGCGACTTGGCGAAAATGCCGCACCTTTTGTGTCGGCGGATACCGGTTGAATCCGTCGGGCTGAACCGGATGATTATGCTTATGCTTTCAAAGTGACCCCGGAAGAGTCCGCTTCATTATGATAGACGCCAAAATCTCGTAGTTGAGCATTTACGAGCGCGATTTCGCGACTACTCTGTCCCGCTGTACCGATATGCGGGAAGCAGGGCAGCGCGTTAGCCTGGTGCCTGCGCGAAATGGAAAAGACGTACCGCGCTCTCTCCACGCGCGGTGTACGCAATCTGGAAGGCTTCAACCAAAAAGTCGAACAAGCCAAAGCGGCAGGCAAGCCGCTGCTCAATCCGTTACGCTTGAACCTTCAGCAACCTGAGCCACTGGAAAACTGCCGATGATCTGTGCTGTTATGACGAACTTGCCGACCTGATGATGACCGAACGCAAGCTGTGAGCAGCAAAATCGCCCGCTCGCCCAAAAAGCGCGCGCGCGGCATACACATGATGTGCGCACCAACGCCCAAGCGCTGATGTGCTGAACCGGCTGATTAAAGCCCAACATCCGACGCGGTATGGCGTTTACCGTGCBAAGCAAAAATGCACAGCGCTACCTATCTCGACCAAAATGGGCGCGGACGAATGCTCAAATATGGCGATTTCGCTGTTCTGCAACCGCGCAGTGCCGAACCGACCCGCTGCAAGGCACGTTTGTTTTCAGACGGCGAAGTGATCTAAGTCGTCACTACGTCACAAATCGCAAGCCCCGCGACTATATGGAAGTCTGCTCAGCGGCAGAGCCGCGCTGGAACCTGCCAATATCGTPTAATTCGAAATGCAGACAGCGACGAATTTATTCGATCAGGCACCTGCGCTATGTTTGGAAAGCAAAAACCTTCATTTTCGTTTCGACGCGCAGTATGCGTATCGGCTATTAACCGCGCGCAAACTGTGAGGCACTGGAAAATGCGGGTATGCTTCTCTCTCGGACCTTCAGCGCAGCCGATAAAATTTTGGCGCACAAAGGCAACTTATTA

**SEQ ID 4082**

SEQ ID 4082  
MGLAATLYLAISLISIFDMGDPSPWSHSSPVVEDAANWGGFLPGAYVADVGYTLFGWSFWNWIAAACVVLKYNRLHAKQTENEAYNHKIAAAALFVLTVFSPVLEYFVLGGKYADSLFVVGAGG  
MVGIRVGAVFAMWLIGKSGSLILILVLLLSLSLIVQISWLEFLNAGRAVQNRILSALSGKVMALKKRRPPIHTKGTGVDQNTNRMMVKEAKNIKATKPVALPEGSSNRSKVAVSAPPPIQIP  
SLFEDNEVQQNGEYHKPTLNLRLIPDESPVSNINPAELERTAEILISGLAEFIGIGVQVVSATSGPVITRYIEIPAGQVKGSQIVALSODLARSMSLSQSVRIVETIAGKNTWIEILPNDRQD  
VMLSEILSSPFAEAKSLITVALGKDIAGTPVVGDLAKRPHLLVAGHTSGSGKSVGVNGMTMSMLFKATPEEVRFMIDPKMEILSYIDGIPHLLCPVWTDMREAGQALNWCVAAEMEKRYRL  
LSHAGVRNLEGFNQKVEAKAGKXPLNLPFSLNLDEPEPLEKLPMTVVVIDELADLMTTERKAVBQQIARLAQKARAAGIHMTVATQRPSPVDVVGTGLIKANIPTRNAPTQSKIDSRTILID  
QMGADELLKYGDSLFLQPGSAEPTRLQGTFSVDGEVHQVNVYKVSQADYTIETGLLSGEAALETANINPNADSDDELFDQAVAYVLESKRTSISLQRLQRLIGYNRAANLMEALENAGIVS  
PSDLNGSRKILAHKHL

**SEQ ID 4083**

SEQ ID 4083

ATGAGCACCTCTCTTCGGCAAACGCCCAAGCCATGACTGCCAAACACATCGGCCGCTTCCCGCTATCGGAGTTGGACAGGTGATTGATTGGCAGCGATCGAACAACTACCTGATCGTC  
AAAAAACCCGTTACCTCCGAGACCGCGCGCGCTCCGCCCATCCCTCTGTCGTCCATGTTCAAAGCCGCTCTGCCCGACAATGGCACAGCCTCTCCGATCCCGAACTCGAACACAGCCT  
CATCACCCCGCATCGGTTTCAACCTGCTTTTGCCGTTTTCGAGCAGCGGCATCCCCGGTTGCAGCACCTTATCCCGCTACCCGTAATTCGCGTATGCGCGGGCAGCCTATTTCGGGCTGCTC  
AAAGTGGGTGTCAAAGCCACCTGAAGGCCGATGTGTTGAACCTGTGTAAGCCGCGCAACAGGCTAAGTGCGCCCGCTGCCGCC

**SEQ ID 4084**

SEQ ID 4084  
MSTFFRQTAQAMTAKHIGRFPLSELDQVIDWQPIEQYLIRQXTRYLRDRRGRPAHPLSSMFKAVLPGQWHSLSDPLEHSLITRIGFNLPCRFDGPGIPGCSTLCRYKRFYARAAYFGLL  
KVGVOSHLKAMCIANLLKAANRLSAPAAA

**SEQ ID 4085**

SEQ ID 4085  
ATCGCGGTTCAAATATCGTACCGTTGCGCTGTTTGCTTCCCCATGTAGGGAAGAAGGTTTATCATTTTATCAACACAACAAATTTAAGGCCTTA

**SEQ ID 4086**

MRFKYRTVALFASPCREEGLSFYQH NKPKGL

**SEQ ID 4087**

SEQ ID 4087

ATGATGAGCGTAACTGTTGAAATTTTGAAGAAATCTGGAACGCGAAGTAGTGTGTGCCCTGCCCTTGGTCCGAAATCAACGAGAAACCGATAAAACCTGAAACAAACCCACGCGTGCAA  
AAATCGACGGTTTCCGTCGCGGTAAAGCACTTAAAAATGATTGCCCAATGTACGCTGCGAGCGCGCAAAACGACGTGATCAACGAGCTGGTGCAACGCCGCTTCTACGATGTTGCCGT  
TGCCCAAGAGTTGAAAGTGGCAGGCTACACCGTTTGAAGCGCTTGAAGAGCAAGACGATAAAGAGTCTTTCAAAGTTGCCGCCATTTTGAAGTGTTCGCCGAAGTCGTTATCGGCGAT  
TTGTCTGCAAGAGAGTGCGAAAAGTAACTCCGCTTCGCTCGGCGATGCCGAAGTCGACCAAACTGTAGAAATCTTCGCGTAAACAACTACCCGCTTCAACCATGTTGACCGCGAAGCCCGAA  
ACGCGCGACCGCGTCATCATCGACTTTGAAGGCAAAATCGACGGCGAACCCTTTGCGCGCGCGCAATPCAAAACCTACGCGTTCGTTATTTGGGCGCGAGTCGAAATCGTGCCTGAAATTTGAAG  
CGGCGTAGTGGCATGAAAGCGGGCGAAGTAAAGACGTTACCGCTCACTTCCCTGAAGAATACACGCGCAAGAGATTTGCCGTTGGCGGTAAATCTGCGGTTCCGCTGAGTAACTGCAATGTT  
TCCGAGGCCCACTTCGCTGAAGTCGATGCAGATTTTGCAAAAGCCCTTGGGTATTCGCGATGGCGATGTGCCAAATTCGGTGAAGAGTGAAGAAACCACTGAAGCCGCGAAGTGAACGCC  
GCGTGAACGAACAAACCAAGAAATCCGTAATGAACGCGCTGATTAAGCCGCTAGATGTGAAAGTTTCCGCTGCTTTTGGTCAATGAAGAAGCCGCCCGCTGGCAACGAAATGAACAAAA  
CTTCGTTAAACCAAGGATATGACCGATGCGCGCAACTTGGATTTGGCTTTGGATATGTTCAAAGAACAAGCCGACGTCGCGTATCTTTGGGTCTGATTTTGGCCAACTGGTTGACGAAAAAC  
AACTTGAAGCACTGAAGGCGCAATCAAGCCGCTTGTGCCAACTTCGCAGAAAGCTACGAGAGTCTCAAGAAAGTGAATGACTGGTACTACGCGAGTACTTCCCGCTGCAAGCCCGCA  
TTTCTTTGGCAGTAGAAGCAACGTTGTTGATTTCGTTTGGGCAAGCCAAAGTAAACAAAAAGCTTTGTCTTTTGACGAAGTGATGGGCGCGCAAGCC

**SEQ ID 4088**

SEQ ID 4088  
 MMSVTEILELWLERKVVLSLPWSEINAETDKKLKQTPRRRAKIDGFRPGKAPLKMIAQMYGASAQNDVINELVQRRPYDVAVAQELKVAGYPRFEGVEBQDDKESFVAALFVFPVSVVIGD  
 LSAQEVEKVTAISVGDAEVDQTEILRRQTRFRNVDRREARGDVRVILIDEGKIDGEPFAGGTSKNYAIFVLGAGQMLPEFEAGVVGMKAGESKDVTVNFPPEYHKGKDVAGKTAVFTITLNV  
 SEPTLPEVDADFAKALGIADGDVAMREEVKKNVSRVERVRVNEQTKESVMAALIKAVELKVPVALVNEEAARLANEMKQNFVNQGMTDAANLDLPLDMFKEQAERRSVSLGLILAKLVDEN  
 KLEPTEGQIKAVVANFAESYEDPDQEVIMDYADTSRLQAPTSIAVESNVVDVFLGKAKVNNKALSFDVEMGAQA

**SEQ ID 4089**

**SEQ ID 4089**  
 ATGAAAGGAGAGCAAGAAATGTCTTTTGATAACCATCTTGTCCCTACCGCTTATCGAGCAGAGCGGTGCGGGTAGCGTGCAATTCGATATCTATTCCCGGCTTTTGAAAGAGCGCAATCGTATTTC  
 TGTGTGGCCCGGTAAACCATGAGTCTGCTAATCTGGTGGTCGCCCACTGTGTGTTTTGGAAAGTGAGAAATCCGGATAGGATATTTCTTCTACATCAATTCCCGCGGGCTCGGTAAC  
 GGCCGGTATGTGCGATTTACGACAGATGAATTTTCATCAAGCCCGATGTATCGACTTTGTGCTTGGGGCAGGCGCCAGTATAGGCGCGCTTATTTGTCGCGCAGGAGAAAGCAAACTC  
 TTCGCCCTGCCCAACAGCCGGATGTATGATTACACAGCCTTTAATCAGCGCGCGCTTTGGCGGTGAGCATTCGCATTTGAAATCCACGACGCGGATGTTGGTGGAAATCAAGAAAACTCA  
 ACCGCCCTGATGGCGAAACATTCGCGCCGCGATTTCGCAGATTTGGAGCGCAGACCCGACCGTGTAAATTTTCATGTCTGCCGAAGAAGCAAAAGAAATATGGTTTGATCGACCAAGTTTGGGA  
 AAACCCGCGCTTCTTTTCGGGCTT

**SEQ ID 4090**

SEQ ID 4090  
 MKGDEMSFDNHLVPTWIEQSGRGERAFDIYSRLKKEIVFLVGPVTDSEANLVVAQLLPLESENPKDIDFFYINSPPGGSVTAGMSIYDTMNFILKPDVSTICLQGAASMGAPLLSAGEGKKR  
 FALNSRIMTHOPLISGGLGGQASDIETHARELLKIKEKLNRLNAKHCGRLADLERDTRDRNFMASAEAKYGLIDQVLENRASRL

SEQ ID 4091

SEQ ID 4091  
ATGACGCAACCCGATCGAAAACACCCAAACTCTGGGGGGTCAATTGCCGCCGCGCATTCATCCTCGTGATTAACATCGGCATGAGGATGACGCTCGGAGCTGTTCGTCCAACCCGTCGTCA  
ACACACCAGGAATTGAACATTTGCCAGTTCAGCCCTCATCATCACGGTTTTCACACTGATGTGGGGCGPATTTGCAACCAATTGTCCGGCGCGCTTCCGACCGTTTCGGCGCGTTTCAGGGTATT  
AAGCGCGGTGCCCTCTGCTCGTCTCGCGCTGCTCGTGAITGCTCCACATCCGACTTAATTGGGGGCTGATGATTCGGCTCGGCTGCTGCTCGCATTCGGCACCGGTTCGGCGGGTTT  
TCCATCATTAATGAGACAGGTTCGCCGCCAAGTCCCCACACACAACCGCGCTTGGCATCCGAGTACTGTTCAACCGAGGCGGTTTCGGCAGGACAATTCTGTTTCGACCGCTGGTTCAAGGAC  
TCAAGGACTGCTGCTCTGCCGAAGTTCGGCTGGACGGGTACATTTTACGTTTGGGGCGCAATTCGCCCTGC

**SEQ ID 4092**

SEQ ID 4092  
MHTPASKTEPKLVAVIAAAAFILLITIGMRNTLGLFVQPVVNTTELNIAQPSLIITVQLNGVLOPLSGALADRFQAFVVLSSGALLVVCACLIASNIPTTWGLMIAVGLLLAFGTGSGGF  
STIMGVAIAOVPHTKRGSLAGLVNAGGSAGQFLPAPLVQGLKDSSSCPKSAGRVIHPTFGAQSPC

SEQ ID 4093

SEQ ID 4093  
ATGGCTAAAAATGGGGGATTTTCTTTGTTCCGAAAGAAAGAAAAACGCTTTATCTTTGAAGCGAGGCATTCTGCTCCGACAACTGGTCAACGGCGAAGTATCCGGTTTACCGAAGAAG  
AGCGACGCGAAAAATCGGCAAAACCGCGCATCCGCCCGTTGCAGATTACCGGTGTGAAACCAAGCTCCAAAGCGCAAAATCACACAAGAAGACATTACCGTTTTACCCCGCCAGCTTTCCAC  
GATGATTAAAGCGGCGCTGCCGCTGATGCAGGCATTTGAAATCTGTGGCGCGCGGACACGGCAACCCGTCTATGACGGAATGCTGATGGAATCCGAGGCCAAGTGGAAACAGGGCAGCTCG  
TTGAGCCGCGCATCTCAAAACCAACCGCAATATTTGCACCGCTTCTACTGCAACCTGGTTGTGGCGGGCGAAGCGGGCGGTGATTTGGAAAGCTGCTGGACAATTGGCAATTTACAAGG  
AAAAACCCCGAGGCTATCCGCAAAAGGTAAAAACCGCGCTAACCTATCCGGTATCCGTATCGCCGTGCCATTCGGTTGGTATTTCGTGATGATGATTTTCGTACTGCCCGCTTTTAAAG  
AGTTTACGCCAATATGGGCGCGGAGCTTCCCCCACTGACCCAAACAGTGATGGATATGTCCGCACTTTTGTGCTCATACGGCTGGATGGTGCTGATCGCATGGGCTTTCGCTATACGCG  
TTCCCTAAATTGAAGGCGCGTTCGATTAAATPCCAACGGCGTATGGATGOCATACCTGCTGCTATGCCGATTTTCGGAGACATTTCGCGAAGAGGACGATGCCCGCTGGGCGAGGACGA  
CGGCAACGCTGTTTGGCCGCGCGGTGCCCTTTGGTCGATGTATTTGGAATCCACTGCCGCGCGCGCGGCGCAATTTAATCTATGAAGAAGCACCCCGGAAATCCGTACGCGCGTCATCCAAGG  
TCTGTCTATGACTTCGGGGATGCGTGGCAGCAAGCTGTTCCCAATATGATGTTCGAGATGTCTCCATCGCGAGGAATCGGGTCTTTGGAGCATATGCTCAACAAGCGCGCGAATTT  
TACGAAGACGAGGTGGACAATCCGTCGGCAGCGTCCGCTATGATGGAGCGGATTAATATTGTGATTTTGGGCTTGTGTCATCGGTACGCTTCTGGTCGCTATGTATCGCGCTGTTC  
ACTTGGGCAACGTTGTCGCG



## SEQ ID 4094

NAKNGGFSLPARKKRFIPFGRHSASDKLVNGEVSAPTEBEARKKLAKRGIRPLQITRVKTSKRKIQTQEDITVTPRQLSTHIKAGLPLMQAFETVARGHNPSTMLMEIRGQVBOGSS  
LSRAPSNHPKYDFRFLCNLVAAGETGVLSELDKLAITYKERTQAIRKRVKTAIYFVSVLIAIGLVFVMMI FVLPAFKEVYANMGAEPLPLTQTFVMDSDFFVSYGWMVLIALGFAIYG  
FLKLRKRSIKIQRMDAILLRMPFGDIVRKGTIARWRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATREIRTRVIOGLSMTSGHRATELFPNMLQMSIGEESSGLDMLNKAEEF  
YEDEVNNAVGRLSAMMEPIIIVILGLVIGTLLVANYLPLFNLGNVVA

## SEQ ID 4095

ATCCGGAAACACCTTCATTTTGGGGAAATCCGCTCATGAAAGAGTCCAGCAGTATGGTTACCGGCCGCTGCTGACAGAGCGACACCTGCATATGCGTCCGGAACCGCTCTTTCGACA  
TGAATCCCGTGTCCGCTAACAGCTCCGCGTTCGAGGTAAAGCCGTTTCCGCTGTCTTCCGCGCGCGCTTGGGAAAACGAAGCCGCGCCGCTTCCGCGCTCGGCATAAGCGGTAA  
ACTGCGACACAGCAGCAGCGCGCGCGGACATCTTCAAGACAGGTTTACGTTCCGCGCTTCTGCTTCAACACGCGCAAAATGTCGATTTCGCGGATATAGCGTGCATCTTTTC  
TGTGTGCTATGCGTTACACCGAGTAACACGACAAACCGCGCTGATTTCGCGCGAGTTTCTCGCGCGCTTCCGACACGACATCCACCTTTCGACCTACCGCTTTCTGTATGACCGCA  
CGCAT

## SEQ ID 4096

IRNNLHFWGNPHERVQYGYRFPVVAERHLMRAETPCFDMNFVSA\*QLRRSQVKPLRLFCRRGLKRRPPACRVGIKRLRHQOHRADIPQROVLARFVFKHQMCDPVGDIACIFF  
CVAMRYTE\*HDKPAVDFAGFRAGFGHDIHLCTYRFLYDRTH

## SEQ ID 4097

ATGATAAAACCGAACCTGAGGCGCAAGCTCGGCTCTCCGCGCTGATTGCTTCTTCCCTGTATCTTCCGCTGATTGAATTACGCTTTTTCGCAAAAGTTGTCGAACCTTCGCCCTT  
TTAACGACACCGGGCGGACATCTTCTCTATACGATCGCGGTGGTCTGTTTTT

## SEQ ID 4098

MIKPNLRPKLGSSALIAFLSLYSSLVLYAFPAKVVELRPFNDTGADIFLYTHFVVLFF

## SEQ ID 4099

ATGAAGATAACACACTGCAAAATTAAAGAAAGAGTACAAAAGAACCGCTCCGTTCTTTGTACCGGAAGTTACCGCCGTTCTGCGCGCGATATTTGGGTATCCATCCCGATTCCGCGG  
CACTGTTTTTACCGTAAATCCGACCGGTACCAATCATCGTTTGGCTTGGCTGCGGATGAGGTTTTCGAGGCGCCCGCGCGCGCGCGCAAGCTGTTTCGCGCGCGCGGTAAAGGCGAG  
ACGCGGTTCGCGCGCGGTAGGAAAAGCGGTGTCTTCCGCAATCCGAAACGCAACGGCGCGGCTATACCGTTGCGGAGGACAATGCGAGCGCTGAAACGTTGCTCCCTGCGGTCAAAAAA  
AAATCATCCGCGAGGTATTTGTTATGCGGATAGCCCGCGAGCGCGGCAAGTCGAGCGCGCGGTTTACCGTTGCGCGCATCAACCGTTTCAAGGAAATTTGCAGACCGTCGGAACCA  
CATTAACGCGATTGGGAATTTTGAATCAGGCAAAACCGCGCTTGCAGAAATACAAAGGATCGACCGCAAACTTTCCCGCGCTTCT

## SEQ ID 4100

MKIYHCKLKKEVQKEPLRSFVPEVTARSAADILGIHPDAAALPYRKIRTVNHRLLAADEVEFEGPAGPASCFFGRRKGRRGRAVGKAVVFGIPKRNGRAYTTVAEDNABETILLPAVKK  
KSCRTVLPMPIARAAAASRTAVLPAASVTPRNLTQVGTTLTALGTGIRQWAPENITTESTANLSRRS

## SEQ ID 4101

ATGAACACACTCCAAACCGCGCAAGACGATCAAGTCTCTCATCGATCATATCACCGTCCGTTTCCAGAACACCGCGTCTTATCCAATCTATGACCAACACCGACACTGCCGATGCAAAAGCCA  
CCGCAATGACAGATTAAAGAAATGAGCGATGCCGCTCGGAAATGGTGGCGATTACCGTCAACAGCCCGAAGCCGCTCCAAAGTTGCGGAAATCCGCGCGCGCTTGGACGATATGGGCTA  
TGCCACACCACTGATTGGCGATTTCATTTTAAACGGCGAAGCGCTTGGCGGAAATTTCCGAATCGCGCAAGCATTTGCCAAATACCGCATCAATCCCGGCAATGTCGCAAAAGCGGTA  
AAAGCGGATGAAAAATTTGCTTTTATGATTCCGACTGCTGCTGAAACGATAAAGCCGTCGATCCGCGTAAACTGGGTTCTTTGATCAGAGCTTCGCAAAACGATATGATGGATGCCA  
ACCTCGTTTCTTCCGCGCGCGGAAACCGCGCGAAGTGAAGGAAGCACTGATTGTCTCCGCTTTGGAATCTGCGGAAAGCGCTTCTATTTGGGACTGCGCGGAGCAAAATCATCCT  
GTCTGCAAGTACGCGCGGTTCATGATTGATTGAGTTTACCGGAACTGGGCGAGCGTTCGCTATCCGCTGCAATTTGGGTTTGACCGAAGCGGATGGGCGAGCAAAAGCATTTGTC  
GCATCAACCGCGGCAATATCTGTTTGTCTCAAGAAAGAAATGGCGACACCATCCGCAATTCACCTCACTCCGGAACCGCGAGCGCGCTACTCAGGAGGTGCTGCTCGGCGAAGAGATTT  
TACAGACTATGGGTTTCCGCTCGTTTACCGGATGGTTACCGCTGCGCGGATGCGGCGGTACCAACGATACCGTATTTCAAGAGCTGCGCAAGATGTTCAAAATTAACCTGCGCCAAA  
AATGCTATATGGCGTACCTTTATCCCGGGGTGAATCCCTGAACGTTGCGGTAATGGGCTGCGTTGTCAATGGCCCCGAGAAAGCAAAATGGCGGACATCGGAATCAGCTTCCCGGT  
ACGGGGGAAACACCGCTCGCACTGTTTATGTAGATGGGAGCGCAAGTCACTGAAAGGTAATAATATTGCAAGCGAATTCCTAGCTATTGTAGAGGAATATGTTAAACCAATTATG  
GCAAAACAGTCTTAAACGCAATAAGGAAAGTACTCCGATACAGTCTCTA

## SEQ ID 4102

MNTLQRRKTHQVLIDHTVSGEAPVVIQSMNTWTDADAKATALQIKELSDAGSEMVRIITVNSPEAAASKVAEIRRRLLDMGYATPLIGDFHPNGERLLAEFPECGKALSKYRINPGNVGKV  
KDEKFAFMIRTAENDKAVRIQVNWGSLDQSLAKRMDANLVSSAPKPEEVMEKALIVSALESABKAVLLGLPEDKILSLCKVSAVHDLIQVYRELGSRCVYPLHLGLTAEAGMSKGI  
ASTAALSULLQEGIGDTIRISLTPEPGSPRTQEVVVGQELIQTMLRSFTPMVTACPGCGRTTSTVPQELAQDVQNYLRQKMSIWRTLTPYGVESLNVAVMGCVVNGPGESKLADIGISLPG  
TGETPPVAPVYVDEKRVTLKGNLIASEFLAIVEEVVYKYNKSSRNKRGKVIPIQSL

## SEQ ID 4103

ATGGCAGCAGATTTAATCGGCAACAGGGGTAAATATGCTTTTAAAGCCATCCAAACGAATCTCTTTATTACTTGTCTTTCCTTGGGCGCGTGAGCACTTCTTACCGCCCTCGCGGG  
CAGAAAAAGCCATCAGGTTTCCAAATATCAAAACCCAGTTGGCGATGGAATATATGCGCGGTGAGCACTACCGTCAGGCAACCGCAAGTATTGAAGTGCTTTGAAATCGAACCTTAAAAA  
CGAATCTGCTGCTGCTGCTGCTGCCGAAATCTATCAATACCTGAAAGTTAACGACAGGCGCAGGAAAGTTTCCGCGCAAGCCCTTCCATCAAAACCGGACAGTCCGAAATCAACACAC  
TACGGCTGCTTCTGCTGCGCGAGGCTCAACCGCCCTGCCGAATCTATGGCATATTTTCGCAAAAGCCCTGCGCGACCCACCTACCGGACCCCTTATATTGCAACCTGAAATAAGGTATAT  
GCAGCGCAAAACAGGGGCAATTTCGATTGGCGGAGGCTATTTGAAACGTTTCCCTCCACGCTTCCCATGCAAGTCCGCAACCAATCTGACCTTAAAGAACTGGCGCGCAAAATGCTGCGCGGCA  
GTTGGCGGATGCCGATTACTACTTTTAAAAAATACCAAGCAGGTTAGAGTCTTTCAGGCGGATGATTTCGCTGCTAGGCTGGAATAATGCAAGCCCTCGGCAACGCTGCGCGCGCATAC  
GAATATGAAGCAATATGACGAGCAATTTCCCTACTCGAAGAAATTCGCAACCGCTCTCACCCTGCA

## SEQ ID 4104

MAADFNRTTGVMPFKPSKRI SLLLVLALGACSTSYRPSRAEKANQVSNIRKQLAMEYMRGQDYRQATASIEDALKSNPKNELAWLVRARIYQYLKVNDAQESFRQALSIXPDSAEINNN  
YGNFLCGRNLNPAESMAHFDKALADPTTPTFYIANLWKGICSAKQGFGLAEAYLKRSLLAQPFPPAPKELARTKMLAQGLDADYVFKYQSRVEVLQADDLLGLHKLAKALGNVQAAY  
EYEAQLQANFPYSERLQTVLTGQ

## SEQ ID 4105

ATGAAAACCAATCTGCTCAACTACGACCTCAAGGGCTAACCCGACATTTTGGCGATATGGGTGAAAAACATTCGCGCGCAACAGGTTATGCGTTGGATGCAACCAATCCGCGCGCAAA  
ATTTTGACGAAATGACCGATTGGGCAAAATCGTTCGCCATAAATGAAACGACAGGCAAGCATGAAATTCAGCTGATGATGTCGAAGAACTTTCAGAGCGCACTCGAAAAATGGCT  
TTTGGATGTCGCTACGCGGAAACCGCTGGAAACCGTCTTATCCCGGAATCGGATCGCGGACGCTCTGCAATTCCTCGCAAGTCCGCTGCGCTTTGGAATGTACATTTTGTTCGACCGGC  
CGGCGGGCTTCAACCGCAATTTAACCGCTGCCGAAATCATCGGACAGTTTGTGTGGGCAAAACAAAGCGATGGGCGTTACACGCAAAACAGAGCGTGTGATTTCACACCGTCTCATGATGG  
GCATGGGCGAGCGGATGGCAACTTCGACAAATGTCGTACCGCTTGGAGCATCATGCTGGAGGACCAAGCGCTACGGTTTGGAGCGCGCGCGCGTAACCGTTTCCACTTGGGTATGCTTCC  
CAAAATGGACAGGTTGCGCGATGTCATGCCGTTGGCGTTTCCCTCCACGCTTCCAAATGCAAGTCCGCAACCAATCTGACCTTGAACAAAAATATCCCTTGAAGAAATG  
ATGGCGCGATGCCAAGCTATCTGCTCAAGCGCGGAGGATTTCATCACTTTCGAGTATGTGATGCTGGAAGGTCACAGTAAGGCAACATGTCATCGAACTTATTAAGCTGGTCA  
AAGATGTTCCCTGCAAAATCAATTTAATCCGTTTAACTCTTCCCTAAATTCGGGATATGAACGTTCAAGTAAACGAAACATCCGTTTTCAGAGATATCTGCAACAGCGCAATTTGT  
GTTTACCGCTTCAAAAACTGTCGCGAGCATATGATGCCCTGCGGACAGTTGGCAGGTGAGTTTCAGTAATAACCGCGCGCAACAAAAATGCGAGCAGATTTTATCGGACACAG  
GGG

**SEQ ID 4106**

SEQ ID 4106

MKTNLLNYDLQGLTRHFADMGKEKPPFRKQVNRWMMQSGAQNFDMTDLAKSLRHLKNEQASIELPKLMMSQESSDGRKWLDDVGTGNGVETVFPFPSDRGTLICISSVQGALECTPCSTG  
RQGFNRNLTAAELIGQLWANKAMGVTPKNERVINSVVMGCKGEMANFNDVVTALSTMLDDHGYGLSRRRVTVSTSGNVPQMDRLRDVMPVALAVSLHASNDEVNRQIVPILANKYPLKRL  
MAACQRYLVKAPRDPITPFEYVMLDGVNDKAQHAYELIELVKDVPCKFNLIPTNPPNSGYERSNENIRIPRDLQQAEPVTVVRKTRGDDIDACGQLAGQVQDKTRRQKWKQQLIGQQ  
G

**SEQ ID 4107**

SEQ ID 4107  
TTGATACATACACCGCCCAATTCCTATTTCAGACGGCATAAAATATATCCATGCCCTCTGAAAACCTCTGTTGCAAAAGACTTCAAACTCAAACCTTGCCCTGCCCTGCAATTTTTATTGGAAG  
CCTTAATT

**SEQ ID 4108**

LIQYTAQFLFRHKKIYPCRLKTLLOKTSNOTCLPCNFLFEALI

**SEQ ID 4109**

EQ ID 4109  
ATGGCGATTGAACGTACCATATCCATCATCAAACCCGATGCCGTGCGCAAAACGTTATCGGCAAAATATACAGCCGCTTTGAGGAGAACGGTCTGAAAATCGTTGCCGCCAAAAATGAAGC  
AGCTTACCTCTCAAAGAAGCCCAAGAAATTTATGCGGTTCTATAAGACCGCCCTTCTATGCGCGATTGGTTGAATTTATGACCGCGCGTCCGGTTATGATTTCAAGTACTGGAAGCGCAAAA  
CGCCGTTCTGAAAACCGCGAACTGATGGGGGCGACCAATCCACCAGAAGCCGAGAAGGCACGATACGCGCGACTTTGCCACTTCGGTCAGCATTTAAGCCGCTACACGGTCCGACAGT  
GTGGAAAATGCGCGTTTGGAATTTGCCCTACTTTTCAGCCAAACCGAAATCTGCCCCCGT

**SEQ ID 4110**

SEQ ID 4110  
MAIERTISIIKPDVAGKNVIGKIYSRFEENGLKIVAANKQLTLEA<sup>2</sup>QEPYAVHKDRPFYAGLVEFMTGGPVMIQVLEGENAVLANKRELNGATNPTEA<sup>2</sup>EGTIRADFATSVSINAVHGSDS  
VENALEIAYFFSQTICPR

**SEQ ID 4111**

SEQ ID 4111  
TTGGCTGAAAAAGTAGGCAATTTCCAAAGCGGCATTTCCCACTGTGCGAACCGTGTAACGGCGTTAATGTGACCGCAAGTGGCAAAGTCCGCGCGTATCGTGCCTTCTGCGGCTTCGGTG  
GGATTGGTCGCCCCCATCAGTTCGCGGTTTTCAGAACGGCGTTTTCGCCCTCCAGTACTTGAAATCATTAACCGGACCGCGGTATTAATTCACCAATCCGGCATAGAGGGGCGCTCT  
TATGAACCGCATAAAAATCTTTGGGCTTCTTTGAGGGTAAGTCGCTTCATTTTGGCGGCAACGATTTTCAGACCGTTCCTCTCAAAGCGGCTGTATATTTTGGCGATAACGTTTTTGCCGAC  
CGGACCGCGCTTCACATCAGATCCATATGCTGACGTTCAATCGCCATGCTATATCTTATTTTACTTAAGAAGATCAAATCGGTATTCTACCAAAAAA

**SEQ ID 4112**

SEQ ID 4112  
LAEKVGNPQSGIFHTVGTVYGVNADRSKGVRAYRAFCGFGSIGRPHQFAVFQNGVFAQYLNNHRTAGHKFNQSGIEGAVFMNRIKPLGFFEGKLLHFGGNDFTVLLKAAVYFADNVFAD  
GIGFDDGYGTFFNRHAISLFLKKNDIGILPKK

**SEQ ID 4113**

SEQ ID 4113  
TGGTGGCTTCCCGGGCGGCAACAACGGCGGCAACAACGGCGCCACCCACACACCCCAAGCCACACACGGACAAAGCCTCGGAGAAGCAGTCAAACCGCCTTCAAAACCCCAAGCTACA  
TCCTGCTGCACCTGAGCTTTTTCGGCTGCGGCTTCACATGGCTTTTCGTAAACCCAC

SEQ ID 4114

WWLAGGNNNGGNNAHTQHTQATHGQSLGEAVKTAFTKTPSYILLHLSFFACGFHLAFLVTH

**SEQ ID 4115**

SEQ ID 4115

ATGAAGAAACCCCTGTTGGCAATGTGTGCCGCTTTTCGCCCTTAAAGTGCCTGCGCGGACGGCGGAAGAGGACACCGCCGCCCTTTACCCCGGCAGATTAGCGACCGTTTCGGTGGGACACTATTGCA  
GTATGAACCTTGACCGAACAACAACGGCCCCAAAGCCAGATTTTTTTTGAACCGCAAAACCGCATCAGCCCGTTTGGTCTCCACCGCTCAAGCAGATGTTCCGCTTATACCAAGCTGCCCGAAGA  
GCCAAAGGCAATCCGCGTGATTATACCTTACCAGATATGGGCAATGTATACCGATTGGACGAATCCTTAATGCCGACACGGAGTGGATAGATGCGAAAAAAGCGCTTTTATGCTATCGACAGCGGC  
TTTATCGCGGATGTGGGCGCGAAGACGCGCTGCCGTTTCGCAACAAGGAGCAGGCTGA AAAAATTTGCAAAGGATAAAGCGCGCAAGTGCTGCGGTTTGACGATATGCCCGATGCTTACA  
TTTTTCAG

**SEQ ID 4116**

SEQ ID 4116  
MKKTLTLLAIVAVFALSACRQAEAPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKPDQPVWFSTVVKMFGGYTKLPEEPKGLRIVTYVTDMGNVTDWTNPNADTETWIDAKKAFYVIDSG  
FIGGCGAEDALPFGNKKEQAEKPAKDKGGKVVVGFDMDPEAYIFK

**SEQ ID 4117**

SEQ ID 4117  
ATGAATATATAGAGACCAACTTTTAAAGACCCGCGGTTTGAAACCAACAGCCCGCTGACCTGGTATCAGCGTGCTCACAACCTGCCAACTTCATCCGCGACGACGACAGGCGGCGCCA  
TCGAACACCTTGACCGGCTTTGGACGACCTTGATGATGTCTAAACGCGAAAGAGAACCGTTTTTATGGCAGGAGTTTGGCTTCCCGCAAGTTCCCAAAGGGCTTTATTCTATGCGGAGT  
CGGACGCGGAGACGATCTTCFATGACGCAATTTTTTCGGCTGCCTCCCTTACCGCCGCAACGCGCGTCCACTTTTCATGCCTTTATGGCGGAAATCCACCGCGGCTGAAAGCCCTGAAA  
AGCGAAAGCAACCCGTTGAAATCCGTTGCGCCGAGATTACAAAGAAACCCGAGTATTGTGTTTTGACGAAATTCATGTGACGATATTGCGGATGCAATGATTTTAGGCCGCTGTGTGG  
AAAACCTGCTTAACAGGGCGGTTGTTTTGGTGGGACTTCAAATACGCGCTCTCCGAACCTCTACCCGCAAGGTCAAACCCGGAGCGGTTTTCTTCCACAATCGCGCTCATCGATCCAG  
TCTGACGCTCTTAAACGTTGACGAGGGGGAAGACTACCGGCTGCGTACCTCCGCCCCGCCGAGATTTCTTTCACGCTGCCAATGAAGAAAATGAGGCAAACTGGCAAACTGTTCAA  
GAAATGACAGGCATTACCGATTTGAACCCCGGCATCAGCACCATCCAGCGCGGAAATTCCTCCCAAGCCGAGTCGCTGTATACCTATGTTTTCAGGTTTGGAAACACTCTCACCGCAAGAAAAGGCGGAGGCGGACGGCTGACTTGGCTGATTGA  
CCCGCTCACAGTCCGACTCTGTATTGTCGGAACATTATGAAATGGGTTTTTATTTTCAGGTTTGGAAACACTCTCACCGCAAGAAAAGGCGGAGGCGGACGGCTGACTTGGCTGATTGA  
CGTACTTACGATTTCCGGGTCAAACTGTGTGCCACCGCGGTAGATGTCAACCATATCTACACGGAAGGCGATTTTGGCGAAGAAATTACCCGACACGCCGACCGGATGTCGAAATG  
CAGTCCGAAGTTTATTTGGAACAGCCGCACTGACCTTATCTCCCAAGGCTTCAGCGGA

**SEQ ID 4118**

SEQ ID 4118  
MNNRDQLFKAPPFENHSPITWYQAASQLPNFIRDDAQAIAI EHLRLWTLELMPKRRKRNFLGRSLRSPQVPKGLYFYGGVGRGKSLFMDAIFPGCLPYRRKRVHFHAFMAEIHRLRLKALK  
SESNNPLKSVAABITKTKTVLPCDFEYHSDIADAMI LGRLEENLNLNEGVLVATSNYPASELYPQQGNRSGFLPTIALIESSLTVLNVGGEDYRLRLTRPAEIPPTPANEENEAKLAKLKF  
EMTGITLNPNGISTIHGRRI PHKAESGRITWFDRLALCFSPRSQSDYLYLAEHYEMVFLSGLEQLSPQEKAEARRLTWLIDVLYDFRVKL CATGAVDVNHLYTEGDFAEKFTTETASKMVM  
QSEVYLEQPHPLTLPKASGG

SEQ ID 4119

SEQ ID 4119

SEQ ID 4120

LAFFVEKNNDAAKGGISKGGVLIWCRYEPKCLLFQAAF

SEQ ID 4121

SEQ ID 4121  
TTGTCCTCCTTCATATTAAACGCGAGCCTGAAATAAAGGCATTTTGGCTCATATCTGCACCATATTAAACGCGCGCTTGTCTTATACCCCTTTGTGCGGTCATTATCTTTTCCAC  
GGGAAACGCCAAGTTTGAAGGAAATCATTTATAATACCACGGTAAGCATTTTCTTTCT

SEQ ID 4122

SEQ ID 4122  
LSSFNKTQPEIKGILAHICTILKRRLCLYPLCARHYSFPRETPSLKEIYNTSGKHFLS

SEQ ID 4123

SEQ ID 4123  
TTGGAGGGGGCGAAAACACACAGGAACAGGTTGCTTATGCAAAATTCGCCAACGAATAATACGAAGCCCGAAAGTGAAGTAGGAAATACGGGGCATTTTAAATGTT



## SEQ ID 4124

LEGAKTQOEQVAYANSATNNTKPESEVGNITGDFNV

## SEQ ID 4125

ATGAATTTGCGGTCTATTGCGCGATAATCCGGAATAACCGCTTGGTGTGATTATTGGCTTCCGGCTTGACGTGTACGGAACAAAATTCATTACCAAAATCGAGCTTCGGCGCTT  
ATGCGGCAGAACATCAAGTGGTGTGGTTCGCCCCGATACCGGCCCTCGCGGAGAGCAAGTCCGGAACGGTCCGCTTATGATTTAGGACAGGGGCGAGCTTTTATTGTAATCGCACCGA  
ACAGCCTTGGCGCGGCAATTAATCAATGTATGATTACATTTTGAACGAGTTGCCCGCTGATTTGAGGAGCAATTTCTTACCAACGGCAACGTTCCATATATGGGGCAATTCGATGGACGGA  
CAGCGGCATTGGTATTGGCACTACGGAATCGGGAACATTAACAGTGTTCCTGCTTTTCCGCTATTATATGCGCAAGCCTCGTACCGTGGGGAGAAAAGCCTTACTGCTTATTATG  
GGAAGAAGCGTGAATAATGGCAGCAATATGATGCTAACTCACTCACTCAACAGGCTATAAAGTGAAGGTATGCGTATCGATCAGGGCTTGAAGATGAGTTTTCGCCACACAAATGCG  
TACCAAGATTTTATCGAAACCTGCTGCGGCAATCAGCAATCGATGCGGTTCCATAAAGGATACGATCAGCTATTACTTCATGCCAGTTTATTGGTGAGCATATCGCTTAT  
CAGCGCGCATTTTGAAG

## SEQ ID 4126

HKFAVYLPDNPENQPLGVYIWLISGLTCTEQNFITKSSFRRYAAHQVVVAPDTGPRGEQVFNAAAYDLGQAGPYLNATEQPWAANYQHYDYILNELPRLIBEHPPTNGKRSIMGHSHDQ  
HGALVLALNRNREHYQVSAPSPILSPSLVFWGEKAPTAYLGRDREKQVQDANSLIQGYKQVGRIDQGLEDEFLPTQLRTKDFLETCAAANQPIIDVRPHKGYDHSYVTFIASFIGEHLAY  
HAAFLK

## SEQ ID 4127

TTGAGCCGAAAGATTACGATAAAACCAATCAAGATGTGTGTTAGACATCAACAAATGGGGCAATTGACCAACCTTTGAATGTATCGCAATGTAAACGTAATGCGTCAGGCATTAGAAA  
GTGCACACCGAGGTTGGGACAATCCATCATCATCGCGTAGCGGATCGAGCAAGAAATTTCAACCGCTCCGTCCCAATCGTAACAGGCGGTGTTTGAAGAGCTTCGGCATTGTTGG  
TGTAAAGCGCGCTCCGAGCTTCCGAAATGTGGAGGATTCAATGAAAGCGGATATCAATAGAACCACTTTGTGACCCATGCAATGACCCCTGATCAAAATCAATGAAGCTTTGAGTTA  
ATGCACGAAGGTAATCGATCCGCGCTGTTTATTCATTAC

## SEQ ID 4128

LSPKDYDKPIKIDVLLDINKNGIDHTFECIGNVNMVRALESARHGWSIIIGVADAGQEISTRPQSVTGRVHKGSAPGGVGRSELPRMVEDSMKGDIOLEFFVTHAMTLDOINEAFEL  
MHEGESIRAVIHY

## SEQ ID 4129

ATGTGCTCAGGCAAGGCTATTTTGTAAATTAAGAGGAAAGCAATGGAAATGAACAAACCGATTCAACCATCAATCTCGTCCGCGGTGGCAATTCGCCCTAACCAACCTTAC  
AAATTTGGAAATCGACGTGGAATGCGCGTAAGACGAGGTGTTAATTCGTAAACCCACACTGGCGTGTGCCATATGATGCAATTTACCTATCAGGAAGCGATCTGAAGCGTATT  
CCTGTGTGCTTGTGACACGAAAGTGGCGGTGTGCTGTGCTGTGGCGAGGCTGTGTAAGCGTAAACCGGTAATACGCTCAATTCGCTTTACACCGCAGAATGTGGCGAATGTAG  
TTTTGCTCTCTCGGTAAACCAATTTATGCGCTTCAGTGGTGATACACAGGTAAAGGCTTAATGCCAGAGCGCAGCAGCGCTTTTCTTATCAAGGTGAGCGGATTATCACTATATGG  
GCTGTGCTGCTTTCAGTGAATATTCGTGTTGTTGCCAGGTTTCACTGCGCAAAATCAACCGGAAAGCCCAACCAAGCAAGTATGTTGCTCGCGTTCGCGGTTTACCACTGCTATGCTGC  
GGTACATAACACGCGAAAGTACAAGAGCGGATTCGTGTTGCCGTGTTGCTTGGAGCGATTGGTTTGGCTGTGGTCAAGGTGCGCGTCAAGCCAAAGCGGTGCGCATATCGCCATT  
GATACCAATCTCGCAAAATTCGAGTTGGCAAAACAGTGTGTTGTCAC

## SEQ ID 4130

MILRQGYFVNEIRKTMENKQTDSTIKSRAAVAFAPNQPLQIVIEDVEMPRKDEVLIRNTHGVCHTDAFTLSGSDPEGVFVVLGHGAGVVAVGEVSVSPKGNHVIPLIYTABEGCEB  
FCLSGKTNLCVSVRDTQKGLMPDGTTRFSYQGPPIYHNGCSTFSEYSVVAEVS LAKINFRANHEQVCLLGGVTTGIGAVHNTAKVQEGDSVAVFGLGAI GLAVVQGARQAKAGRIIAI  
DTNPAKFLAKQKCN

## SEQ ID 4131

ATGACTTATACCACTGCCAAAGCTGCCGAAAAATAGGCATCTCCGCCACACTTTACGCTTTTACGACAAAGAGGCTTGTGCTTAATATCGGACGTGATGAATACGCTAACCGTGTGT  
TTACCGATAACGATTTCGANTGGTGTACTTATGCAATGCTTGAAAAATACGGAATGAGCTTAAAGACATCAACGCTTTGCGGAATGTACCGTCAATGGCGACGATACCATTTGAAGA  
ACGCTTTCTCTGTTTGAATAATCAATAGAAAAATGTGAAGTGTCAATTTGCCGAATTAACACGTTATTATTAGATTGCTTGAATACAAATTTGGCGTTTACCAAAAGCGAAAGCAATTAGGC  
TCGGTAAAGCTGTAAATTTGCCGCAAAATCTCTGAAACGGCT

## SEQ ID 4132

MTYTTAKAAEKIGISAHTLRFYDKBELLFNIGRDEYGNRCPTDNDLQWLYLLQCLKWTGMSLRDIKRPABCTVIGDDTIEERLSLFFENQIENVKQIAELKRYLLDLEYKLAFYQKAKALG  
SVKAVNLPQIPETA

## SEQ ID 4133

TTGGCAGAAATTTTTCGCGCAAAAACGGCAGCATCTTCTGGCAAAAGACGTAGAGTACAGCGTAAAGTCTTGGTTGACACCATGACCCGATCGCTTCCCGGAGGTCAAGCATCGAAA  
TTCGCGGTTTCGCGAGCTTCGATTGGAACCATCTGCTGCCGCGATCGGTGCAATCCCAAAACCGGCGAGCGCTGGAAGTACCTGAAAAACATGTACCCCACTTCAAGCTTGTAAAGA  
ATTGCGCGAGCGGTGCACTTGGCTTTAAAGAAAAATGCCAAT

## SEQ ID 4134

LAENVFAKNGTHILLAKDVEYSVKVLVDNTRSLARGQRIEIRGFGSPDLNHRPARIGRNPKTGERVEVPEKHVPHKPGKELRERVLDALKENAN

## SEQ ID 4135

TTGGCGGCAATCTTCTGCCAAGCGAACCAATTAACCTAGACTTTGTATGCTGCAACCTTATTCTTGTTCGCGGAGAGTTTGGCTTTCAGCAGGTTCGCCCAAGCTGGTGGTACCGGCA  
TTCGCAATTTGGCGCGGCTTACGCGGATTACGCGGCTTCTTTGGCATCTTTGGCTTTAACGGAAGTTTGTATGCTGCGGTTTTCGCGTCAACGGTAACGATGACGGCTTCAA  
CTTCGCTGCTTCTTTCAGTTTGGTGGTCAAGTCTTCAACGCGGTGCGGTGCAAAATTCGGAACGAGGAGGTAGCTTCTACTTCGTGACAGAGGGGATAACAGCGGCTTTGGCGTCAAC  
AGATTTACGGAACCTTTAAACAAAGAACCTTTGCTGTTACGCTGATGAAGTTGCCGAAAGGATCGCTTCCAGTTGTTGATACCCAGGAGATGCGTTCTTTTCCACATCGATTTGCC  
AATACGAGCGCTTCGACTTCTTCTCTTTTGTATTTCGTACGCGCTTCTTCGCGGATTCGGTCCAAGACAGGTGCGACAGGTGAACAGACCGTCAATGCGCGCGGCGAGCGGACGGA  
ATACGCGGAAATCGGTAATGGATTAAACCGCACCGGAGATTGTCCTCTTGTGCTGCTTGGCGCAAAATCTTCCCAAGGATTTGCTTGGCATTTGTTTCAATCCCAAGAGATACGGCG  
GCGGCTTCTGCTGATTTCCAAATCATGACTTCGACTTCGCTACCCAGTTGTACGACTTTCGCTGCGGCTTACGCTTTTGTGTTGCTCCAGTCCATTTCGAGAGCGTGTACCAAACTTCGATG  
CCTTGTTCGATTTCGACGAATGCGCGTAGTGGTTCAGGTGGATACCTTTCGCGAAGCGGCTGGCTTTCGCGATAACGCGGCTCAGACCGCTTCAAGGATCTTCGCCAGTTGTTTCA  
TACCAAGGAACACGTTGTTTCTTGGTCAATTTCAATACTTTGGCTTCACTTCTGACCGACTTCCAAGACTTTCGCTGCGGTTTTCACGCGACCGCATGCCAAATCGGTGATGTG  
CAGCAGCGCTGATGCGCGGAGGTCAACGAATGCGCGTAGTGGTGTATTTTTCGATGCTTTCGATGACGAGCTTCTTTCGAGTTTTCAGCAGGCTTTCGCTTCTTCAACCC  
AAAGTGGCTTCCAAACGCGCGCGGGAACACGAGCTTGTGCGTTTTCGCTGAGTTTGTATCACTTTGAATTCGATCTTTCGCTTCAAAATGGGAAGTGTCTTTAACGGGACGTA  
CGTCGACCAAGAACCGCGGAGGATGCGCGGATGCTGCTGATCAACGCTCAGCGCGCTTTCGCTTACCGTTGATGATGCGGACAGGATGTTGCGCTTTTCCAGGCTTCTTCCAA  
AGCGATCAATCGGCTGCGGCTTTGGCTTTTTCGCGGACAGTTGGTTTTCGCGAAGCGCTTTCGACGATTCGATGTTAAGGTAACGAGTCAAGTCCGCGACTTTAACTTCAATTCGCTT  
TGAGCTTTTGAATTCAGCTACATTCGATCAGGATTC

## SEQ ID 4136

LAANTSAKRTINSDFVMSATLFLPAGEFGQQVAQAGGTGIRIGGIDGVQCPAFAFGIFGFKGPDAAVFAVNGNDGPNFVAFQFGQVFNAGVCKFGSRQVAFYFVRQGDNSAFGVN  
RPHGTNPNRTFVVADEVAERLAPQLFDTPGDAFFFLHDCQYDGFDFSPFVPAFGFAGFPGRQVQVQVQVDAAGQADEYAEIENGPNRTGDFVSPVVGKFPFPRIGLALPHTQRTDA  
AAPVDPQNHDPDFVQLYDFARVYVFGVPHFGDVIYQTFDALFDFDECAVVGQVGYFAEQAGGLRITAGQTAPRIAPQLPHTQGNLFLFLVERQYFGPNFLTFQDFARVPHATFCQIGDV

QQAVIDAAQVNECAVVGDIFFDDAFDDGAFLQVQGGFAFFTQSGFQNGAAGNNDVVAFVQFDHFEFLDFAFKMGSVFNQTVQDQTRQECADAADHNGQAADFPTVDDAGQDVAVFHGFFQ  
SDPIGCAFGFFAGQGFPAEAVFDGFDGNGNEVADFNFNFALSVEFSYIDQGF

**SEQ ID 4137**

EQ ID 4137  
 GTGGGGCGGTATTCGAACCATTTGTCGGCGCGGCTTGCAGACCGGTTTCGGCGCGGTTACAGGATATTAAGCGGCGGTGCCCTCTGCTCGTCTGGCGCTGCCGTGATTCGCTCCAAACATCCCGACT  
 TATTTGGGGCGGTGATGATTGCGGTGCGGCTGCTGCTCGCATTCGCGACCGGGTTCCGCGGGGTTTTCATCATATATGGGACAGGTGCGCGGCCAAAGTCCCCACACACAACACGGCGGCTTGGCAT  
 CCGGACTGGTCAACGCAAGCGGGTTGCGCAGGACAATTCCTGTTGCGACCGCTGGTCTAAGAGACTCAAGAGACTCGCTGCTCTGCCGGAAGTCGGCTGGACGGGTACATCTTTACGTTTGGGGC  
 GCAATCGCCCTGCTGATTCCTGCGCGCTCATGTTGGCTGGCGGCGGCAACAACGCGGCGCAACAACGCGGCCACACCCAAACACACAGGACACGAAGCTCTGGAGAGAGCAG  
 TCAAAACCGCCTTCAAACCCCAAGCTACATCTCTGCTGACCTGAGCTTTTCTGCTCTGCGGGCTTCCACATGCCCTTCTCGTAAACCCACCTACCCACGGAAGTGCCTCTGTGCGGACTGCC  
 CGCCACCGCTCTCGAATCTCATCTCGCCATCATATCGGACTGGCAAAACATCGCCGGTTGCGTGTTCAGGC

**SEQ ID 4138**

SEQ ID 4138  
VGR<sup>1</sup>L<sup>2</sup>I<sup>3</sup>T<sup>4</sup>V<sup>5</sup>R<sup>6</sup>R<sup>7</sup>A<sup>8</sup>C<sup>9</sup>P<sup>10</sup>F<sup>11</sup>R<sup>12</sup>R<sup>13</sup>V<sup>14</sup>Q<sup>15</sup>G<sup>16</sup>I<sup>17</sup>K<sup>18</sup>R<sup>19</sup>C<sup>20</sup>P<sup>21</sup>A<sup>22</sup>R<sup>23</sup>L<sup>24</sup>R<sup>25</sup>L<sup>26</sup>P<sup>27</sup>D<sup>28</sup>C<sup>29</sup>L<sup>30</sup>Q<sup>31</sup>H<sup>32</sup>P<sup>33</sup>D<sup>34</sup>L<sup>35</sup>L<sup>36</sup>G<sup>37</sup>A<sup>38</sup>D<sup>39</sup>C<sup>40</sup>R<sup>41</sup>R<sup>42</sup>A<sup>43</sup>A<sup>44</sup>R<sup>45</sup>I<sup>46</sup>R<sup>47</sup>H<sup>48</sup>F<sup>49</sup>R<sup>50</sup>R<sup>51</sup>V<sup>52</sup>F<sup>53</sup>H<sup>54</sup>Y<sup>55</sup>G<sup>56</sup>T<sup>57</sup>G<sup>58</sup>R<sup>59</sup>R<sup>60</sup>P<sup>61</sup>S<sup>62</sup>P<sup>63</sup>H<sup>64</sup>T<sup>65</sup>Q<sup>66</sup>T<sup>67</sup>R<sup>68</sup>L<sup>69</sup>G<sup>70</sup>I<sup>71</sup>R<sup>72</sup>T<sup>73</sup>Q<sup>74</sup>R<sup>75</sup>R<sup>76</sup>R<sup>77</sup>F<sup>78</sup>G<sup>79</sup>T<sup>80</sup>I<sup>81</sup>P<sup>82</sup>V<sup>83</sup>T<sup>84</sup>A<sup>85</sup>G<sup>86</sup>S<sup>87</sup>R<sup>88</sup>T<sup>89</sup>Q<sup>90</sup>G<sup>91</sup>L<sup>92</sup>V<sup>93</sup>L<sup>94</sup>P<sup>95</sup>E<sup>96</sup>V<sup>97</sup>G<sup>98</sup>W<sup>99</sup>T<sup>100</sup>G<sup>101</sup>T<sup>102</sup>T<sup>103</sup>Y<sup>104</sup>W<sup>105</sup>  
A<sup>106</sup>I<sup>107</sup>A<sup>108</sup>L<sup>109</sup>L<sup>110</sup>P<sup>111</sup>S<sup>112</sup>V<sup>113</sup>S<sup>114</sup>W<sup>115</sup>L<sup>116</sup>A<sup>117</sup>G<sup>118</sup>G<sup>119</sup>N<sup>120</sup>G<sup>121</sup>N<sup>122</sup>N<sup>123</sup>A<sup>124</sup>A<sup>125</sup>T<sup>126</sup>Q<sup>127</sup>H<sup>128</sup>T<sup>129</sup>Q<sup>130</sup>T<sup>131</sup>A<sup>132</sup>Q<sup>133</sup>H<sup>134</sup>Q<sup>135</sup>S<sup>136</sup>L<sup>137</sup>G<sup>138</sup>E<sup>139</sup>A<sup>140</sup>V<sup>141</sup>K<sup>142</sup>T<sup>143</sup>A<sup>144</sup>F<sup>145</sup>T<sup>146</sup>K<sup>147</sup>P<sup>148</sup>S<sup>149</sup>Y<sup>150</sup>I<sup>151</sup>L<sup>152</sup>L<sup>153</sup>L<sup>154</sup>S<sup>155</sup>F<sup>156</sup>A<sup>157</sup>C<sup>158</sup>G<sup>159</sup>P<sup>160</sup>H<sup>161</sup>I<sup>162</sup>A<sup>163</sup>L<sup>164</sup>V<sup>165</sup>T<sup>166</sup>L<sup>167</sup>H<sup>168</sup>L<sup>169</sup>P<sup>170</sup>T<sup>171</sup>E<sup>172</sup>V<sup>173</sup>A<sup>174</sup>L<sup>175</sup>G<sup>176</sup>L<sup>177</sup>P<sup>178</sup>A<sup>179</sup>T<sup>180</sup>V<sup>181</sup>A<sup>182</sup>S<sup>183</sup>T<sup>184</sup>S<sup>185</sup>I<sup>186</sup>A<sup>187</sup>I<sup>188</sup>G<sup>189</sup>L<sup>190</sup>A<sup>191</sup>N<sup>192</sup>I<sup>193</sup>A<sup>194</sup>G<sup>195</sup>C<sup>196</sup>V<sup>197</sup>P<sup>198</sup>S<sup>199</sup>G<sup>200</sup>

**SEQ ID 4139**

SEQ ID 4139

ATGTCGTGATTGTCGTGATTGTCGCCGCTTTGCCGTGCCCTTTGGCAGCAGTTTTCGGGGCTGCTGGTCGGCAGCTTCCCTGAATGTCGTGATTACC GCGTACCCGTTATGATGGAACGCGGCT  
GAGCGGTATTTGCCAAGAACATTTAACCTGCGCGCTGACCGAGATGAAGACCGCTACCTTCAACCTGATGAAGCCGGATTCTCGTGTGCCAAATGCCGTGTGCCGATACGCGCGTGGCA  
GAACATCCCGATTGTCAGTTACCTGCTCTCGCGCGCAAAATGCGCTTCTGCCAAACCAAAATCAGCATACGTTATCCCTTAATCAGAGCTGCTGACCGGGGTPATTGTTCCGGGCTGCTGCGC  
TGGCAATACGGCTGCTCTGGATTACGCTGCGGCGGTTGTGATACTAGCCGCTTTTCGTGATTTCCCTGACCTTTATCGATGCGGACACCCAATACCTGCCCGACTCGATGACATTACCCCTGA  
TCTGGCTGGGGCTGATATTAAATTTGGACGCGGCGCTTCGTGCCCTTTGCAAGCTTGCCTTTTCCGTCGGTTCGCGGCTATAGCTTCATATGGCTCTTATGTGCAGTGATAAACTGCTAC  
AGGAAAAACCGGTATGGGCAACGGAGATTCAAACCTGATTGCCGATTTGGCGCGGTGCTTGGGATATCCGCAATGCGCGTGCATTTTGTGTTTCTCTCTGATCGGTTTGGTCGCGGCA  
ATCGTTATGCGCGCTGCCAAGGGGCGGCATTTTGCCTTCGCGCCCGCACTGACAGTTTCGGGCTGGATAATTTTACGGCAACGATTCCGATGCGCGGCGGTCACTGCTGCTGACCC  
ATCCGGTGAGA

**SEQ ID 4140**

SEQ ID 4140

MSDLSVLSPPFAVPLAAVLGLLVGSFLNVVTVRVPMMERGWTVFAKEHLNLPLDDESRTFNLMPDSCCPKCRVPIRAWQNIPIVSYLLLRGKCASCQTKISIRYPLIELLITGLVFLGLVA  
WQYGSWITLGLGLITAPLISLTPIADTQYLPDSMTPLPLNLGLIFNLDDGFPVLPQSAVLGAVAGYSSMLLCAVYKLLTGKTMGNGDFKLIALGAMLGISALPVLIFVSSLIGLVAA  
IVMRVAKGRHFAFGPALTVSGWLIPTANDSVNRVNWLTHTPVR

**SEQ ID 4141**

SEQ ID 4141

TTGGAAGAAAGCTTTACCTTGCAGAAATGAACCCGGGTGAGGTGATTACCGCTGAAGTAGTGCCAATCGACCAAAACTTCGTACCCTTAACCGCAGGTTGAAATCAGAATCCCTGATCG  
ATGTACGCTGAAGATTCAAAAACGCTCAAGGGCAAAATTGAAGTTAAAGTCGGCGACTTCGTACCCTTACCATCGAATCCGTCGAAAAACGGCTTCGGCGAAACCAAACTGTCCCGCGAAAAACG  
CAAAACGCGCAGCCGATTGGATCGCTTTGGAAGAAGCCATGGAACACGGCAACATCTGTCTGGCATCATCAACGGTAAAGTCAAAGCGCCCTGACCGTTATGATCAGCAGCATCCGCGCA  
TTCTCTGCCGGGTCTTTGGTCGACGTACGTCGCCGTTAAAGACACTTCCCATTTTGAAGGCAAGAGATCGAATTCAAAGTGATCAAACCTGGACAAAAACCGCAACACCGCTGTGTTTCCCT  
GCGCGCGCGTTTGGGAAGCCAATTGTGGGTGAAGAACGCAAGCCCTGCTGGAACAACTGCAAGAGGCTCCGTCATCAAGCGATCGTCAACAGTATTCACCGATTCACGGCGCTTCGTTGA  
CCTGGCGGCATCGACGCCCTGCTGCACATCAATCGGATTTGGCATGGCGTCGGTGAACACCCGAGCGAAGTCTTGGAAATCGGCTCAGGAAGTTGAAGCCAAAGTATTGAAATTCGACCAA  
GAAAAACAACGTGTTTCTTGGGTATGAACAACAATCGGGCGAAGATCTTGGAGCGGTCTGACCCGCCGTTATCCGCAAGCCACCCGCCGTGTTTCGGCAAAGTATCCAACCTGACCGCACTACG  
CGCATTCGTCGAAATCGAACAAGGCATCGAAGGTTTGGTACACGCTCCGAAATGGACTGGAACAACAAAAACGTACACCCGAGCAAGTGTACAATCGGGTGACGAAGTCTGAAGTCAT  
GATTTTGGAAATCGACGAAGCCGCCGCGGTATCTCTTTGGGTATGAACAATGCCAAGCCAACTCTTGGGAAGAAATTTCGCCCCCAACCAACAAGAGAGACAAAATCTCCGGTCCGGTT  
AAATTCATTACCGATTTCGGCGTATTCGTGCGCTGCCCGGCGGCATCGACGGTCTGGTTTCACTTGCTCCGACCTGTCTTGGACAGCAATTCGCGGAGAGACCGGTACGCAAAATCAAAAAG  
GAGAAGAAGTCGAAGCCGCTGATTGGCAATCGATGTGGAAAAAGAACGCACTCTCTTGGTATCAAACAATGGAAGGCGATTTCTTCGGCAACTTCATCAGCGTGAACGACAAAGGTTT  
TTTGGTTAAAGGTTACCGTGAAATCTGTTTGGCGCAAGAAAGCTGTATTTCGCCCTGTCTGACGAAGTAGAAGGCTACCTGCCTGCTTCCGAATTTGCAGCGACCGCGTTGAAGACTTGAAC  
ACCAAACTGAAGAGGCGGACGAAGTTGAAGCGCTATCTGTTACCGTTGACCGCAAAAACCGCAGCATCAAACCTTTCGTTAAAGCCAAAGATGCCAAAAGAACGCGGAGGCACTGAAC  
CCGTCATGCCGCCCAATGCGAATGCCGGTACCACCACTTGGCGGACCTGCTGAAAGCCAAACTCTCCGCGCAACAAGAA

**SEQ ID 4142**

SEQ ID 4142

LEESPTLQEMNPFGEVITAEEVVAIDQNFVTVNAGLKSESLIDVAEFKNAQGEIEVKVGDPVTVTTIESVENGFGETKLSREKAKRAADWIALEEAMENGNLISGIINGKVKGGFLVMISSIRA  
PLFGSLSDVDRPVKDTSHSPFGKEIEFKVKILDKKRNNVVVSRRAVLEATLGEERKALLENLQEGSVIRGIVKNIITYGAFVDLGGIDGLLHITDLAWRRVKHPSEVLEVGVQEVAKFLPQDQ  
EKQRVSLGMKQLGEDPWSGLFTRRYPQATRLFGKVSNLITYGAFVBIHQIEGLHVSEMDWINKNVHPSKVQVLGDEVEVMILEIDEGRRRISLGMKQCCQANFWSEFANENKGDKISGAV  
KSTIDPGVFVGLPGGIDGLVHLSLDSWTSGESGEAVRKYKKGEEVAVLAI DVEKERISLIGLQVDEGDPFGNFISVNDKGLSVKGSVWDAKGAVALSDVEVGLPASEFAADRVEDLT  
TKLFGDEVRRAVITVVDKRNRSILKSVAKDAKSKREALNSVNAANANAGNTTSLGDLKAKLSGEQE

**SEQ ID 4143**

SEQ ID 4143  
GTGCCGCTGAAACCTTATTTACCGGCTGCGGTGCCAAGGACTGCAGACACCCACCAACCAACCCGCACCCCTTGGCGGTGTACCGAAAAGAGTTATATATGCTATGGAAAATTTTGC  
TCAGCTGTGGGAAGAAAGCTTTACCTGCAAGAA

**SEQ ID 4144**

VPSETLPTRLPCOGLQPTNPTRTPWRCTEKSYSICLNKILLSCHWKALPCKK

**SEQ ID 4145**

SEQ ID 4145  
GTGGGTGCTCGAGTCCTTGGCACGGCAGCGGGTAAATAAGGTTTCAGACGGCACATGGAAATTCATGCTGTCTGAAGCGCAATGCGGGCGATTATACCTGAAAAAT

SEQ ID 4146

SEQ ID 4146  
VGVCSPWHGRRVNKVS DGTWK FMLSEAQCGRLYLKI

SEQ ID 4147

SEQ ID 4147  
ATGCCGTCTGAAGGTCATACCTCTTTTCAGACGGCAATTGCATTGATGCCGCCACGCCGGAATCCGAACCGGGTTGCCGGCTTCTGTCCGACGCTTTCCGGGACGGCGCGCTTCGGCTGTGCT  
TAGACAACTCGCTCTTTAAACACAGGTAGAATTCGCCCCCAACGGGAACACACACCTTCAGACGGCAAAACCCATACCCCAAAACCATCAGGAATCCCCCTATTGAACACAGACAAAAAGTCATCGC  
CATCGACGGTCCGGGCGCATCGGGCAAAGCACGGTCGCCGGCCGGCTTGCCGCGCATTTGGGATACGATTATCTCGATACCGGGCGCTCTACCGCTGACCGCCCTATATGCACAAAA  
CAAGGCGTGGAAATGGCAGATGAAGAAAAAGTTTCGCCACTTGGCAAAAAATCGCCCGCGCTATTTTCAGGCAACCGCATCTTACTTGATGGCGAAGAGCTTTTCAGACGGCATCCGGACG  
AAGCCATCGGTATGGGCGCATCCGCAGTTGCGCAATGGCCCAAAGTCCGCGCGCACTGCGCAACGCCAACCGCGCTTTTCGACCGAAAAAGGACTGGTTCGCCGACGGACGGGACACCGG  
ATCGGTCGCTTCCCCAAGCGAACTCAAAATTTTCTGACAGCCGAATCTAAAAATCGTGCGCAACGCCCGCGCAAAACAAATCGGCATTCCCTCGAAGGTTTCACATTCGAGCGCATC  
CTGTCCGACATCGAGACCAAGACAGAGCAGACGAAACCGCAAGGTTCGCCCTGAAACAAACAGCCCGATGCCCTGCTTTTGATACGAGCGCTTAACCTAGACAGAACTGTAAAAA  
AAGTCGCTTGATTGGTATCGTAAAGTT

SEQ ID 4148

SEQ ID 4148  
 HPSEGHSTFRRCIDARHAGIRTGLPASVGRFPGRRRSVCLDNRLPKQVESAPTGMTFFRRQNPFYKPSGIFLMNRQKVIADGPGASGKGTVAARVAALGYDYLDTGALYRLTALYAQK  
 QGVEMHDEENVSALAKKLPAVFSGNGRILLGDGEDVSDGIRTRAIHGASAVAQNPVKRAALLQRQDFITKEGLVADGRDTCGVVFPQAEKLFIATSKIRAEERAKQIQIGPEGFTFERI  
 LSDIETRDEADNRNRKVAPLKQQPDALLDTSRLTTEETVKKVLWDYRKV

**SEQ ID 4150**

**SEQ ID 4151**

**SEQ ID 4152**

**SEQ ID 4153**

**SEQ ID 4154**

**SEQ ID 4155**

SEQ ID 4156

SEQ ID 4157

SEQ ID 4158

SEQ ID 4159

ATGTCACAACTCAAACCATCGCCCTGACCGCATCAGTCTCTGCCGTTTGTTCGGGTTTCTCTATATGCCAAAACACCTCATCACACCAAGTCGGTTAGCGATTATGCGGTTAAACTCTT  
CAATATCTGACCTGCCACCGCAAAAACATATTTTCCAAATCCGGCAGCCTGTGGGACGAGCTGCGCCAGGCTTCCGGATGGCGAAGTCAATCCGMACTGGTAACGCCGCCAGAAAGCAA  
ATTCACTGCGAAGCCGCGCATTTTTCGACAGGCTCGTCAACCGGAGCCGACCTTATATGTACCATATCTGCCAACGAGCTCAAAAAACGCAATATGCCGCCGGAAGCGCCCTGCTTCCCTTT  
ATCGAAAGCGCTTCTGTCACCAAAAGCAAAATCAACGTCGGCGCATCGGCCCTGTGGCAGTTCATGCCCGTCAACCGGACGCTTACGGCTTGGAAAAAACACCGGTTTACGACGCGAGG  
ACGACGCTTAGCGAGCTACCGATTGCGCGCATCAACTCATATGTCGAATATCTCATGGAATCTTCCGACGATGCGCCCTGCGGCTTTCGCGCTACAACTGGGGTAGGAAGCACTGCGACGCGC  
CGTCAACCGCGCCCGCGCAACGAGGGCTCGAACCGACCTACGAAAACCTTGCCTATGCCAACGAAACGCGCAACTATGTCCCAAGCTGCTCGCCGTGCGCAACATTATTTGCCACCCCCCAA  
TCTTTGCGCATGAATATCAGCGACATAGACACAAACCTTATTTTACGGCAGTGGAAACGGGCGCTGCGCTCGAACAGAAAGCCATCGCCCGGCTTGC CGGCATCACGCAAGCGAGCTGCT  
TGCCTCGAATCTGTCATTCAACGTCGCCCGCTTCATCCCCAAAACAAACCGAAACGCTGCTGCTTCTGTCGCTTTCGCGCAACCTTCCAAAGCAACTACTCTCAACGCGCGACCGCGACG  
CCTGTTTATCGGGAAGCTATACGCTTCCGCTCGCCGACCGCTTCCGCGACATCTCGACATCTCGACGATGAGCATTTGCCGACATCAAAACGCTCAACAACTGGAAGCGCAACTCTGCTC  
AAGCGAGACGAGGAGCATCTCTTGTGCGCAAGAACCGCAAGACCTCTATACGCGGATCGAAGGATTCGTCGTTTTCATCGACATCTGACAATACGCGCGACGATCAACGTTTCCAAATATTCGCGGAC  
GCACGCTGAACGTCAGCATTTGCCGAATCCAACCCGCGCGCGACAGACAGCGGACATTACCGTGCACCTTTTGC CGCAAGAAACCGTTCGTCAGGAACCCGATCCCTTGTTCGCGATTAC  
CGAACCCGCTTTCGACAGCGCGACGCGCAACCTCAAAACGAAAAACAGACTGCCATCGCTGCTGAACCCAAACCGCAACACTCGCGCAGGCTATCCCCCAAACGACATGCAAGCGCGCA  
GACGAATCACTGCGAGCTTGTGCGCGAAACAACTTGC CGCGGCGAGGCTGAAGAAACATCTTCGCGCTCATCGCGAGGCTGACACAGTTGTCGCGAAACACAACATTCTCTATCTCGCAAC  
ATACCGTTGTCGCGCGACGCGCAACCGCGCGACGTTTGGAAACCGCGCTAGAACAGCTGCGCAAGCGGACGCTTCCCCGCTCCATCGGCACATCAACCGCTTGTAGAGAGCGGCA  
CACCGTTTCAACATGCGCAAAACGCTCAACGCTCAGGCTAGGCTAGCGCATGATTTGTGCGCAACATCTCAAGGCAACACCATCCAAAGGACGAGTACTCCGCTGGGCTAGGACGCTCT

GCCCAAAACCGGTATTGAAAAAGTATCTACACCGCGCGCAAGGCGACACCTTCAAAAGTATCGCGCGCGCTTCAATATCCATATCGACGACATCCGCGCGCTCAATCCCAACTGAACA  
CCATCAATCCGGGACAGAGGGTCAAACTGATTGGAAGC

**SEQ ID 4160**

NSKLTIALPASGLSVCPLFYAQTSSHQVGLAIMRLNSSLIDLPPTKQYFQSGSLWDELQGFPMGEVNPFLVRRHESKPIASRSYFDRVVRNRSRPTMYHLANEVKKRNPMAEALLPF  
IESAFVTKAKSHVAGSLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNLYQLVYGLFGDWPLAFAYNWNWEGNVGRAVNRARDQGLEPTYENLRMPNERNRYVFKLLAVRNIATPQ  
SFGMNISSIDNKPYPQAVEPGRPLDNEALARLAGITQSELLALMPAFNPAPFIPKNNRKLPLVASVQTPQSNYLNAPDSLFSWEVYTPAARTSLSDISTATGMSIADIKRLNMLNGLV  
NAGRSILVAKNGRTLHTASESVSVIDINTPDYRNSMFPAGTVNVSIAIQPAAATQADITVAPLPQETVTRTPDPLVRIETEPALATAAAQPTQEKQAMPSETQATLAQVIPPDMQAA  
DELMQLVARNRLRRQAETLSAVIGTPTVAEHNISSSPQHTVAADGKRRARLETTRVAKADGEAETSPLHASIHRVVEGDTLFWIAKRYNVSVADLIVANNIKGNTQKQGVRLQAAP  
AQTRIEKVSYTARKGDTFKSLAARFNIHIDIRRLNPNLNTINFGQVRLIGS

**SEQ ID 4161**

ATGCATCCATATTCGCTCCGTTTCAACAGATTGCCTGCCGATATTTTATCCAAACAGGATTCTGTCAAAAACACATCGCGCGCCCATTTCCGAATCCGCATAAAGTTCTGTAAAC  
TTGACGCTTTTTCAGTCAACAGTACCATCGGACGATATAATATGTTTATCCCGGAGTATAATCATGTCCAAACTCAAAACCATCGCC

**SEQ ID 4162**

MHPYCVRFQIACRYFIPNRI SVKKHIGRPFNPHKVPVKLDAF SVKQYHRTIKYVSAEYKSCPNKPSF

**SEQ ID 4163**

ATGGATGCATGTTTGAAGATACGGCGATGGGGCGGTATGTTGCAAAATTGGAACAGGACTCTTTAATCGGTATGTGCGCTCATACGCTTTTTCGGGAATGTGTGCGGTTTTCAGTGGGG  
GTGAGTGGCTGAGCGTCTGTAAGACATGTCTGTGTCGCGGAGATATGTCATGTGCGCGGAGAAATATGCTTTGCGGATATGCTGCTTTTTCGGCATACGCTGGA  
ATGCGCGTACCTTCGCAAACTCTGTGCGAAGCGCACCGGATATGAAACCGTCCGACGTTTGATGCTGACGGGTTTCAATCCGTATTCGCTTTGGGGATTCGCGGTGTTGACGGT  
TTCGCTGTCGCGGAAAAACGGTTTGTGTCGCGCTGCCGAGTTGAAAGGAGCGTTCGCGATGCGGTTTCGATATGAAATTTGGGAAATTCATGCTGTATTCGCTCCGCTTTCGTCGC  
TCGGGCAAAATACGCTTTTGGCGGTTTATGAAAGCGCGGCGGAGTGTGTCGCGCAATGTGCGGATGTACGGTTTGGTTTGGTCAAAAGGCGCGCGGCGTAACGCCCTTCGCGC  
GTGGGACGGTATGGGGCGGCAAGCCCTTGGCGGGTGGCGGAGGGTTCGGAT

**SEQ ID 4164**

MDAWEFTAMGRYVAKLEQDFNRYVASYRFGMCVQVGGWLSLSEIVCVPRDMMSAENMALADVADMLLPHTECGVPSQILSEAHRIKPSGRIMLTGFNPYSLWGFCEWFDG  
VRLPEKRFCLPLPELKRQLADAGFDIEFGKFMVYLPVSLGQIRPWRFMKAGDRWPPQCAAVYGLVLVKRAAGVPLPAWDGTWGGKALAGAARVAD

**SEQ ID 4165**

GTGCGGCAAGGGTTGCGGATTAAGGACGCGCTCTTTACAGCGCATCTGTGAGAAGAAATGTGCGGAGGGTTATGCGCGAATTCGCGGAAGTGAAACGACGTTGCGCGCATCGCGC  
CGCATATTGAAGAAAAACGGTGAAGCCGTGATATTGCGCAACTGAAGCTGCGCTGCGAGATCAATCCGATTGGGGGAGATTGTTGCGCGCGCGCAGGTTTGTCTCGCGCAGGCG  
TGCCAAATATCTGATGTGCGGTTTCAAAACGGGGATTTTGCTGATTCACTTGGGATGTGCGGCGAGTTCGCGATCTTACGCGCTCGGACGAGTATCGCGAGCGCGGACAGACAGAT  
CACGTCGATATTGTGTTTTCAGACGCGCAGGTCATGCGTTACCGGATCCGAGAAAGTTTCGCGCGGATCTTGGTATGAGGGAATCGAAGAAGCTCATCCGCTGTGGAAGAACTGGGGC  
CGGAGCTTTTTCGCGAGGCGATTTCACGCGATTATCTGTATGCGGGGCTGAAGCGCGAGAAACGCGCGTCAAACTGCTCTGATGGAACAATACGCTGTGTCGCGCTGGGCAATATTA  
TGCCAACGAGAGTCTGTTTCAGGCGGGCATTTGCGCCACCGCTCTGCCAACCGCTTAAAAAGAAAGAGTCCGCGTTTGGTTGAAACCGTCAAGCGGTGTGTCAGCGCGCCATTGAA  
ACGGGCGGAGTACGCTGAGGATTTTGTGACAGCGAGCGCAAGCGGCTACTTTCAACAGGAATATACGGTGTACGGGCGGCACAAATACGCGCTGCTCCGCTGCGCGGTTTGGTTG  
TGAAAGAACTTTGGGCGCAGCGCGCATGTTTATTCACGAACTGTCAAGAA

**SEQ ID 4166**

VRQGLRIKGRPSRRHLSEMSGVMPLEVEVETTLRGLAPIHIGKTVEAVILRQLKLRQINPDLGEILSGRQVLSGRRAKYLIVRFQTGILLIHLGMSGSLRIPTPSDGRIGRPDRHD  
HVDIVSDGTVMRYRDPKRFKAILWYEGIEERHLEKLGEPLSEAFCTDYLYAGLKAQKRAVKLALMDNTVVVGNGNIYANESLFRAGISPHRANRLKKKECAVLVETVKAQLQRAIE  
TGGSTLRFVSDGKSGYPQEQEYTVYGRHNPCLRCGLLVKKEQLGQRGTFTCTNCRK

**SEQ ID 4167**

GTGCGTCCGCGTGGCGGTTTGGTTGTGAAGAAACTTTGGGGCAGCGCGGACGTTTATTCACGAACTGTGAGAAATAGGGCGGAAACGGTTTTCAGCGCATTTTATCGGTATGCC  
GTCCGACGTTTCAACAACAAACACCGATTATCGGAAAGAAATGCGCATGTCTTCAA

**SEQ ID 4168**

VPFVRRFGCERNFGAARHVLHLELSEIGRKTVDGILSVCRPNVSTNTDYRRIERIANHFV

**SEQ ID 4169**

TTGCCCATGTCTTCAAATAAAGCTTCATTTTACACGCTCTGCGCGCTTGTGCGGCTTGACGCTGCTGTTCAAAACCGGCAAAACCTGCGCGTATTGACGCGCGCTGCCCAAGT  
CGCGCAATCGGGCAGTTATAGCGTTGGGCAAGGCGCTTTGCGCGCTTTGGATATCGGATTGGAGGTGGGAGACCCGACCCGACCGTCTGCTTGGTTGCGCGCAACCAAGT  
GTCTGCGCTGATATTTCGCGATGACGCGGTTTATCCGAGTAGCTTTATCGCGCAAGCAGGAATCAAAAGCTGCGCGTATTGGGCAAGATGGGCGAGAACCGGGAACGTTTCATC  
AACCGCAATTTCGCGCGGCGGACATCGAACCGATTAACCGCGCGCTTCCGAAACCTTGCAACCGCGTCAAAACGTCAGTTTTCCTGAGGCGGCAATTCCTCGGACTGGGGCTCTGCG  
CGTTCAAGGCTGCGCTGTTCACATCCGCCATCGATGCGGGGCAAGGTTTGGCGGTGCGACTGCGTTTATGACGAAACGGGAAAGGACGCGCGCTCGTATGCGGATGTCG  
TTTGGCGACTGCTGTCGCGAATCTGTCTATGAAAACTGACTATCAAGTCGATTTCGTTGCGTGGCGGACGCGGCAAGCGGAGACCGGTTATGCTTTAAAGATAAAATCGAA  
GAAAGCATCCGCTGCTGTCGAGCGATGCGGATGTTGCGCT

**SEQ ID 4170**

LFMSSNKASFFTRRLRLCRLTVWLFTKGNLRGIDGGCPKSRNRVIALGKALALDILGVEGRPAPEHPNGVLVAANHVSMLDIFAMSAVYPSFIAKQBIKSWPVLGKMGQNAQTVFI  
NRNRRDIEPIINRAVCETLRGQGVNSFPPEARTSSGLGLLPFAALFQSAIDAGAKVLAVALRYDYDETKRTARPSYADVGLPTCLWRIVSMKLTIKVDFVCVADAESEDRYALKIKIE  
ESIRAVVAGDAVAV

**SEQ ID 4171**

TTGCGCTCGGCTGCTGCTGCAATTGCGCACCGGTTCCGCGGGTTTCCATCATTTATGGGACAGGTGCGCGCCCAAGTCCCAACACACAAACCGCGCTTGGCATCGGACTGGTCAACGC  
AGGCGGTTTCGCGAGGACAAATCTGTGTCGACCGCTGGTTCAAGGACTCAAGGACTGCTGCTTCCCGGAAGTTCGCTGGACGGGTACATTTACGTTTGGGGCGCAATCGCCCTGCTGA  
TTTCTGCGCTCATGTTGCTGCTGCGCGGCAACACGCGCGCAACACGCGCGGCAACACCGGCAACAGGCTCGGAGAGCAGTCAAAACCGCTTCAA  
AACCCCAAGCTACATCTGCTGCACTGAGCTTTTTCGCTGCGGCTTCCACATCGCTTTCTGTAACCCACCTACCCACGGAAGTTCGCGCTGTCGCGACTGCGCGGACCGCTGCGCTG  
ACATCCATCGGCTCATCGGACTGGCAACATCGCGGTTGCGTGTCTCAGGCTGATGACCGGACGCTTCAAAGGAAACACATCTGCTGCGGACTTACGCTTACCGCTTACCGCTGCGCATG  
TGCTGATTACATCTTCTACCCAAACCGACTCAACTTTTACATTTTTCGCGCGGCTGCGGACTTACATGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTTCCG  
CACCGCTACTTCCGACCGCTGTCGAGCTGCTGCTCACCACCAAACTGCGCGGATTCCTGCTGCTACATCGGCGGCTGCTGCTTACACAACTCGG

**SEQ ID 4172**

LPSCCSHSAFVPAFPLWDRSPKSPHTNAWHPDWSTQAVRQDQNSHRWFKDSRTTRPARSLDGYILRLGNRPADSARLMVACRRQRRQRRPHPTPHSHTRTKPRSSQNLQ  
NPKLHPAEPFLRLRLPHRLSRNPPTHGSRVTRARHRLDIHRHRTGKRRRLVRLMHRTLQRKTHPVRTLRLTRRHGADLHLLQNRPLQLHFRRTTRTHMARHRRPDRRRYRQTLR  
HALPRHPVRTGDAHPPNRRIPRLVHRHRRDYTR



## SEQ ID 4173

ATGCGCGCGGTCACCTGGTGGCTGACCCATCCGGTGAAGTACACGATGGGTGCGACTGACCGCGGAATCGGACGCGCAAAATGCGGACGCGCAATATTTTGGCGATTTGGCGGTGC  
CGCGCATCGATGCGGACGCGCGCGCGCACTCGCTGACGGCTTCAGACGGCATCGCCCTCCGGAATCAGGCGGTGTCGGGACACCGCTTTTCGACACACAGGGTTTGTTCGCGCGGA  
CATATTGCGTAAGAAATCTTTGCCCTCCCATCGGCAAGCCCTGCTCGAATCCGTGATGTTGCCGTGATTTTCTCAGAAATCAAAAACAGCAAGAAACCTTTACCGATGCGGTTTAC  
GGCATGTCGAAATTCGCTGCTGACGGAAGCGTCAATTTATCAGCTGATACGGCGTCTGACCATAGCGCACCTTTGAAAAACGATATCGGACGGGTAATGGCAGCGACGCGGC  
TGACGCGCGCGAGGTGGCGGACATCATGCCATCAGGCATCCGAATCCGAACGCGCTGCTGCTTGACAGCATGTACTGCTCAATGACGGCAGCCTCAAAAGCCCTACGTGAGAAAAACAAT  
GCTCTGACCGGTTTATTCAGGGATTTTCGCTCAAAACCAACAAAGGAAAAACAATGGC

## SEQ ID 4174

NAGQVLVADPSGEMTAVGLTGGIGSGKSAAYFADLVPRIDADAAHSLTASDGIALPEIRLFGDTVFDVQGLLRDILRKEIFASPSRKALLESVNLPLIFSEIKKQOETPTDAVY  
GIVRIPLLTEKRQFISLIRRVLTISAPLEKRIGRVMARSGLTRGEVADIISHQASESERILLADDVLLNDGSLKSLREKTHLHAFYSGIFASKPTQGHNG

## SEQ ID 4175

TTGTCGGAATGTCGGGTATGATTCGCTTTTGGCGATGCCCTAAGGCTGCGGTACCGGAGTACCTCAAAAGAAATGCCGTAAAGGATAGTTGTGTATAGTGGATTAAATTTAAATCAGG  
ACAAGCGCGGCAAGCCGAGACAGTACAAATAGCAGCGCAAGGCGAGGCAACGCCGTACCGGTCTAAATTTAATCCACTATATCTATGAAATGCCATCT

## SEQ ID 4176

LSEGGMIRFCGLKAAVTGVPQKKCRKDSLLYSGLNLNQDKAAKPQTQIARQGEATPYRSKFNPLYLKHPS

## SEQ ID 4177

ATGCTTGCCATACTGTTGCTGCAATACTGGGACTGGTATCAACAACTGCCGTGCGGTACGTGAGAACCCGCCACCACATACCAAACTATCAGCAAGGCAACAGCAGATGCTGC  
ACCCGCAATGACGAAATATTTGGAACGCCGTGCCGCTGGTACCGATCGCAAGGCAACGTGACGGAATTCGCGGAAACAAAAAGCGCGCAAGCATTCGCCACCCCTGCTTATGCGGA  
ACAGAAATCCAATGCCGGCGGCTTATGAGGCTTCGATGATTTTCGACGGCGCGAGGTTCCGCCGT

## SEQ ID 4178

NLAILLSAILGLVSTTAAAGTSEPAHRHTKHSKANKQHLHPECRKYLERRAAWYRSQGNVQELRENNKARKAFETLFEAEQKIQCRAAAYEAFDDPDGGRFR

## SEQ ID 4179

ATGAGTCTGAAACTGCCGACAGTTTCCCGTTCCTCTCCATCTTATCTGGAAGGAATACAAACTGAAAGGATCGTCATGTCCTCAATAAGATGCTTGCCATACTGTTGCTGCA  
ATACTGGGACTGGTATCAACAACTGCCGCTGCCGCTAGCTCAGAACCCGCCACCGACATACCAAACTATCAGCAAGGCAACAGCAGATGCTGCAACCCGGAATGACGAAATATTTGG  
AACGCCGTGCCGCTGGTACCGATCGCAAGGCAACGTGACGGAATTCGCGGAAACAAAAAGCGCGCAAGCATTCGCCACCCCTGCTTATGCGGAACAGAAATCCAAATGCCGGCGGC  
TTA

## SEQ ID 4180

MSLKLPTVCPFPFSILYKELQTERIVMSVNDACHTVVCTGTGINNCRCRYVRTRPPTYQTYQGGQADAAFRMQEIPGTPCRVVP IARQRAGLARKQKGAQSIHPALCGTENPHPGG  
L

## SEQ ID 4181

TTGTTAAATTTTGCAAGTATGATTTTGGCAGCGCGCGCGGACAAATTCATTTTCTTACCAGTTGGAATTTATTTATGAGATTATATGTTATTTGAATTTGCATATCAACCGGCAAG  
TTTTGTCGGCTGAA

## SEQ ID 4182

LLNFAKYDFCHAAADKFHFLTDWNLRLRLICVNLHRIKQVLSAE

## SEQ ID 4183

TTGCAAAATTTAACAATTCGACGGGCGGAAAAACCGAAGTTTCTCTTTTCGTCGGAATTCCTTATTTTCATCGCCTTGTAGCCGGAGCGGTCAAAAGGCAAAAAATTTACCGTTTTT  
TATCGGTAAAGAATATCAGATAAAACAAATGTTA

## SEQ ID 4184

LQNLITRRGGKPEVFLFRKILISSPCSRSRSGKKPFRFLSVKNVQIKQHL

## SEQ ID 4185

ATGAATACACGACTGATTTAAAGTAACCAACGAGACGGAAGATTGGAAGCCATGATTTGGATAGATTCAACGCTGCTTACTTTGGCGCGCGGAAGGATGGAATATGTTCCGTGT  
CGCAGGTCGAGTTGAAATCGCATATCCAGTTTCACACCGCATCCGACCCGACGACATCCAGCAAAACATCATCAAAAGCGCTGACAGATTAAATTTGGAAGATACCCCGGACATCAATA  
CCTTGCCGACGTTTGGGATTTTCCATCTTCGTAAGTACGCTACGCGGAATACGAGCGCGCCGACCTTTACAAACATGTTAAAGCTCACCGATGCCGGAATACGACAGGCATATC  
CTTGAGGATTCAGCCCGGAAGAAATTCAGCAACTCAACGCTTATATCGAACCAAGCGATATGTCCTTTTCTATGCGCGCGTCAACAGCTCGAAGGCAAAATATCTGTTACAGAAC  
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CGCCCTGCCGACCAACCGCTGGACAACATCAACGACCTGACGCGGAAATAGCCCTGTGTACACTGTGCGCTTCAACTTGGGTGCAATTAACAGCTTGGACGAATTTGAAGGCGTTCGC  
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GCCGACATCTGCAATACGCGCTCGGCAACTCTACTCTGACCGCGCTCATGCCCTCTGAAACAGCTCGCAAAATCGCCAACGCCACCAACCGCATCGAGCCGCGCGGATTTGGTAACGG  
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GGCGTCAAAACCTGCTACTACCAACACCCGCGAGCGCGGACGACACGACAGCGATTTCAAGATGACGCTGCGCTGCTGGCGCTTGAAGATT

## SEQ ID 4186

MYPTDLKVKRDKRLEADLDKIHVVWAAEGLNVSVQVELKSHIQFYNGIRTDIHETI IKAADLISEDPDYQYLAARLAIPLRKLIAIYGEYEPHLYNHVKLLTDAGKYDRHI  
LEDYSREFFDELNAVYDHERDMFSYAAVKQLEGKYLQNRVTRQIYETPQLVLVWAMCLFSKYPKEARLDYVKRFDYAVSTFKVSLPTPIMSGVETPTQFSSCVLIECDDSLDINAT  
TSAIVKYVSQRAGIGINAGRIGLDSEIRGGEARHTGCIPIFFKMFQAAVSCSQQGVGGAATFLFYPLHIEAESLLVLKNNRGVEDNRIQLDVGQINRLLYTRLLIKGNNITLFSFNEV  
SGLYEAPFADQDEFERLYTYEQDPNIRKRIIPADLFSTLMQERAGTGRYIYQVNDHCNTHSPFDPVAVPVQSNLCMEALPTKPLDNDNDPGEIALCTLSAFNLGALNSLDELEGLA  
DLTVRALDALLDYQGYVPEAARTSTNDRSLGIVINAYYLAKNVGRISDGSALGLTHRTPEAIQYLLKASANLAKEYGACTLFNQTVYSQKLPIDTYKDLDAVCGEPLHYDWESLR  
ADIVKYGLRNLSTALMPSETSSQIANATNGIEPPGLVTVKASKDILKQVPEFELKNAYETLWQLPGNEGLYKLVGVMKFVDQAI SANPAYDPKGFEGNKVSMQMLKDLITAYKY  
GVKTLYYHNRDGDADTQTDIQDDGAGGACKI





## SEQ ID 4202

MGRAVPSGASTGQKEALELRDGDKSRYSGKVLKAVEHVNQIAQALIGIDANEOSYIDQIMIELDGTENKGNLGNATLAVSMVARAAAEDSGLEFLYRLGGAGPMSLPVPMNVING  
GEHANSILNIQEFMIMFVGAISPREALRCGAEIFHALKKLDCSRGFPPTVGDGGFAPNLNSHKEALQLMVEAAEAAGYKAGEDVLFALDCASSEFYKDGKYLHAEGRSYTNAEFAEYLE  
GLVNEFPIISIEDGMDENDWEGWKLITKLGKVKVLVGDLLFVTPNPKILAEIGIEKGVANALLVKVNIQIGTLESLKAVDLAKCNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLSR  
SDRMAYNQILLRIEELAEAAAYPGKAAPYQLGR

## SEQ ID 4203

ATGATGCAGACTTTCCGAAAAATCAGCCTGTATGCCGCAACCTTGTGGCTCGGTATGCAGATTATGGCAGGTATATCGCCGACCGGTGCTGTTCAAAATGCTGCCAAAAATGCAGCGG  
GCGAAATTCGCGCGCTATTGTTTCGACATCCTCTCTTGGAGCGGCTTGCCTTTGGGGCAGGCTATCGCTGCCGCTTTCGCCCTTAACCCGCGCGCAACCCGCTCTGCTTTTTT  
ATTGTCGCGCTTTCGCGCAACCAATTTTGGTTACACCCGTTATCGAGGCATGAAATACGGCATGAAAAATGGCTGTTGTCGGTTGCAGCGGATCTTCGGAATGTGGCAGCGTATT  
TCCAGCATGACTTTCATGCGCAACCGCCTACTTTCAGCAGTTTAAAGTTGGCGCTTTCGCGCAAGAGGCGCTC

## SEQ ID 4204

MMQTFRKISLYAATLWLMQIMAGYIAAPVLPKMLPKMAGEIAGVLPDILSWGLAVWGTVLAAPAAALTRRQTALLFLLSALANQFLVTPVIREALKYGHENWLLSVAGGSFGEHNGI  
SSMFFHATALLSAVLSWRLSGKEAV

## SEQ ID 4205

CCCAAAACCGACTCACTTTTACATTTTCGCCCGCGCACTCGGATTCACATGGCTCGCCACCGTCCGCCCGACCGCGCGCTTACCGGCAAACTCTTCGGCAGCGCTTACCTCGCACCC  
TGTTCGGACTGTGATGCTCACCCACCAATTCGGCGGATTCCTCGGCTCGTACATCGCGCGCATGATGATTACACAATTCGGTACTACGGCTGGATGTGTACGCGGATGCCGTACTCGC  
CGGCACGGCAGCCCTGCTTGTCTGCCGCTCGCGAACCAGCGCGCATGACAGAATGCCGTCTGAAACCTTCAGACGGCATTTTCCAAACACCCCGCGCTTTCGGGACTGCACGG  
CACGCAATCAGCTTATCAACCGCAATTAACCGCGGATTAACCGCCATTCAAATAGCCCGCTTTTCCTTCGGGTGTAATAATCATCAC

## SEQ ID 4206

PKTDIAPYIFAAALGFTLAVTAAVTKLPGTRYLATLFLVLMTHQIGGFLGSYIGGIVITQPGDYHMYADAVLAGTAALLVLPVREPRTA\*QNAV\*NLQTPAFSKHPCRFAR  
HANQPYQTANNRRD\*TAIQISPFSLRV\*NHH

## SEQ ID 4207

ATGGATATTAATAACAGCATCACCTTCGGCAACAATTCGCTTTCGCTTATTCGGCGCATCAACGTTTATAGAGATTGGATTCCACCTCCAACTCTGCGCATTAACGCGAAG  
TTACCCGCAAACTGGGCAATCCCTATATCTTTAAAGCCTCTTCGACAAAGGCAACCGCTCGCTATCCATTCCTATCGCGCGTAGGCTTGAAGAAGGCTTAAAGATTTTTGAAAAAGT  
CAAGCAGAGTTCGGCATCCCGCTCATTAACGACGTACACGAACCCATCAATGCCAACCGTTCGCGCAAGTGTGCGATGTCAATCAGCTTCGCGCTTTCGCGCGCAGACCGATTG  
GTGGCGCAATGGCGGAAACGGGCAATGTTATCAACATCAAAAACCCAGTTCCTCAGCCCTTCGCAAAATGAAAAACATCGTGAAAAATTCGCGAAGCGCGCAACGGGAAGCTGATT  
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AACCCGCGATGCGCGTTCTGCGCATCGCGCGTCTGCGCGCACAGCTTTGGATTGGCAGCTTCAGGCGATGCAACCCCGCTTCGCGCGCTGTTCTCGAATCGCACCCCGATCCGAAA  
CTGGCAAAATGCGACGCGCCGCGCTGCGCTACACCTTTTAGAAAAATTTTAAATCGCATCAAGCATTCGACGATTAAATCAAAATCACAACCGATTATTAACAAATCGAG

## SEQ ID 4208

MDIKINDITLGNNSPFVFLGGINVLDELDTLQTCARHYVEVTRKLGIPYIFKASPFKANRSSIHSYRGVLEGLKIFKVKAEFGIPVITDVHEPHQCPVAEVCVDVQLPAPLARQTDL  
VAAMAEATGNVINIKKQPLSPSQMKNIVEKPREAGNGLILCERSSFGYDNLVDMLGPGVMKQTCGNLFPVFDVTHSLQTRDAGSAAAGGRRRAQALDLALAGMATRLAGFLBSHEDPK  
LAKCDGPSALPLHLEWFLIRIKALDDLIKSPILIFIE

## SEQ ID 4209

ATGTTCCGTACTATATCTGGCGGAAAAATCCACCGCCACCGTAACCGAAGCCGATTAACTACGTCGCGAGCATTAACGTCGATCAAGACCTGTAGACGCGGCGAGCATTCGCCCCA  
ACGAAAAAGTCGCGCATCGTCAACCAACAACGCGCAACGTTTGAACCTATACCATTCAGGGAACCGCGCAGCGCGGTGATTGCTGAAACGGTGTGACGCCAGGCTGTACAGAA  
AGCGCATCGTCATCATTTATGCTTATATCAACTTTCGGAACCGGAATCGCGCACACGAACCAAGTCTGCTTAGTGGACGGAACAATAAATCCCGACATCATCTCTACGAG  
CCGCCGCACACCTACTG

## SEQ ID 4210

MFRTILGGKIHRAVTVTRADLNVGSITVDQDLDAAGICPNEKVAIVNNNGERPEYTTIAGKRGSGVICNGAAARLVQKGDIVIMSYIQLSEPLAAHEPKVVLVDGNNKIRDIISYE  
PPHTVL

## SEQ ID 4211

TGGATGCAATTTCGCGCTTCTGTGCGAATTTGAAAAAGCGACGATGCTGCACGCGCGCACTGACGGAATATTGAAACGGACAGCCGCTATATGACTTTTACACCGAAGATACCC  
AAACAAGCGGTGATGCGGCAAAATTTGTCGCACTATGCACTTATATCAAGCTTATGGGCAAAAAATCCGGCTTTTCCGCTTATGATTATATGCCCCCAATATAGAAAGCGAGCA  
AATCTTTCGCGTCAAACTCGATTGAGCGCGAGCATTTCTCAATGATGCGAGAGT

## SEQ ID 4212

LDAPAFPLSELEKADDAARAALTEYLKRSRYIDFHTPTQTSRDAKFVRTMQLIYISLWAKNPAPAVMDYHPANIESDEILAVKLHLGDSIFSIDYES

## SEQ ID 4213

TGGGTATCTTCGGTGTGAAATCGATATAGCGCTGTCCCGTTTCAAATAATCCGTCAGTGGCGCGTGCAGCATCGTGGCTTTTCCAATTCCGACAGGAAGCGGCAAAATGCATCC  
AATGTTTCGGTTGCGAGCGCTGTTTCAATTTTCGCTACAGGAATACCTCGACAGATATGCTTTGACGGTCAGCTCGTCTCCAGAGGACATCTTCTCTCGTCAAAACCTTCGGTGG  
ACAGTGTGGAATAGGGGTGAAAAATCGACATGATGTTCTCTTTG

## SEQ ID 4214

LGIFGVKVDIAAVPQIFRQCGACISVGFQFGQEGGKIQCFGWQAVFIFCLQEYLDKIAFDGQLVFPEDIFFSVKTFGGQLLEIGVKRRHDCSFH

## SEQ ID 4215

ATGTCGATTTTACCCCTATTTCACAACTGTCCACCGAAGGTTTTCAGCGAGAAGAAGATGCTCTTGGGAAGACGAGCTGACCGTCAAAGCAATCTTGTGAGGTATCTCTG

## SEQ ID 4216

MSIFHPYFQQLSTEGFDGEDVLWEDELTVKGNLVEVFL

## SEQ ID 4217

GTGCGCCCGCAAAACCGCAGCGGCGGCACTTCTGCATCGCGTGGCAACCGGTACGAACAACAGTCCGCGCGCGCTTTTAACTGCGCAACCGCGACAGCGCTCCGACACCA  
AATCC

## SEQ ID 4218

VRPAKNGTGSFICIAVATGNTNTSAAPLLICHNADSRSDTES

## SEQ ID 4219

ATGCGCGCGCTTGGCAAGGTTTCCCGCGCGCGCGCTATCGGCATTTTCATCAATGCAGACCGCATTTCAATCTATATCAAGGTGTCCGCTTATGAAAAATCGTTTTATCACAA  
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CGTAAAAACAAAAATAAAGGGCATTTTGAATGCCCTGTACCGCATTGCCCTGCGGATGTTGGAAGGCTGATGATTAACCCCGACGACAAAGACGAGCTGCTGCATCAATACGG

CATCAAAATAAAAAACATTCATATTTTGGGCGGAATCGGCTCGATTGCGGCAATATCTTTATTCGAGGCGGATATTCGGATGAAAAGAACCCTGAAAAATTTCTCTTTATCGGCAGATTTCTTGAAAGAAAAGGGGATGATGATTTTATTCGGGCGGCGGAACAGGTTAAGGGCAAAATACCCCGATACGGTGTTTTACCGCTTTGGGCGCAATCGACAAATACCGCGGGGGGGGGGATTTAGAACGCTTTATCGCCCGGATATTAACGGTTTCCCGGTTTGTGAACAAATGTTTCCGAAGTGATAAAGGCGCATCATATATTCGATTTGCCGTCTTATAGGGAAGGGGTCCCGAAGCACCCAGGAGGCAATGCGCGTTCGGCAGGGCGGTGATTACGACGGATGTCGCCGAGTGACAGGAAACGGTTGCCGACAGGTCAACGGTCTCTGATCAACCTTGGAAATCCCGCATCTTGGCCGAAAAATGATTTATTTTATCGAAAAACAGGGCTGCCCTCCGCTGATGGCGAATGCAAGTTATCGGATTGCCAAAGATAAATTCGATGCCGAAAAAGTCGATTTGAAATTTCTGATATTTTGAAGGCG

**SEQ ID 4220**

SEQ ID 4220  
MRRAWQRFPARRAPYAFHQCRPHQPSYIQGVRLMKIVPITTVASSIYGFRAPIVKLIGKNHQYAFVSEFSNDELIIIRENGVTPVTVRSNRSGVNPFSDIKSTFLIFKALKKISPOLVF  
PYFAKPVIFGTFAAKLAGVPRIVGMLEGLIGFAFTPOPEGIPLKTKIITKIGILIALYRIALPMLGESLIVLNPDDKDELLHQYGIKINHTILGGIGLDLRQYPTSEADIPODEKEPVKFLFTGR  
FLKEKGIDDFIRAAEQVKGKIPDVTPTALGALDKSRGGGGDLERFLIARDIRFPGFVNVSEVIKAHHI FVLPSYREGVPRSTQEAMAVGRAVITTDVPGCRETVDKRVNGFLIEPWPFR  
ILAEKNYIYIENRAEVRIMANASAYIAKDKFDAEKVDLKFLDILKA

**SEQ ID 4221**

SEQ ID 4221

ATGCTCAACTATGCTCAACTATTCCGATATTACGACAATATTATCAACAAGCGGGCAAGTGCCTTTTGCTTACAATGCCAACTACGATAAACTGTGCGGCAATCATTTTGAAACTGCC  
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ACACGGCAACTACTGGAAGCGACAACAGCCCGTTCGATTGTGAACGGGACGCGGCTTCGGAGACAGCGCGTACCGTCCGCGCGGCAATCATCTGGCGCGCGGCCGATTCGGCG  
CTCTTGATGAACAGCTCCCGCAATCAGCATCTGCTCAAAATGGCGGCGAGCGGCGATTTCGCCGCTTCGCGCGCGCGGTGTGGAGCGCAACACCGCTGATGAAGCGTTATCGCCCCAAAATTC  
AAACCCGTTATCAGCGCGATGAGAAGCAGTTCGCTCAAGAAGCGGAAACGCGGCGAGTGGGAACGGGGCAGGGCGGAAAAACGGTCTTTTGAAC

**SEQ ID 4222**

SEQ ID 4222  
MLNYVNSDIHDNIINKAGKCVFAYNANYDKLSANHFENCQIGMHPAAIEGTSLEDNSFINNGSQVKYVSTRFLDWSEGGHGNYSNDSPPDLNGDGFDSAYRDPGLIDQIIWRAPVSR  
LWNSPAISIVKWAQAPPAVLPGGVVDSKPLMKPYAPKIQTTRYQAMKDELILKEATRQSERGRAENGSLN

SEQ ID 4223

SEQ ID 4223

ATGACCTGCCCCATCCCCAAACCCCGTGAAAAATCCCGTTGGTTCATCACTTTTCGCAAGCTCGCTGCCCTTGGCTTTTGGCGCGTATTATTGCCGCAACAAGCGGCTCAAAGCCGTGCTGACCC  
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CCAGCCTTTTCGCGTTTCAACAACAGCAAGGCCAAGGCCAGCTCGAAGGCATGCGCGAGCGGTACTGTGATATCGTTATCGGTACGCACAAATTTGTTGACGAGGACATAAAAATCAA  
AACTTAGGTTTATTGATTATCGATGAAGAACACCGCTTCGCGCTGCGCAGAAAGAGCAGCTCAACGCTTGCAGCCAAATGTCGATCTTAACTACGCGCGCGCGGATTTCCGCGT  
ACCTTCAGCATGGCGCTCGAAGGTCTGCGGACTTCTCGCTGATTACCACTGCACCGAGCGCGCGCTCGCGTGAACAACTTTGTTCAAACGCTTCAGCGAAGCGCGCGCGGACGCG  
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CGTTACTTTCGCGCAACCACTGATATCAGCCCGCAGGGGATTATCTGCTGATTACAGCGGATAAAAAATACCGGCTGGCAGGGCGCAGCAAAATTGAGTTTGCAGCGGAAATGGAAGAC  
ATCGAGGTACAGGATCAATACCGTCAAACCGTACTAAAAACCTGCAAGGCAACGCTTGCCTCAAGGAAT

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HTCPIPKPREKSRWFNLSSQSLPLALARYLPHKRLKAVLTQDAEQALRLQTAWRFFRPHDTAVFLPDWETLPHYERFSPHQDLVSRLSALWQIKSGAADVLFPVATAMQKLPVPVFLAGR  
TFWLKGTQGLDIGRLKTLDLVADAGYNHSHVVAAGEFAVRGGIVOLFPMGSEFPYRIDFLPDEIKTSIKTPTDTQRTISPVSEIRLLPAHEFTPTDSEAQIKFRSFRBEVDGNPNDAAVYKA  
VSNHGPGAGVEYLLPLFPFENELETFLFDYTGEDALFVSLGDVHABANRPNWVDKSRYAMAQGDETYPLLPQHLYLSADVFAGRLLKNYQGVLPVDSGKAHSLDLAVNRQSDPLQALKDFQ  
TAFDGRITLLCAESLGRRETFMLGFLQONGLKAKPVSDMQGFLSAHEPLMITVAFLAYGFKLGLGSSSQOQTVPASEGEGKAVTDQTFPSASATNPLPSPLPQERBQSAAAVSDGLKAAAVS  
TESSLYLVASDLHGQTRQQSAPSPVUGEWEKGAQVAAQSAIAVITESDLYQTVARSRVNRRKKRAAVSDGILLRDLAEIINIDPVVHEEHGIGRYTGLVTMDLGGETNEMMLLEYAGEAQL  
YVPVSQHLISRYSGQAHESVALHLKLGSAWNKAKRKAEEKARDTAAELINLYAQRAAQSGHKHFEINESDYQAFADGPGYEETEDQAAAIAAVIKDLQAKPMDRLVCGDVGFGKTEVALR  
AAFVAVHGGKQVAVLAPTTLVVEGHAQNFADRFADFPVKVASLSRPNNSKATKATLBMADGTVDIVGTHKLVDQDIKFNKLGILLIIDEHRHFGVRQKQERKLRANVDILMTATPIPR  
TLSHALEGLRDFSLLTTAPSRRLAVKTVFKPFSBGSVREAVLRKLRGQAVFLHNEVDITENMRKELETLPEARIQVAGHQJLERRELEQVMDPLPQRRFNVLICSTIIETGIDIPNANT  
IINRADKPGFLAQHLQLRGRVGRSHHQAYAYLLTPEYITDKAEKRLDAIAADELHAGDFTLMAQDLERTRGAGEILGEGQSGSEMQVGFTLYTEMLQAVRDLKKGROFDLAPLIGITTEIK  
LHSPALLPEDIYCPDIHERLVLYKLAETVCVQKINATHELVDRFGLTEQPVKTLIESHHLRLAAKBLGIDATDATSEAVTVTFGRKHCHIDPTGILLIQDKKYRLAGADKLRFAAKEN  
TEVRINTVKTVLKTHGKRLPKGN

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SEQ ID 4225  
ATGTGCTTTAAAAAGCAGCCGTGTCCATGGTTGACGGCTGCGCGCTCGGTTGCGTGTGTATCATCGGCTTCCCTGTGTCGGTTCCCATTAATCGGGCGGCGGTCAAACCGGCTGCCACAGT  
TTAGAGCTTAATTTTCTAAACTTTACCACAAGTGCACCGGGCAACAATCCCGCGGCTTTCAGACGGCATCGCGCACCCCTCAGTGTCTAAAA

## SEQ ID 4226

MCFKKAASVMDGCAIGSVCIIGFLCRFPLIGGRSNRLPQFRVNFNFPTTKCTGQGSAGLSGIAHPHVLK

## SEQ ID 4227

ATGGACACGGCTGCTTTTAAAGCACATCGAATCCGCAATCCGCGCATTTTTCAGACGGCATCGACCTGATGCGATACCTGCCGGAAGACAAATGGCTTGCCCTGAAGCAGCGGGT  
TGCTGTTCGCCCTTCTCGACAAAAACACGGCGGGCGCAAGGCGAGTCAGTTTGAATCCAAAGAGTCTTAAGGATTCGCGGGCATACCGCGTCCCGCTTACGCTGCGTACCGGCATCGA  
AGGCGCGCTGGTGTTCAGCCTCTGCAAGAGTTTCGGCGGCGAAGCGCAAGTCGCACAAGGTTTGGACATGATTTTCAAAGGCGAAGCGCGCGTTCGGCGTTACCGAACCCGAAACCTCC  
GGCGCGCGAATTCACCGCAATGCACTCTGCTACGAATATACCGACGACCAAAACCTTTACGTCAACGCGCGGAAATACCTGCGAGGCAATTCGCAAGCGACTTCTCTCGTTGCGG  
CCAAAGAGCGCAAAACCGGCAAACTCGCCAAAGTCATCGACCTGCTGCTGCTCCCAAAACATACATCCGCTGCGAAACCTTCGCATCCGAAGCGCTGCGCGCGCTCGGTACGCGCTCAA  
CCGCATCGATGCCGAATGCTTCGAACCGCGGTGATGAACCTCTCCCGGGCGCAGCTGCGCGTTCGCGCGCTTCCAAACATCTTTATCCGCGACCGCTGCAACTGATCGGCATGACG  
CACGGCATTTAGGAATACATCTTTCGAACCTGAACCGATATGTCGCAACGATATCAGATTGCTGATACGAAACCGCGGAAATCCAAACCGCGCATCAGGTTTCGGAATCTTTTACC  
GCTACGCTGCGCATTCGCTTCGCGCGCTGCGCGCGCTGCGCCATCAATTGATGGAGCGAATCGTCAAAACCTTCGCCACGGAATACACTTACCGCGCGCGCAATGTTGCAAAACCT  
CTTGGCGCGAAGGTTTGAAGCGCGACACCGCGGCAATATCGCATCGATATCGCGCTTCACGATTTTGAAGGCGGCAAGCATATGCTTTATGCGGAAATTTACGACCAAGTTC  
GTCCGCGCCACCGCGGAAGAAAAGAGCAGGCATTAAGTTGGACAAAACCAACCTGCTCGACCGCTGCAACCGCATGTCGCTTTGCGCGCTGCGCGGCTACGCTTTGCGCG  
AAGACATTCGCGCATCTCTGCGAGGAACACACCTGACCGCGCTGCGCGCTGCAAAAGATCTTCATCGGCAAAATCATCGCGCGACTTTTGTCTTCGTACAGGAGGAACAGAAACAC  
CACAGCTTCTGCTGAACGACATCCGCAAGATATATTGGACTCCGATATTGCGGA

## SEQ ID 4228

MDTAALFKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKHGGRKGSQFEIJEVLRIAGHYGVVFTLRTGIEGALVLPQLEFPGGEAQAAGLHMFKEGGGLGVTEPETS  
GAALAREMQSYETTEDQTYIVNAAKYQWNSQDFLIVAAKERKNGKLAKVIDLLVPKTYIRCTELASEGLRAVRYAVNRIDAEMPATAVMKLSRGDAAGLRAFPQNIPIRSRLQILGET  
HGIMEYILDLNRYVRNDIRFVDYERRRIQRHVSSEILYRYVCHSVFVAPVAHQLMANIVKTLATEYTYAAQMLQLKLGKGFERGHGPNGLAIDIRPFTIPEGNMLYAEIYDQF  
VRATAEKEKAGIKLKNQTLRLQTDVRFPAVARDYALPEDIRSFLEHTLADCAIQKVFYIKLILARLFVFPQBEHEDTAFILNDIRKDLDCRYCG

## SEQ ID 4229

TTGCGGATAGCGGCAAAATACGGCGCGAGGAGATTTCCGGCGCGCAAAAGGCAACCGCGCATTCCTGCAAAACCGCGGATTCGCGCGGATACCGCAATTCGCGCTCACCTCTGTGCC  
GCTTTCCTACTTACCTTATTTGTCGGAATGTGTTTATGAAAGAGAAAATATCTGCCGCTGCGCAATTTGTTTGGCGGCTTTGTCTGCTGTACGCGGATGGAGGCGCGCACACCGCGG  
CAAA

## SEQ ID 4230

LRIAGKYGRQISGGAGKNRHSAPPIAADTAFRASPLCRFPYPISECYVYKKEKNTAAGNLPGGFVCLYGDGPGHTPGK

## SEQ ID 4231

ATGGAGCGCGCACACCCCGGCAATGAAGCCCAAGCCCCCGCGCGATGAATGAAAAAGAAAGCGCGCGCTTTGACGCGGACCGGTACCGGTATCCGACAGCGGTTTGGCG  
CCATATCAATATGTCGCGCTTTTGTGGACGATGAAGTCGGGAAAGGGGATTTTCCAGGCGGAAATGGCAGGATTTTGTGACAAAGCGGTTCACAAAGCGGACATCGTCAAGATTATGCA  
CCGACCTCCACATCGCGCTCCGTGGTATGTTTCCGACCGGAAATTCGGCGAGGCGCAATTTACGCGCGCGCGAGGTTTATGCGGAAAACCGCGCGGTATCGATGATGTCGGCA  
AAATAAGCGGTGCTGCGGAGCTTATCGTGGCGATTATCGGATTTGAACCAATTCAGGCAAAATACGGGCGATTTCCGCTGTCGCGGACGCAATTCGCGCTTTAGGCTTTGATTTATCCCC  
GCCGCGCGGCTTTTCCAAAAAGAAATGCTGAGCTTTTAAAGCTGCGCAAAAGAAAGCGCGGTGATGTTTTCGCTTTAAGGGCAGCTATGCGGTGCAATGGGTATGCGCAATTTAT  
GCTTCGAGCTACCGGAAATGGCGGTGATTTATGACGGGACGACATCGGATATATGGGCAACGTCGCTGATGTCGCGCATCGGTTCGCAATTTATGAGCAGCAGCGTTGGCGC  
ACGGCGGTAATAATGTTGCTGTCGCGGAGTTGCGCGCGGTGCGGATGTTTCAGGCAATCTTTGGCGAAAAACCGCGCTGACCGGACGCGTGGCGGATTTGAAGCGGTACGCGCATCATCC  
CGCGGAAACGCTCGCAGATGATGAAAGCGGTTTGTTCAACTGGAACCGCACCGCGCGGTGTTGAATATTTATTTGGGCTTGAACATTTTATACGGGTATGCGAGTACAACACAG  
CCGGATGATGTAACGGCGGTACGGGACATTCGCAATTCGCTCGCGCGCGCGGATTTG

## SEQ ID 4232

MEARTFRANEAQAPRADEMKEKSRPADAAPVPSDSGAANANVRVVDDEVKGDVFSQAEWQDFDKAAAYKADIVKIMHRPSTSRPWYVFTGNSGRAKPHGARRFYAENRAVIDDVAQ  
KYGVPAELIVAIIGIETNYKNTGSFRVADALATLGFDPYPRRAGFPQKELVELLKLAKKEGGDVFAPKGSYAGAMGMPQFMPSSYKMAVDYDGDGHRDIWGNVGDVAASVANYMKQHGHR  
TGGKMLVSLATLAPGADVQAIIGKPTALTRTVADLKAYGIIPEGTLADDEKAVLFKLETPAGVPEYIYGLNPFYTVWQYVNHSMRYVFAVEDIANSLGGPL

## SEQ ID 4233

GTGGCGGAGAAATGCCGAGTTTGTATGAGTGCAGGATAAATGTGATTTGCGCGAGCCAGATGTAACCAACCGCGCTGAAGCGGGACAG

## SEQ ID 4234

VARENAEFDECRINVYLREPDVKTAEAGQ

## SEQ ID 4235

ATGATGCTTTATTTTTCGCGCATACCGAACCAAGAGGGACACTATGCACACATCCGCGCTCCGTATATGGCTGAAGCGCGTGTGATCTGCGCGCGGACATTTTTCAGACGG  
CATCGGCGCGCTGCTCCAGCTTTCCCGCAAGACAACCTTCCCGAAATTTTTCGCGCGCGCGCGGGCGGATACGATCAAACTGGCTCCCGCGTATATCAAAACCAACTTTATATCGA  
CAACCGGATTCAGATTGAAGGGCTCCGCGACCTTCCGCAACCATCGAAGGGGCAAGAGCGGGCGTACCATAGCCGTACACGCGCGGACGTAAGCTCCGCAACCTGACCGTTACCGGT  
TCCGCTATGAGCTGCCAGCAATGATGCGGTTATTTATCTCGAAAAAGCGCGCGCGCGCGCTGTTGAACACACAATAATTTTGATAATTCGTTCCGCGTATACCTTCATGCTTCG  
CGATGCGATGCTGCGCGGATGCGGACCTTTCGCGGTGATGAGCGCGGCAATGGCGCTTACCGTTTGAAGCAGCGCGCGCGCGGATGTTGAGCGGATTCGCGGCAACGACATTTTC  
CAAGGGCGGGACGCAATTTTTCGAATACGACGCGCACACACCTATAAAAAACCGCGCTTCAGCGACCTGCGTTTCGCGCTCCCATATATGACCAACGACGAGGTCAGCGG  
AATATTTCCGTGGGCAACAATATGGGTATGTCGTGATGTTTCCGAACCGCTCAAAGTGTTCGACAAATATCCGCTCGCGCGCGCGGAT

## SEQ ID 4236

MMLYFVRPYRTKQDTHMTSALRIWLKAVLILAAAGSIPTASAAVHVHSPQDNLAEIFARARAGDTIKLASGVYQTKLYIDKPITIEGPADRSATIEGDKSGRTIAVHAPDVTILRLNFVTR  
SGMSLPAMDAGIYLEKAAPRALVEHNIFDNSPGVYLHGSADAMVRENKIVGDATLVRNERNGVTVWNAAPGAQVVGNDISKGRDGIFSNSTHTNTYKNNRFSDLRFVHYMTNDSEVS  
NISVGNMGVYLMFSERLKVFNDIAVGSRD

## SEQ ID 4237

ATGGCAGATATGAAGAAAATACCCCTCAAAACCTGCGTCCCTGCTTTCCGAAAGCTTGGGACATACCGATTGTTGTCACAGCTCTCAACGCAATGATTAATTTTTCGCGCGTGGCGCA  
AAAAATGTCGGGGGAGCGTTTCGACCTGATTATCGACACATTCAAACAGACAGGGAATFACGTGTCGCGCTTCAGCGGCTGTTTTCATCTGCGCTCGCGCAATACACATTTATCGGC  
ACTCATCAAACTCGGCAATTTTTCGCGCGCACAGCTTTCCCGGGAATGGGCAATACGATATACGAACGCTTCAACCGCTCATATAAAGATTTTGCAACTTGGCGGAAGTCTCTCTTAT  
CTTTTCATTCGAAAACGACGACAAATGGCTGCAACGCTCAATATCCGCAATGGCTGGTTTATACGAACCTCATCCGTAGCCACGCGGAGCGCTCAAAATTCGAGACGCGGGGACATCG  
GCTTTCGCGATGCGCGTTTTCGCGCGCATCGAAATGCTGCTGCTGAGCGCATCGGAAGCATCGAACCGGATCTCATCCGTATGCGCGCGCGCTGCTGGAAGCGGATTCCTCTCTGCT  
CGCGCTCCAAACGCGAAACCGGCAAACTGCTGCAACACTGCGCAACCGGCAACCGGCTTACGACACCGCGGCAAGTATGTTTCGACCAATGTTTCAGCGGATTCGCTATTTGCGGT  
CGCAAGGGACGCGCGCGCTCGGTGCTGCGTCAAGTCGCGCACTGCTCGAAGCACTCGCGGACGCGTAGGCGCTGGAAGCTGCTACAGACATACAAACCGGTGCGCGCAACA  
GCAACCGGCTGACCATGCGCGTATGAACCTCTCATCTACGCGCGGTGCAACATACAGCACCGCGGCACTGCGCGCGGACGATCGGTATGCTGCGCGCGGATTCGCAAAACAA  
AAGCGCACGCGGCAACACTATACACCGCAACCGCAAGAAATTTTCAAAATGTTTACTTCGCGGACGAGGCGCGCGCGGATCATCGCGCTGATGGCGCTGCTCAAAATCCGCAATCGCG  
ACACTCGACCTCAGTCCCTTCTGCTCTCTTGTGCGGTGGGTTCACTACGCGCATCGGCTTTATGATCATCATATGCTGACTGCAACGCTGCGCAACGAGCGCGGATGACTGCGG  
CCAGCTTTGCGGAACAGGTGATCTCAACGAGGCGGCAAGCGGTGGAACAACACTTCCAAGCTCTCATCGACGATATGCGCTCCCAAGCGTGCCTGCTTCGCGCAAGCTTTCCAT



CGCCATCCCTTTTGGCGTGGCCATATCGTTGGCTATGCCATCTGTACCGGCTGCCATCTCGATGCCACACCGCCGCTACCAAGTTCAATCCATAGACATCATCAATCATCTTACC  
CTATGGTATGCCGCTATTCAGAGCTTGTGGCTGTCTGCTCCGCGATCATCGAGGTTTTTTCGACACCGCGCCGACTACCTCAACCTGCCCAACGCTTCAATCCCTTGTCTGC  
GTAAATCATGCGCCCGGCGCCGCGCTCCGCGCTTACATCCACAAACACACGCTCGCTGGTGGCACTTCATCTTCGGAATGCTCTTGGGTATGACCGGCTATTTCCGACA  
CTCTCTCGGGCTGGCGTGGACATCCGCCACGTCGCTTTCTCCGCCAACCTCGGCTATGCGCGCTCAGCGGCAACGTCGCTTGGTACATTCGTACTCGGCTTTTTCAGCGTCTC  
GCCATCGGCTTGGTCAACCTCTGCTCAGCTTCAGCTCGCTCTGCTGCGCTCGCTCGCGGCAAAAATCGGAGCATCCGCAACCTGATCAAAAGTTTTTGGAAATCAGATTA  
AAAGCAATCCCTTGCATCTTTTCTCCCGCGCAAGGACAGGACATCTCTCTCGGACAAGCT

## SEQ ID 4238

NADMKKITPQNLRLSLSLGHDTDFVNLNALIKFLRRGGKKCAGERFDLIIDTFKQDRELLSRFSRCFYTLAQIHTYPAIKLIGIFSRHSFAREMGIRIYERFNPYSYKDFANLGEVFLY  
LFHSENDKWLQTLNIRQLVLYELIRSHAEPKLTAGIRLADARLRAEMLSVWTASEAIEFDLIRIAPRLLEADSSVALQRETAFLVEHYRNGTAPYDFAHLEVMFDCQFSQIDYLR  
RKGTAGSGSSSVKVAHLERLRQTVGRLLKLLTDIQTGAGNSRLTIALMNSLIYADEVQYSTRHLRRSSIRMLARSITENKSHGHEHYITRNKKEYFKMPSAAGGGGIALMALLKIRIG  
TLDLSPFLASLSAGFYIGFMIHMLHCTVATKQPMATAASFABQVDLNEGGKADNLSKLLIDVCRSQSVAVFNVSIALLACASIFGYAHLRYLPILDHAATAAYQFKSIDLINHPT  
LWYAAIAGLWLPSCGIIAGFPDNRADYINLRQLRFPNPLRLKIRMPRRVLAAYTHKHGYSLVGNFIPGMILLGHTGYPHLLGLPLDIRHVFSSANLGYAAVSGNVGFTFVLGIFSVL  
AIGLVNLVCSFSLALFVALRSRGTKIGSIRNLKISFPMQIKSNPCILFLPPAKGQHPSPDK

## SEQ ID 4239

ATGAAGATAACACTCGAAATTAAGAAAGAGTACAGAAAGAACCGCTCCGTTCTTTTGTACCGGAAGTTACCGCCGTTCTGCGCGCATATTTTGGGTATCCATCCCGATTCCGCGG  
CACTGTTTTACCGTAAATCCGACCGTTGCCAACCTCGTTTGGCTTGGCTGCGCATGGGCTTTTCGAGGCGCCCGCGCGCGGGTGGAGCTATTTTCGCGGACGCGGTAAGGCG  
ACGCGTTCGCGCGCGGACGAGAAAGCGTTGTCTTCGCGCATTCGGAACGCAACGCGCGGCTTATCCGTTGCGCGGCAATGCCGAGCTGAACGTTGCCCGCTCGCGTCAAAAG  
AAATCATGCGCGGACGCTATTTGTTATCGCGATAGCCCGGCGGCGCGCAAGTTGGACGCGCGGCTTTTACCGTTGCGCGCATCAACGTTCCAGGAATTTTCAGACCGCTCGGAAC  
ACATTAACGCGATTGGGATTTTGAATCAGCAAAACGCGCTTCGGAATAACAGGAAATCGATCGTAAACCTTTTCGCGCTCTTGAGGGAATCGAATTCGACTTAACCTCGG  
CACACCGTCCCGGACGCTAAATCTCGCGGATCGGTGGAAT

## SEQ ID 4240

MKITHCKLKKEVQKEPLRSFVPEVTARSAADIIGIHPDSALFYRKIRTVANHRLALADGVFEPGAGPGSGYFPGRRKRRGRGAAGKAVVPGIPIKRWGRATVVAADNAEPETLPPAVK  
KIMPDGIVYADSPGSRGLDAGGFTCRINRSKEFADRRNHINGIDGFWNQAKRALRKYNGIDRKPFPFLRECFRLNFGTSPRQLKILDRDGI

## SEQ ID 4241

ATGACCGACGCAACCATCCGCCACGACCAAAATTCGCCCTCGAAACCTTCCCGCTCAGCCTTGAAGACGAAATGCGCAAAAGCTATCTCGACTACGCCATGAGCGTCATTGTGCGGCGG  
CGTTCGCCGACGTTTCGCGACGCGCTAAAGCGGTGACCGCGCGCTACTGTACGCGATGACGAGCTGAAAAATACTGGAATGCCGCTACAAAAAATCGCGCGCATCTCGCGGACG  
CATCGGTAAATACACCCCAACGCGGATTCGCGAGTTTACGACACCATCGCTCCGATATGGCGCAAAATTCGCTATGCGTTATGCTGATAGACGCGACGCGCACTTCGGATCGGTGAC  
GGGCTTCCGCGCGGACCATGCGCTATACCGAAATCCGATGCGGCAAAATCTCACATGAAATGCTGCGAGACATTGAGGAAGAAACCGTTAATTTTCGCGCGCACTACGACGCTAGCGAC  
ACGAGCGCTTGTACTGCGGACCGCTTCCCCACACATGCTCGTCAACGCGCTCGCGGTATCGCGTTCGCTATGCGGACCAACATCCCGCGGACAACTTCACCGACACCATCAACGCGT  
TCTGCGCTCTTTGGAGCAACCCAAACCGAAATCGACGAATGATCGACATTAATCAAGCCCCGACTTCCCGACCGGGGCAACCATCTACGCGCTTGGGCGCGCTGCGCGAAGCTATAAA  
ACAGGCGCGCGCGCTGCTATACGCGTAAAGCCATATCGAACCCATAGGCAAAACGCGGACGCGGAAGCCATCGTTATCGACGAAATCCCTTACAGTCAACAAAGCCAAGTTGG  
TTCGAGAAATCGCGGATTTGGTTTCGCGAAACCGTGAAGGCAATTCGAGCTCCGCGACGAATCCGACAAATCCGGGATCGCGCTGTTATCGAGCTGAACGCAAGCAAAATGCGGA  
AGTCTCTTAAACCACTCTACAACTGACTCCGCTGCAAGACAGTTTCGCGCAATATATGTTGTTTTCGTCGAGCAACCGCGCTGTAAACCTGAAACAGATTCTCTCCGAATTC  
CTGCGCACCGCGCGGAGGTGTTACCGGACGTACGCTTTCCGCTGAAGAGGCAAGCCATGAAGGCAATATCGCGAAGGCAAGCGCTCGCACTGTCCAATATCGATGAATATCATCA  
AGCTCATCAAGANTCGCCCAACGCGCGGAGGCAAGAAAGAACTGCTTCCGCGCTTTCGCGCAGCAGCCTCGTTGAAGAAATGCTGAGCGCTTCCGCTGCGATTGGAATGATGCG  
TCCGGAAGGATTGCTGCAACATTTGTTCTGAAAGAAAGGTTATTAACCTGAGCGAGATTGAGGAGATGCTATTTACGATGAGCTCGCAACCTGACCGGCTCGATCAGAAAGAA  
ATTATCGAAAGCTACAAACCTGATGGGTAAATATCGACTTTCGATATCTCTCAACCCGAAACGCTTACCCAAATCATCTCGTACGAACTGGAAGAAATCAAAACCACTATG  
GCGAGCAACGCGCGAGCAATCAACCGCTTCGCGCGGACATTCGCGATGAAGACTTATTCGAAACCTGTTTGTGTCACACGCGATGACTATTTGATGCTTTTACC  
CACGACTATCAGCTCAGCTCGCGTCCGCGCGCGCGGCAACAGCGCGCTCCGATTAACAACGCTATCCAGCTGGAAGAGGCGAAAGTTCAGCGGATTC  
AACCTCGGCAAGTGCCTACGATTAAGGTTTACAACTGCCGAAGGCGGACGCAACAGCGCGCGCTCCGATTAACAACGCTATCCAGCTGGAAGAGGCGAAAGTTCAGCGGATTC  
TGGCAGTACCGAGTTTCCGGAAGCAATACGCTCTTTCGCCACCGCGGAGGATGTTGAAAAAGTCCAATTTCCGCTTTAAAAACGTCGCGCGCAAGGCAATTAAGCCATCGC  
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GACGAAGCGGAAGATGCCGACATCGAAACGAGATTTCAGACGACCTCGAAGACGAAACGCGGCAACGCGGCAACACCTCGCAAGCGGCAAAACGCGCTGCGCTCGCGTCCGCGCA  
GCGCGGTTTCGCGGCTATGCGCTGCTGCGGCAAAATCGTCAAGCTGATTAACCTTCGCGCTGAAACGGAAGAGCGGTTTGAAGTTTAAACGCCACCGCAACGAGATACG  
AAAACGCAACCGGATTCGCGGATTCAGCGGCAAAACGCGGCAAGGCGGCAAGGAGTATGCAATTAACCGCGGAGCGCAACGCGGATTTGTTGCGGCAACCTTGTGCGGCAACCGGAC  
GATTGATGCTGATTACAGCGCGCGCTGCTTATCGTACCAAGTGAACAAATTCGCGGAAACGCGCGCGGCGGAGCGGTAAGCTGATTAACCTGAGCAAGCGGAAACCTTGG  
TATCGCTGGAACGCTGTCGGAAGACGAATCCGAACCTTCCGCGCTTCTGTAATTTCAATGTAACCGAAGCGGAGCGGAG

## SEQ ID 4242

MTDATIRHDKFALETLPVSLDEMRKSYLDYAMSVTVGRALPDVRDLKPVHRRVLYAMHELKNNWNAAYKKSARIVGDWIGKYHPHGDASVYDITVRMAQNFAMRYVLIDGQGNFGSD  
GLAAAMRYTEIRMAKISHEMLADIEETVNFPGNYDGEHEPLVLPTRFPTLLVINGSSGIAVGMATNIPPNLTDITINACIRLLDEPKTEIDELIDITQAPDPTGATTYGLGGVREGYK  
TGRGRVVRIGKTHIEPIKNGEREIVIDEIPYQVNKALVEKIGDLVREKTLEGISELRDESDKSGMRVVIKLRNENAEVVLNQLYKLTPLQDSFGINNVVLVDGQPLNLKQLSEF  
LRHREVRVTRTLFRLKARHEGHIAEGKAVALSNIDEIKLIKESPNAAEAKELARPWRSSLVREMLTRSGLDLEMRPEGLAANI GLKKQGYLSETOADAILRMSLRNITGLDQKE  
ITIESYKNLKGKIIDFVLDLSKPERITQIIRDELEIKTNYGDERSEINPFGGDIADIEDLIPOREMVVTLTHGGYIKTQPTDYQQRGRGKQAAATKDEDFIETFLVANTHYDLMCT  
NLGKCHWIKVYKLPPEGGRNSRGRPINNVQLEBGEKVSAILAVREPPEQYVVFATQGMVKVQLSAFKNVRAQGIKAIKLEBDYLVGAAQTGGADDIMLFNLSGKAIKIRFNEYWEKSGN  
DEADADIEPIESDLEDEADNENWLPSPKNGVRPSGRGSGGLRGMRLPADGKIIVSLITFAPIETESGLQVLTATANGYKRTPIADYSRKNKGQGSIAINTGERNGDLVAATLVGETD  
DLMLITSGGVLIRTKVEQIRETGRAAGVKILINLDEGETLVSLERVAEDESLSGASVISNVTEPRAEN

## SEQ ID 4243

GTGGCGGATGGTTGCGTGGCTCATGTTTCAATGTTTCGTATGCGCAAAAATTTGTTGCTTATTTTAGCATATTTTCGACATGAAACGGTGGCGGTTATGCGGCT

## SEQ ID 4244

VADGCVGHGFNVSYGKLLLLILAYFDMKRCGGYAV

## SEQ ID 4245

TTCGCTCGGTCATGTTTCAATGTTTCGTATGCGCAAAAATTTGTTGCTTATTTTAGCATATTTTCGACATGAAACGGTGGCGGTTATGCGCTTGAACACGCTCGGATTAATAATGCGG  
AGGAATTTTCGTGGCGGAGTTTTCGAGAAACCTGCTTGGCGGACTTGTGTGCGCGGCTGTCGAGCTTTCGCGCGGAAATGACTGTTTCAGACCGGAGAACGATTTTCTTGTTCGCG  
GCGGATTTCGTATCAGATTTTCAAGGATCAAGTTGTTGCTGCGCGTCCATCAGCGTTTCGCGGCAATTCATTTGCTGATGAGGAATCGGGGCGCAAGAGGATGATGTTCC  
GCGCATCGCATCGATACCGGATGTTTTCAGCAGGTACCGCGCGGCTGATGGGATTTTTCAGGTTGCGG

## SEQ ID 4246

LRRSNFQCFVWQKIVAYFSIFRHETVRLCRLKHGADYNABEKISWRSLSRNLPMWTCAAVSVSWRANDCFRPNQSFCSARISLSRPFKDSRLLPARASISVSRHSICMRKSGAKEVCS  
GASASIPDVFSRYAARSMGFFKVR



## SEQ ID 4247

ATGATGTCCTCCACCATCAACGATGCTTACCGCACCTTGAAAAATCCCATCGACCGCGCGCGTACCTGCTGAAACATCGGGTATCGATGCGGATGCGCGGAAACATACCTCTTCGCCC  
CCGACTTCCTCATGCGAGCAATGGAATGGCGGAAACGCTGATGGAGGCAAGGCAACACCTTGAAATCTCGATAACGAAATCCGCGCGGCAACAGAAAACTGTT  
CTGCGGTCTGAAACAGTCACTCGCGCGCAAGACTCGACACCGCGCACAAAGTCCGCCAAGGAGGTTCTCGACAACTCCGCCACGAAATTTCTCCGCATTA

## SEQ ID 4248

MMSSTINDAYRTLNKPIIDRAAYLLKTSIDADAPHTSFAPDFLMQMEWRETLMPEARAGNLESKNLNEIRAEQKLPGLKQSFARQDCDTAAQVVRQGRFLDKRHEISSAL

## SEQ ID 4249

ATGGAACCGGCGGCAAGGCGCGTAGGTTTGTTCAGTTTTCGGTGCCGATATCGAAAGCGGTTCAATCCGGAAGAGGTTGAAATATTGGGACATAGTAGGATGATAAATGTAAGAT  
TTTGGCAGAAACTGTTTTCCTTA

## SEQ ID 4250

MTGGGAGVGLPVVFADIESGFNPREBEILGHSRMINVRPQKTFVAL

## SEQ ID 4251

TTGATCTGTCGCGCGCTTTTATGCTTAAACGTGGAAGCTCTCGCCGAGCGCAGGAGTCTTTGACATGGGGTTTCAAATTTGAAACCTTCTCGCAATCTTCTTTGGTGTAAATCG  
ACTTGTGTGCGTCCAGATAAACAAGCTTTTCGGTTCGATATAATGCGCGCGCGTGTCTTCGAAAATCAGGTCGTGCGCGTGGCTTCATCGACAAATCAAGGTTGACGCCATCC  
CCGAGCAGCGCTGCTTTTACACCAACGCTAGCCCAAGCTTTGCCGCGTTTGGCGAGATAGTCATGTATGTTTTCGCGCATCTCGGTAAGGTAATCATATTTCTTCTTGTG  
TACCGCCCGGACGATCCGAAGCGCGCGCGTTCGACGCGCATTTGGGACGATCGCTCTGAAGGGCTTTATCTGTTTCC

## SEQ ID 4252

LILSRFYALNVEALAAAAGVFDIGVFKFETFLQIFGVGIDCAVQINQAPRVDIRAVSFENQVAVGFIDKFVVRHPRAAAGFTQAYAQAFAPGEIVIDVFCGLKGNHISLL  
YRPGIRSGRFRHCGTTPSEGLYLF

## SEQ ID 4253

ATGACGGGATCGAGTTTCCGCGCGGACGATTCGGCATTCCCGCTTTCGAGAAATGTCGGCTTTTGGTTTGTCTTTATAAGATTATTCGGTAATTTATTCGCGTTTTCGGTTTGT  
GTGTCGCGGAATCTCAAGGATTTCTGTATTTCGCAACGCTGCGCGGGAACCTCTATACCGCGGAAGCCAGCAGGTTGGCGAGTGCTCTGTCAGAA

## SEQ ID 4254

MTGCRFPGRIRHRSRFRNVGFVVFIRLFGNYSALRLCAAGISRDSLYLATVRETSIPKASRLASASSE

## SEQ ID 4255

GTGAATATCGGAATAGTTGACATAGTTGAGCATGATGCCCTAATCGCGGCTGCCGACGGCGATATTGCGAACACTTTGAGCCGTTCCGGAACATCAGCACATAGCCCATATTTGTTGCC  
ACGGAATATTTCCCGCTGACTTCGCTGCTGTTGGTGTACATATAGTGGACGGCGAAACCGCAGGTCGCTGAAGCGGTGTTTATAGGTGTTGTCGCTGCTGTTGGAATAAATGCGGT  
CCGCGCTTTGGAATATGCTGTCGCGACGACCTGCGCGCGCGCGCTTCCAAACGGTAACGCCATTGCCCGCTCAATTCACGCGCAAGGTCGATCGCGACGATTATTTCTCGCGCAC  
CATCGCATCGCGCAGAACCATGAAGGTATACGCCGAACGAATATCAAAATATTTGTTGTTCACCAAGGCGCGCGCGCGGCTTTTCGAGATAAATACCGGCATCCATTTGCTGGCAGG  
CTCATACCGGAACGGGTAACGCTCAGGTTGCGGAGCGTTACGTCGCGCGCTGTACGCGTATGGTACGCCGCTCTTGTCCCTTCGATGTTGCGGAACGCTCGGACGGCTTCAATCG  
TAATCGGTTTTCGATATAAAGTTTGGTTTGTATATACGCCGAAGCCAGTTTGTATCGTATCGCCGCGCGCGCGCGGCAAAATTTCCGCAAGGTTGCTTTCGCGGGAACCGTGACGAC  
GGCTGCCGATGCCGTCTGAAAAATGCTGCGCGCGCGCAAGTATCAGCACGCCCTTCAGCCATATACGAGCGCGGATGTGTGCATAGTGTCCCTCTGTTTCTGTTTCGGTATGGCCGAACAAA  
TAAAGCATCATTAATGTCCTGTTTATAGCGAAACGCCGTGAACGGTACCGCAAGCGTTTGCTTA

## SEQ ID 4256

VNIIGVIVDVEHDLIAAADGIVERFEPFGKHQIHIAHIVAHGNIAADFVAVGVHIVDGTQVAEAVVFIGVVRAGIKNAVPPFNVVADDLRAGRVFNGNIAALIIHAQRIADDFILAH  
HRIGRTMKVYERILKNIIVFNQARGGFPEINTGICWQAHGTGNGQVAERYVRVYGTGTPALVPPFDGCTVGRPFNRNRFVDIKFGLIYAGSQFDRIARPGAGNFKGVVLGRNVDD  
GCRCLKNAAGKYQHGLQPYTERGCVHSVPLFRSVWPNKIKHNSNVFVFIAPKETVRQAVHL

## SEQ ID 4257

ATGAGCGTAGGTTGCTGAGGATTTGTTTCAAACAGGTGCTTACTGTTGAGCGGGCGGAGCTACTACAAATGAGTTCGACGCGGGTAAGGAAGTGTTCGCGATGCTGTTTTCAGAG  
GTGTCATTTCCGCCAAGTCGCTTCGCGCATGATTGCGAGGGTGTTGATTTTCGATTTTCGCTCATATCCCGCCCAAGGTTGCTGATGGGGGTGTGACGGAGGAGCAGAT  
GGTGGAGTTCACCTGTGTGCGCGTTTCCGTGCGGGCGCAAAAGTATTTTTCGCGTTTCCGATCCGACCCAGATGCCGCAAAATCAGAAAACCGTTTCTCGCCGAGGATTCGGTTGAG  
TTGGTCAATGTCGAGGATGACCACTTGGCGGTTTTCGCTGATTGGTGGGTTCGCGTTTCGACATCGCTGCTTCAGGAGCTTGGGAGGGGCAAGAGGAAGAGGAAGCCACACCTGTATA  
TCGACAAACGAGGAGGAGAGAGCGCCCTGTTCGAGGTTTATCCATAAAATCTTGTGCGATGCTTTCGATAGCGGGGATCCGACATCCATTTTCAGTTTACGAACACAATGCGGTAT  
CCGTTTCCGTGTTGAGCGGCGAGTCCGCGAGGTGTTTCAGCGGCCCATTCGCGTAAGGGGGCAGCTTCCTTCCCGGATTAAGGTATGTCGCTTTCGACATTTCCGAAAAACGGATACCG  
CAGGACGGTAGGATGACGCTGACCTTTCAAAGCGCGGCAAGCTGTCGATTTCCGTGTCAGCACATTCGCCGACCTGTTTGGCGAAAAGGTGCTGATGCGGATTTTGAATTTTCGATGCGG  
CGCTTTTGAACATCGACCGCTCGGTTTTCGAGCGCTTCAGAAAAATTTGTTTGGAAAGCGATTACCGCTCTTACGGGATGTTGCTGTTAAACCGTCCGAGGGTTTCGGTTAAGCGGT  
GTGCTCTATACCTGTTTGAATATTTGAATACGAGTCCGTAATAATTCGAACCGCGGAAGACCTTCGCGAGATTAACTGCCGGCATCAATCAGGTTAAGCTCAATGATAAGCAGGTT  
CTGACTTTTCCCGCTGCTTTGAAGTCTTCTTCGCTCAGGACCGGACATCATTTATGTTGCTGAGATTCGCTGATTGGAAGTCCCGATATTTCGAGTTAAGGCGGCAACACAGGCGATA  
TGGTGTTCACACTGCACAGAAATATGCGCGCGGACGTTGTCGCGTATGCTGAATATGGTGTGCGCGCTTTAATATTCGAGTTTCGCTCAGCTGATTATGGCGCAGCGTCTTT  
ACGCGAGGCTGTGTTGAGCTGCAACAGGAAGTGAACCGCGCTGCTCTGCTTTGAAGGAAGTCCGTTTACCGATGAGGATCTTCCAAAGATTGGAAGCTTTACCGCGCGCTCGGT  
TGCAGCGTTTCCCGGGGCGAGGTTATAAGGGCGGTGATGAGGTTATGCCATCAGCGGAAGAAATGACCGGTGATTTATGAACAACGATCAGGAAGTGGGTATTTTGGAGG  
TTGCCATTAAGGAGGATGTTGTTGATTTGCGCGCGCGGTATTTTGAATAATTCAGGGGCTTACTTTCATGGAAGAGGTAACGGCAATACCAAGAT

## SEQ ID 4258

MSVGLLRILVQNVVTVERAHYINESQAGKEVLPPLFSDGVISPKSLAALIARVFSYSLDLRHYPRHRLMGVLTPEEQVVEFHCVPVFRRGDKVFFAVSDPTQMPQIQKTVSANGIAVE  
LVIVEDDLQAGLLDWGSRSTSLQLGEGQEEESHLYIDNEEAEDGPVFRPIHRTLSDALRSGASDIHFEPYEHNARIREFRVDGQLREVVPPIAVRGQLASRIKVMRLDISEKRIP  
QDGRMQLTFQKGKQVPDFRSTLPTLFGEKVMRIILNSDAASLNDQLGPEFFQKLLLEAHRPYGMVLVGTPTGSGKTVSLYTLNLTATESVNIAETAPAEINLPGINQVNVNDKQ  
LTPAALKSLFRQDDPIINVGEIRDLETADIAIKAAQTGHNVSTLHTNNPATLSRLMAMGVAFPNNIASSVSLIMAQRLRLRLSSCKQEVERPSASALKEVGFTEDELDKWLRYAVG  
CDRCRGGQYKGRAGVYVEMPISEEMQVLMNNGTEVGLDWAYKEGVLDLRAGILKIMQGTTSLEEVTANTMD

## SEQ ID 4259

ATCGCGTCCGAACCGCGCGCTTCGGATCCGTCGCGGGCGGTACAACAGGAAGAAATATGATTACCCCTTACCGAGAAATGCGCAAAACACATCAATGACTATCTCGCCAAACGCGGCA  
AAGCTTGGCGGTACGCTTGGGTGTAACCAACGCGCGCTTCGCGGATGCGGTACAACTTGAATTTGTCGATGAAGCAACCGCGACGACCTGATTTTTCGAAGGACACGCGCGCGCAT  
TTATATGACCCGAAAGCTTGTGTTATCTGGACGCGACACAAGTCGATTACCAACAGGAAGATTTCAGGAAGGTTTCAAATTTGAAACCCCAATGTCAAGACTCTCTCGCGCTCGCGC  
GAGAGCTTCCACGTT

## SEQ ID 4260

MPSEPPAASDPGAVQGRNMITLTENAARKHINDYLAKRGKGLGVRLGVKTSGCSGMAYNLEFVDRANGDDLIIFBHGARYIDPKSLVLYLDGTQVDYTKEDLQEGFKFENPNVKDCGCG  
ESFHV

## SEQ ID 4261

ATGGCATACAGCGATAAAGTAATCGACCACTACGAAAAATCCCGCAACGTCGGCACTTTCGACAAAAACGAGAGTCGTCGGCACCGGCATGGTCGGCGCGCCGCCCTGCGGCGACGCTGA  
TGCCTCTGCAATCAAGTGAACGATGAAGGCATCATCGAAGATGCGAAATTCAAAACCTACGGCTCGCGTTCGCCATCGCTTCGTCAGCCCTGATTACCGAGTGGGTCAAAGCGAAAG  
TCTGGATGACGCGCTGGCAATCAAAAACAGCGAAATCGCGAAGAACTGGAATTCGCCCGGTAAAAATCCACTGCTCCATCTTGGCTGAAGATGCGGTAAAGCGCGCGTTCGCCACTAC  
CGCAACGTCAGGAAACAGA

## SEQ ID 4262

MAYSDKVIDHYENPRNVGTFDKNDSVGTGMVAPACGDVRLQLKVNDEGIIEDAKFKTYGCGSAIASSSLITEWVKGSLD DALAIKNS EIAERLELPVKIHCSTILAEDAVKAAVADY  
RKRQENR

## SEQ ID 4263

GTGGATTTTACCGCGCGCAATTCCAGTCTTCGGCGATTTCGCTGTTTTGATTGCCAGCGCGTCATCCAGACTTTTGCTTTGACCCACTCGGTAATCAGGCTGGACGAAGCGATGGCG  
GAACCGCAGCGTAAGTTTGAATTCGCATCTTCGATGATGCCTTCATCGTTCACTTTGATTTCGAGCGCATCACGTGCGCGCAGGCGCGCGCCGACCATGCGGTGCGGACGGACT  
CGTGGTTTTTTCGAAAGTCCGACGTTTCGGGGATTTCGTAGTGGTCGATTACTTTTATCGCTGTATGCCATGATGTTGTTTCTTAAAAATATCGTGGTTTGTGATTGTTT

## SEQ ID 4264

VDFYRRQFQFFGDFAVFDCQRVITQFAFDPLGNQAGRSDDGTAAVSFEPRIFDAFTVHFDLQAHVVAAGGRADHAGDGLVVFVESADVAGIFVVDVTFIACHDVVSLKYRGLIMP

## SEQ ID 4265

TTGGAGAAGCTGAAAAACGAAAACTATTTCGGGTGTTGGATAAAGATAAAATTCGCCGAGCGTGCAGCCTATTATTGAGCAGGTTGAACGCTCTACATCTTTTCGTGAAGAAACGGCA  
GAACATTCGCCCTGTTTATGACACAATTCGCAATAAAAAACGGTTTTTCAGATACATTGGCAAAATATCTCTGCCGAACAAATGATTCAAGCCTGTATTCAGGCATACCATGCGGATAGCAG  
CTTATTGGCAGCCTAATATTAGACAATTAGACAATTCGTCTTTTCAGAGCAGCTAAAACATCAACAAACACGATATTT

## SEQ ID 4266

LEKLNENYLRVLDDKDKFAERAAYYLDELNVLPFFREGNGRTLRLFMTQLAKNGPQIHWQNI SAEQMIQACIQAYHADSSLLARLIIRQFRTIVFPRILKHQQTTF

## SEQ ID 4267

ATGAGTAAATACGGTGGTGAAGACGTAATCTATATGAATGATGGTGTATTTAGAAATAAATTAGCCATTCAAGATCCACTTAAATTTAAAAAAGGTGSAAGAGACATTTCTGCTATTTC  
GCCAAAATCTGCTTTTGCAACCCATTACAGGCAATTCGATTTCGCGCAATTTACAGACCATTTCATCGCAACTGTTTGGCAATGTTTA

## SEQ ID 4268

MSKYGGEDVIYMN DGVFRNKLAIQDPLKFKKGRKRFHYRQFSAFATHYRQFRFGAFTDHSRTVWQCL

## SEQ ID 4269

ATGGAGAATTTAGAAATTAGCCGACAACTCAATATGCAATGCAACTTCTAAAGATTGGTAAAAACAAATATTGAGAAGAATAAGAAAAATTAAACAAGGTTT

## SEQ ID 4270

MENLEISRQTYAMQLLKIGKTNIEKEIRKIKQRF

## SEQ ID 4271

ATGGCGCGCGCATTAAAGATTGATGTCAAACAAAGGCTGCTGAGAAAGAATACCATGAAAGTTAAATTTAATTTGCCAAATGGTTATAAACGTATTATTTATGAAAAATTTTGAAC  
AATTTGACTTAGATTATGAACAAGATTAGACGTATTAAAAAAGATATTGAATTTGCTTTATCTGTTATTGAATACAAATCGATCTATATTCAAAAAATCTCTTCTTATTGAGAATAA  
AATCATTTTGTATTATCAAGGAGGACATCATCTGATATTATTGATCGTGATAAAGGAAGTTTGAAA

## SEQ ID 4272

MGGALRLMSNKGRLRNKTKVKIINLPNGYKRIIYGYFEQFDLDYEQDLVDLKKDIEFALSVEYNRSIFKKFSSLFENKIIFVYQGGHLDIIDRDKGSLX

## SEQ ID 4273

ATGACCGTCAAAACCCCGCTTACCTCGACTACGCCGCCACCAACCCGTTGACAAAACCGGTTGCCGAAAAATGATCCCTATCTGACTGAAACCTTCGGCAACCCCGCTCCAACAGCC  
ACGCATTCGGCTGGACGGCAGAAGAAGCGCTCGAAAAGCCCGCGCGACATCGCCGCCCTGATTAAACCGCGACCCCAAGAAATCGTCTTCAACAGCGCGCGGACCGAGTCCGACAACCT  
CGCCATCAAAAGGTGCGGCAAACTTCTACAAAACCAAGGCAACACCTCATACCGTCAAAACCGAACACAAAGCCGTGCTGACACGATGCGCGAATCGAACGCCAAGGCTTTGAAGTT  
ACCTACCTCGCGCTGCAGGAAACGGTTTGATTGATTGGAAGAATCAAAAGCCGCCATCCGCGACGACACCATCTGATTCCATAATGTGGGTGAACACGAAATCGGCGTGGTGCAAA  
ACATTCGCCCATCGCGCAAAATCTGCGCGAAGCGCAAAATCGCTTCCACGTCGATGCCGCCCAAGCCTGCGGCAAAAGTGCTGCGATGTCGAAGCCGCAAAATCGACTTGCTCTGAT  
GTCCGCGCACAAAGTGTACGGCCCCAAAGGCATCGCGCGCTGTACGTCGCGCAACCCGCGCTCGCTCGAAGCCCAAATGCACGTTGGCGGTACGAGCGCGTTTCCGTTCCGCG  
ACATTCGCCGACCATCAAAATCGTGGCATGGGCGAGGCTTCCGCATCGCCAAAGAAGAAATGGCACAAAGACACAGCGCACTACCTGAAACTGCGCGACATCTTCTCAAAGGCATCGAAG  
GCATCGAAGAAGTCTATATCAACGGCGACCTCGAACCCGCGCCCGAACCACTGAACGTCAGCTTCAACTTCGTCGAAGGCGAAAGCGCTGATTGCGGTGAAAGAACTCCCGGTATC  
CAGCGGATCCGCTGCACTCTCGCTCGCTCGAACCAGCTACGCTCGCGCGCTTGGCGCGCAACGACGAACTGGCGCACTACCTTCGCGCATCACTTCGCGCGCATGACACCGAA  
GAAGAAGTGCAATTCGCGCGCAGAACTGATCAAAATCGCAAACTGCGCGAATGTCGCGCTGTGGGAAATGTTCAAAGACGGTATTGATCTGAATCGATTGAATGGCGCGCGC  
AT

## SEQ ID 4274

MTVKTPVYLDYAATTPVDKRVAKMIPYLFEFPGNPASN SHAFGWTAEAEVEKARADIAALINADPKIIVTSGATESDNLAIKGAANFYKTKGKHLITVKTEHKAVLDTMRELERQGFV  
TYLGVEQNLIDLEELKAIRDFTILISIMVWNIEIGVQNI PAIGEICRERKILAFHVDAAQACGKVPVDVEAAKIDLLSMSAHKVGPKGIGALYVRRKPRVRL EAGMHGGGHERGFRSG  
TLPTHQIVGMGEAFRIAKEELAQDTAHLKLRDIFLKGIGIEEVIYINGDLEHRAPNLNVSFNPVEGESLIMAVKELAVSSGSACTSASLEPSVLRALGRNDELHSLRLITPRMTTE  
EEVQFAELIKSKIGKLELSPLWEMFDGIDLNSIEWAAH

## SEQ ID 4275

ATGCAAAACCGTCAAAACCTCGCCAACAGGAATCGAACCTGTATTTACGCTTAGGAGGCATACGTTCTATCCGTTGAACTATGGCGAGCCGAAA

## SEQ ID 4276

MTVKPRQQESNLPTLRRHTFYPLNYGEPK

## SEQ ID 4277

ATGGCGTCTGAAGGCAACAGGCTCTCAGACGGCATTTATAGCCAAACCGCTTGGCGTACCGTTTCAGGCGGTTTCGCTATAAAAACAGGCACATTGAA

## SEQ ID 4278

MASEGNRSSDGIYSQTACRTVSGGFAIKTGTFE

## SEQ ID 4279

GTGTCCGATAAGGTTGGAAAAGACATCCGGAATCCGGATTATTGAAAAAGATCTTAAATTATAAGGCAACGAGCAAGCAGGGCAAGAAAACGAGTAGGCGGCGCGGGGTTTCCGCC  
GCCATTCAAACGTCGCGCAGACA

## SEQ ID 4280

VSDKGWKRPESGLLKKILNYKATEQSRARKRVGGAGVSARHSNVRQT

## SEQ ID 4281

CGGTTTGACACCGTTTCTTCCAAAAGGCATCGATTTCAGCGGGCTTTTCTCGCTCAAACCTTGTTCCAACTGGTTTCTGACCAACTCGAAAGGCTGCGGTCGGGGTTTTTCCG  
ACCGCGCGAGTTTGAACAGGTAATAGCGTTCGCCCAATTTGACCGGATTGCGGGTAACGTCGCCACGGTTTATACCGGCAAACTGCGAAGCCAGCGCTCGGGAAGCTGCTCGCCGATAA

TGAAACCGTGCGAACGCGTCTCGTCTGGATAACGCTTCATCAGCCCTTCAAAGAAGACAGCCCTTTGAGCAGGAGCTGCTGCGCCTGACGCGCCTCCTCTTCGGTTGCGAAGCTGAACCTGCTGCAATTTGATCATGTCGGATTTCGCGCTCATAAACTGACGCGATGCGCTTTCGGAAACCGTTTCCGAACGTTTCCAGAAAACGGAGCTATCTCTCGGCATAAAAAGACGCTTCGCGGATTTTAAAGCGGTTTGGACATCCTTATCCTTATCCAAACCTTCCTTCAATGCCCTGTTTTTCAAAACTTCCAAAGTTTGCAGCGCGGACGGCATCGTTTCGGATTGCGCTCGCCGTCGCGTCTTGGAGCATCTCCGCAATCGCGGTGTGCTGCTGCAATGATGCGCGATGTCGCGCAACAGCATGTACCAACCAAGCGCGGTGCAATTCGGGTGCTTTGGCTGCGCGCAAAACCTGCCAATTTGCAGCAATACTGCGCAGCGGCTTTTTCTGTTTCATGTGATTTCCCTGTGCTGCGCGCGCGGCAAA

**SEQ ID 4282**

RFDTVFFQKQXGIDFQAGFFLPQTLFQLVSDQLERLRVGVFPDRAEFQVIAFAQFDRIAGNVATVHTGKLRSLRQIKLLRHNETVERILLVVRITLHQPFKQPFEQELLRLTRLLFGCRADL  
LQPDHADLPLIKLTOCAFNGRFRFTFKORTDVLGIKRRFGDFKAVLDILILIQFFLQCPVFNQFSLQPADGIVSDCLFVRSIGLLRMPVCLLHDLRHQRHQSRVDFGCGCRKTCQHCNS  
NCGSGLFLPHGIPCPAERQ

**SEQ ID 4283**

TTGGCGAGTAACGCGCAAAACGGGGCGCTCAAACTCAGTGCCATCAGCGAAGCCCAAATATATCCTCTCCTATCTCGAGCAATTGTGCGGCAAACTCGCGCGCGCGGACTGGTGTGAAA  
GCCTGCGCGGGGCGGCGGGGTACATCCTCGCGCCCTCCGCGCAAAATCAACATCGCCCAATCATTTCCGCGCGCGAAGACGGCTGGACGCGAACCATCGGGCAGCAAGGCCAA  
CTGCCACCACGGCGGCGCTGCCTGACGCACGACCTTTGGGAGAAATTTAAACAAAACCATCAACGACTATCTCGGCAGCGTTACCTTGCAAAGCATCATGAAACAGAAAAACAACGGCGAC  
GGCAGCGCGCTGCTCAATTTACACACATCCAT

**SEQ ID 4284**

LAHNAVTGAVKLSAISERQNTISLSYLEQLFGKLRAGLVESLEGPGGYTLAAPPAQINIAQIIISAAEDRLDATQCGSKANCHGAPCLTHDLWENLAKTINDYLGSVTLQSIIEQKNNGD  
GSRVVVQTHIH

**SEQ ID 4285**

TTGGTGGTCAGTCTCATGGTGGTGGTTGCCCGTGTCCGGCTTTTTTATAGTGGGCGGAATTGTCCAATATCTGAGTGTTTCACTCAAGTATGGGGAGCTGTTGCCGATTGTTTGTGTTAAAT  
GGCGGTATAGTCTGATTTTGCCTTTATTTGTTTGGTTTTTGAAATCAGTTAGTTATGTTTTTGGAGAGCGCGGTGGGGCGTTTTCGCCGGCAAGCGGTTTCAAAACGATTTGATTATATTT

**SEQ ID 4286**

L V V S L M V V V A R V G F F I V G G I V Q Y L S V S V K Y G G A V A D C L F K W R Y S L I L L Y L F G F L N Q L V M F P E E R R L G R F A G K R F O N D L I Y P

**SEQ ID 4287**

ATGAAACGCTGATTGAGCAAAATGACCTGCATTTGAAGACTTGCACCGCGTGTGCAAGCGCAAAATGCCGCGTATGTTTTACGATTACATCGATTGCGGGTCTCGTGGACGGAAACGACTTTATAGGAGAAATACCTTCGGATTTCAAAGATATCCGCTCCGACAAAAGGTATTTGGTCAATATGAGAGGAGCGCAGCCTCGAAACCAAAATGATCGGGGGGGATGTGAAATATGCCGCTGCGCATTGCGCCAGCGGTTTTACCGGCTGGCACACGCAGCAGCGCGCAAAATTTTGGCGCGCGCTGCGCGCGGAAGTTCCGATTTCGGTTTACGTTGTCACCATTGTCCATTCTCTCGATTGGAAGACGTTCCGGAACACACCGCCGCGCTTTGGTTTTCAGCTTTATGTAGTCGCGCAGCCGCAATTTATGAAACCAAGATTAAGCGGATTCGCGAATTTGGTATGTCATGCGCATTTGTCAGGTTTGGGTCAAGCCCAAGACATCAAAACAGCGCTTCCGCGCGGAAACCGACCATGCCCAATTTAATCAATTCGCGCAACAGCCCGCAATGGTGCATGAAATGCTGAACACGGAACGCCGACAGTTCCGCAATATCTGCGGACACGCCAAAAACGTCGCGGATTTGTCTTCACTTTCTTCGTGGACGGCGGAACAGTTTCGACCCCGCTTAAGCTGGGACGAGGTGCGCGGATTAAGATTTGTGGGGCGGCAAGCTGATTATCAAAAGGCATTATGGAACCCGAAGACGCGGAAAGGCGCGGAAAGCGGTCCGATGCAATGGTCTGTTTCAACACCGCGCGCCGCCAGCTCGACGATATCTGTGCCCATCAAGGCTTCCCGCATATTGTTTTCCGAGTCGCAGCGACATCGAAGTTTGAAGTGGAACAGCGGTATCCGCAGCGTCAAGATATTTTGAAGCGGTGGGCTTTGGTGCAGAAAGCAGATGATAGCTCGGCGCTTCTGTATGGTCTGATGTCGCAAGAAAGCGTCAACGCCCGCGCTGGAGATTTGTACAAGAAATGGATGTGTCTGATGCGCTTTCGCGGACACCGCGATATTCAGATGTGCATGCTCCGATTTTGAGGAGTAAGGATTTGGGCGACGGAAACCGGTT

**SEQ ID 4288**

MKRDL SKMTCIEDLHRVAKRKMPRMFYDYIDSGSWTETTYREWTSDFKDIRFRQKVLVNMBCRSLETKMIGGDVKMPVALPTGFTGMHADGEILAAARAEKFGIPFTLSTMSICSIEZW  
 AENISAPFPWQLYVMRDEFMENLIKRAKDAKCSALVLTADLQVLGQRHKDIKNGLSAPFKPTIANLINLATKPEWCMKMLATERRTFRNIVGHAKNVGDLSSLSSWTAEQDPRLSHDDV  
 ARIKDLWGGKLIKGTNEPEDAEKAAKSGADALVVSNHGGRQLDDTVSAIKALPDIVSAVSGDIEVWMDSGIRSQDILKANALGAKGTMIGRAPLYGLGAYGEEGVTRALEILYKEHDVS  
 MAFTGHRDIOVDASILRSKDWGRETV

SEQ ID 4289

[illegible]

SEQ ID 4290

MANNNKTLFDWDERKSMLEEMEQTDFPALPEFVSNNLKYPPFEWQKSALENFVIFDRTSKLDFPDIKNRPHTLLFNMATGAGKTMIAAILIYYPERKYRHPFLPFVNKNINIVKTEYNNPI  
DPHTPKFLFTEKILQGDFTVPIRIRKVFETFSQYSDGIEIKFTSIQIKLYNDIHTFERENQTLADLHELNLVILGDDEAHHLNAQTGKKQGOLEKEMNERTSDAEIERKGEHWHVLIELLAKN  
GNPGQNVILLEPTATLPENAEVQKYADKIITKPLGKEFLQGYTTEINLVSGTLNKKERVLEHALLFAWYRHQIALKYGIANFKPVMHLPRSKTIDESKADYSAPLNNVENVQADDFSLFTTF  
STLSLSDNNANEOGKTRTEQALKPMOENKFEPVHLANWVKONYOKHNVIITNSETNKTTEKTDSOTEKILLANLEADNPRAIPTVDRLTEGWDVIALFDIVELYEGONGGGSNKKSGKT

AAATVSEKQLIGRGVRYPPFAFEQKQPNRRFPNDHQHELRILEEFLYYTHDEQSRYYITELKNELKDGYPKEDDDKVLITFKLKSEFADNKDFRELLIWANKKIPNPNKASNNADSLQA  
NPQTLSQVGHNGQLLQEQTPADENDETARQIGQNNPTQTIKSEMERHIFNKALHTKGNSQSLFHPDRLQSKLDIQNKNELQNKLLKDWQIEFLGLEQDKQVRPDDKLAGCLKILEV  
EKHLNESDIPFIGTKEFPKKLWEIPGTGPKQVKKDDIKTALATQNDVYMDNFAGTGLEBALIQIPISARLGDLSQYDVHELIRNEEVFKLNFADGEGFMPDFVLLLKQKQKSSSDSDV  
DFLHYQIPIEPKGGLHVENDSWKEAFLKSITVEYGRDKILQKNTPHYRLIGLPFFTQHQXNQPTFLPLGAASLEK

**SEQ ID 4291**

[illegible]

**SEQ ID 4292**

SEQ ID 4292

LLNNDELKRHPVFEVNGVLVFKLQDFRFLDKHSINNSYTKYANRIGLTDGNRFLKDNSDIVLDFPFKQDLVNGGQSTEEGEETYFKRNNSPASQPASQPASQPASQPASQPASQPASQPASQPASQPASQLYTKLTRKRQEITFNQTLAFDEIDRLFDAKAFSKFSRHPTADGKQVGEIKRRSDGTPAENLIITKGNLLIAMSLSLAKRQGVKLIYIDPPYMTETDSFAYNDKFSHSTWLTFTMKNRLEIAKELLKDDGLLVFQCDDKRBQAYLKLVLDEITFTRENTINCLIAVKMSEPSGNKMAHTSHRLPEKIKETILYIKNRKLIKLNPITREKSEWDEYNNITLENPTQDEKKFIDLIVNSQTEKNKEINGFNLKEIDILKGLISPISTVQKLAQLNLKDNVEIKWLDNAYRIVRTAAASSVKKLADBEKICQQQFVSVLSKRIKLIYVKSDDYSKDAKAPRVQVLPAEDYLSISLCLWTNNITGTAEGNVLGKGRKPSLEITNIIKLATNDEIDYHLGSSQTAAVAHKNNRQYVIGIBQMDYIETLAEVRMKKVIDGBGGGISKAVNWGGGGEFVYAEISPPNETAKQOTLACENSGIKTLFEGLCERHFLKYNVSNVSPQIIIEPEFQSLALDEBQKMMLEMLDLNQMTISLSEWDEQFAGCLNDDDKALSRAFYQSVKHQAEKKDGE

**SEQ ID 4293**

TACCCGCGGAAAGCCAGCAGGTGTGGCGAGTGCCTCGTCAGATAAGGACTTGGGCGTGTGACGAGGCAAAACCGCGCGGGGAAAGGGTTTGGACGAGACATAGAGCCGATGCGCCCTTCCGTTGGTGGCGCGTGTCCGTTTGGGGCAGGGCGTTTTCATTCGCGCCGGGTTTTCGTCGCGCGGGTTCGCGTCCGTTTCGCGCGGGCGGCGATTCGCTCCGAGTCGATATTTTCATTCGCGGTTCAGGGGCTTGTTCACGATTCGCTTCATCCACATCCA  
CGCCCGGATCTTTCATCTGTCGTAATCAACGATTCGTCGTCAGATTCGGCGGGCGGCGATTCGCTCCGAGTCGATATTTTCATTCGCGGTTCAGGGGCTTGTTCACGATTCGCTTCATCCACATCCA  
CTCCAAAGGCGGCTATGTGTCAGGATGCTTCGATGCTGTCGTCAGGTAGCCCTGCTCGTCAAGGAAATCGATAAGGATGTGGACCGCAGGCGGCTTCCTTGTGTCGAAAGGGGGTGTTCGCGAC  
GCTTTCGCGGTTCAGGATATTCGTTGAAATCTTCCTTCGCGCGGCGATGTGTGACAGCATATCTTCGCTTCGCTCCGCGGATTTGACGCGCGGGCGGGTGTAAATGGCTGAATTCGCGCATCG  
AAAATTCATTCGTTTCCTTCGCGTTCGAGCAGGGGGTTCGCGACGCGCCAGTTTCGACCTTCGCGTTCAGTTCGATACCCGCGCATTCGCAATACCGCGCAAAAGATGTGTGACGCGCTGTGTC  
GAGCTGCTGGGTCTGTTTGAGCTTTTCCGATTAAGGTAAGTAAATGCGGTAATAATGTCAGCTGTGCGGCGCAAAAAATGCCGCAAGGCGTCATTGCATATATAAATGGTT  
TTAATGAGCGGGTTCGGATTCGATACCAATAACAAAAACAA

**SEQ ID 4294**

SEQ ID 4294  
YRGPAGWVRVPRQNRITWAWTRQNRRRERG\*ARQ\*GRVRLVRCRCRFGAGVFSRRGLAAVAWNAVEGVSDDMGGGFGSTFARSFYLYQYRFGHIGGGHACRIEFQCGQGLFQHCFTQHP  
LQGRNVQDVPDAGVQVALLVKEIDKDVDAGGFLVGKGVPARLRVQVLLLETFPAGDVQGLHIFAFVSDLTRGRGVMAEFGIGKIFRFFAFBQGVRRRVPVDFLAFKFDTRHLQYARLLQPLV  
ELGLFLYSD\*GNDNAVKIVIFSLSAQKNAKRHCIIINGFNERNRIPSDNKKQ

**SEQ ID 4295**

TTGGAACAGCGGAAAAAAGACGGTGTGAGCTGCGAAAGCGCCGAAAGCCGTACGCGAAGGCAACAAGATACGGCGTATATAGACGGCGTGGCGCTCTGTACAGTATCCCGCAGTTTG  
AAGTGAAACCAAGGCGACGAAGTAACCGTTTACGTACCAACGTGAAACCATCGAGGACCTGACCCACGGCTTCACTTTTGAAGGCTCGGCGATCGCTATGGAATTCGGCCCCGCAAGCCAC  
TCTCTTCGTAACCTTCAAAGCCGTCGCGCCGGGTGTGCACTGGTACTACTGCCAATGGTCTCTGCCACGCMTTGCATATGGAATGTGCGGTGAGATGTTGTCATCCCAA

**SEQ ID 4296**

SEQ ID 4296  
I E Q A K K D C V E L E K A A K A V R E G N K V R V Y M T A V A P A Y S I P O F E V N O G D E V T V Y V T N V E T I E D L T H G F T L E G C G I A M E I G P Q A T S S V T F K A V R P G V H W Y Y C Q W F C H A L H M E M S G M I V H P K

SEQ ID 4297

SEQ ID 4297  
ATGAGGATTTATAACGATGAAGACAGGCATTCAAACCGAATTAGCCCAAGCCCTGCTATCACACGAAAAAATATGGGGCAACGAAGAAAAAACCATTTTGGCCAAAAACATCCTGTGGAT  
TTGGTGGAAAAAACCGACCCGTCCTAATTCGGTTTGTATTGAA

**SEQ ID 4298**

NR1YNDEDRHSNRISPSPAITRKNMGERRKNHFGQKHPVGFGGKNRPVHYRFVIE

**SEQ ID 4299**

SEQ ID 4299  
TTGATAATATATGTTGATATTTCCGCAAAATCCGATGCATTTCGGACACCCGCCCCGCTTTATCGCAACGTTGCGAAGCCCCCCGAAACAGCAAAGACAGCAAAGAAATTGATTTTATTATTA  
TTTATTATG

SEQ ID 4300

INNM LIFPONPD AFGHPPELSORCERPRKQORQORIDFIITYL

**SFQ ID 4301**

SEQ ID 4301  
TTGCGGAATATCAACATATTATTCAAACGCAGCCCGTATTTTAAACGCCGCTCAGCGGAGGATGCCCGCGTGTTCATCAGGCGCAAGGCTTTCATAAGGCATATTTCTTT

SEQ ID 4302

LRKYOHIIOTOPVFLTAAQAEDAAVFIRRKAFIRHISP

SEQ ID 4303

SEQ ID 4303  
ATGACCAATAAAACCCGCCAAACGCCGGTCAACGGCGTCTCTCTTCGACAAACCAGAGGCCTTCCAGCAACACCGCCCTGCAAAAAGCGCGCGTTTGTTCATGCGAAAAAGCAG  
GGCATACCGCGCGTCTCGATCCTTTGGCAACCGGACATTTTGCCCGCTGCTCTCGGCAAGCGGCGCAAGTTCGCCCAATACCTGCTGGATGCGGACAAAGCGTACACCGCCACGCTGAAACT  
CGGCGCAACGACGACGACGCGGCGATGCGGAAGGAGAAATCATTTCCGCCGCCCGCGCGATATTTCTTAGCCGAATTTTCAGACGGCCCTGCCAAGCACTGACAGGCAACATCGGCCAAGTG  
CCGCGGATGTTTTCGCCCTCAAGCACGAAGCAAACCGTTGTACGAATACGGCGCGCAAGGCATGTGTATCGAAGCGCAAAACGCGCGACATTACCGTTTACTCTATCGATATTGCCGAGT



TTGACGCGCCCAAGCCGTGATAAGCGTGCCTGTCAGCAAGGCACTACATCCGCACTCAGCGAAGGCATCGCCAAACACATCGGCACATTCGCCACCTGACCGCCCTACGCGGCAC  
CGAAACCGCGGCTTTACATTCGCCCAAGCCACACGCTCGAAGCTTTGGCAAAATTTAAACGAAACAGAACCGGACGGCTCTGCTGCTGCCCTGCGACGTATGTTGTTTACACATTTCCCA  
ACCGTTTAAACGATTATGCCGTCCATATGCTCAATGCGGGCAACGCGCGGTTTCGAGGAAGACCTGCCCTCCGATACGCGGTACCGGTTTACACGAAACGCGCCCTTTGTCGGTT  
TGGCGGAATATCAAAAGGAAATATGCCGTATGAAAGCCTTTCGCGCTGATGAACACGCGGCATCTCCCGCC

## SEQ ID 4304

MTNKPAPKRVNGLVLDKPEGLSNTALQKARRLFHAERAGHTGVLDPLATGLIPVPCGEAAKFAQVLLDADKAYTATLKLGEASSTGDAEGRIIAAARADISLAEFQTACQALTGNIRQV  
PPMPSALKHGBKPLIEYARKGIVIERKPRDITVYSIDIAEFDAKAVISVRSKGTIIRLSEGLAKHIGTFAHLTALRRFTAGFTTIAQSHTLBALANLNETERDGLLLPCDVLVSHFPQ  
TVLNDYAVHMLQCGQRPFEDLPSTPVRVYTTENGFRVGLAEYQKEICRMKALRLMNTAASSA

## SEQ ID 4305

TTGAAGACTGATACTGCCAGAATGAACAATCTGATTCGCCAACATTTAGCCGCTATGCACATAGTGATAACCTGCAAAATTGAAGCGGGCATCGTTGCTTTTCAATTCCTGCCAAGTA  
GAGACTATTTCCACATCCGTACTATGGAGGCCCTTTGATGGATTGATTACCGATGACTGATAAGGCGCGGTAAAAATTTGCGCGGTAGAAGCTGTAAGCGCGATGAAATCGTATTGTT  
TGATGGGCGGGAACATGCTATTAACGCTATGTTCTGCGCAAAATATAGCCAAATCAAAAGCAAAACAGACGTTAACTGATTGGATGAATATACCTACCGAGTTCGGATTTCATCTTTAT  
TACAATATAGACTACGAAGATGAATATGAAGATTTCGTCATTCGAAGGACAAGTCCCTTAATTGATGGCGCATCATTAGTTTTCGACTATTAAACGAAATGGCTTTGATGCAATCA  
GCATTGATCTAATTGATGAAAAACATCTGTTCTGTAATTTGAATGAAGAAATTAAGC

## SEQ ID 4306

LKTDTPARMNLIPEHLAAYAHSDNLQIEGHRCPFLSCQGRDTFHIRYYPEPFDGLITDIDKAPVKIVAVEAVSGDEIVLFDGAEHGYNAMPCKDYSQNKQNRITLIDLEYTYRVPILHY  
YNIDYEDYEDYFNSEGVPLIDGRIISFDLSKRNFGDAISIDLIDEKHSVRELLNEELS

## SEQ ID 4307

ATGAAAAACCCCAACGCGGTACGCGCCCAAGACCGGTGTCAGGAACAAATTTAGCGGAGCTTTCGCGAATCGTCCGTACCGGACTGAAAGACCCGCGCGCGGCTTCATCACTATCA  
ACGAAGTCGAAATTAACCGCGATTACAGCCACGCGACCGGTGTTCTACACCGCTTTTGAACCAAGATACGCGGAAATACGGAAGAGTGTGGAACACGCGCGGACACCTCCCGACGGA  
ATTGTCCAAACGCATCAAGCTGTTCAAAATCCCGAATGCATTTCAATACGACGAATCTTTGAACGCGGTATGAGCCTGTCCGCCCTTATCGATCAAGTGGCGCGGAAAAACCGGT  
GAAGAC

## SEQ ID 4308

MKRPQRGYARQDRVKEQIMRELAELVRTGLKDPFRAGFITINEVEITRDYSHATVFTVNLQDREITTEEVLEHARGHLRSELSKRILFKIPLHFKYDESLEGRMSLSALIDQVAEEKPV  
ED

## SEQ ID 4309

TTGTCATCTTCGGCAGTATCAGTCTTCAACCGGTTTTTCGCGCCCACTTGATCGATAAGGGCGGACAGGCTCATACCGGTTCCAAAGATTCTGCTGATTGAAATGCAGTTCGGGGATT  
TTGAACAGCTTGATCGGTTTGGACAATTCGCTGCGGAGGTGTCGCGCGCGGTGTTCCAGCACTTCTTCCGTAATTTCCGCGGTATCTTGGTTCAAAACGGTGTAGAACACGCTGGCGTGGC  
TGTAATTCGCGGTAATTTGCACTTCTGATAGTAGTGAAGCGCGCGCGGCTTTCAGTCCGGTACGGACAGGTTTCGGCAAGCTCCGCGATAATTTGTTCTTTGACACGGTCTTGGCG  
GGCGTAGCGCGTGGGGTTTTTCATGAATATCCTCAGATTGGTGTACAGCGCATTTCTGCGCGCGGGCGGTTGCGAAAGGCGGTATTA

## SEQ ID 4310

LFILAVSVFNFRFRRLIDKGGQAHAFQRFVVFEMQFGDFQDLDAFGQFAAEVSARVQHFPRNFARILVQNGVEHGGVAVIAGNDFVDSDEAGARVQSGTDEFGKLAHMLFFDTVLA  
GVAALGFFHEYPQHQWTAFLPPGRLRKGV

## SEQ ID 4311

AATCAATTTCTATAGTTTAAATAACGAAATCTTGGCGTATAATCGCATCCATAGTTTTTCAAAAGGAAATAAATGTGATTCAAGAAATTTATCAATCAAGAAACCGGTTACGAAT  
ACGCTTTCGCGCAATCTGACTGTAAGCGGTTTGCCGCCCACTTGACCACTGAGAAAAGGAACAAGAGCGATGACTACCTCCAAATGCCCGTAACCATCTGACCAT

## SEQ ID 4312

NQPHSFNNENLGV\*SHF\*FLQKENKMSIQEIYMQETGYEYAFRQIVL\*AVCPFPDQPEKRNKSDDYLMFRNPSPDH

## SEQ ID 4313

GTGTGCGTTCGAGAAACGCGCATGCGCGTTCGGGTTGCCAAGTATAATACTATATCCGTGCTTATCAACGTATTACCTTAAAAATCCCGCGGATTTCGGCTATAATACGCCCTTTCGCAACC  
GCCCCGCGCGAGAAATGCCGTC

## SEQ ID 4314

VCVAETACAVRVAKYNNYIRAYQRI TLKSRRFYNTPPFRNRPGRNAV

## SEQ ID 4315

ATGTCCAACGAAAAACGTTACCTGTTCTTTTTCGCGAAAAATCCAAATCACACGCCAAACACCTGATTGAGGGCAAAAAACGCTATATCTGCGACGAATGCGTGCAGAACTGCCTCGAAATAT  
TGTACGAAGGGCAGCAACGCGCGCACGCTCCGGAATAATGCGCGAGGGAGCGCGAGAAATTCGCGCAAACTGCCACGCGCGCGGAAATCGTTGCCAACCTCGACGATTATGTATCGCGGCA  
GGGCGAGGCGAAAAAGCGCTGCGGTTTCAACCAATTAACAACGCTGCGCCACCGGAAAGCGGCGGTTGCGAATTTGCGAAATCCAACTCTGCTTTATCGGCGGACG  
GGATCGGGTAAACGCTGTTGGCGCAATCTTTGGCAGCAAACTGGACGTGCGGTTGCTGATGCGGAGTGCAGCACGCTGACCGAAGCGGCTATGTCGGCGAAGATGTCGACAAATCA  
TTACCAAACTGTTGGCAAAATGCGATTTCGATGTCGAAAAAGCGCGCACGCGATTGCTATATATGACGAAATGACAAAAATTTCCGCTAAAAGCGACAACCGCTCCATCAACGCGGACGT  
GTCCGCGAAGGCGTGCAGCAAGCCTTGCTGAACTGATTGAAGGTACGGTGGCAAGCGTTCCGCCCCAAGGCGGACGCAAGCATCCGAATCAGGAATTTATCAACGTTGATACGCCAAC  
ATCCTGTTTATCTGCGCGCGCGGCTTTGACAGCTTGGAAAAAGTGATTGCCAGCGCACGAGAAAGGTGGTATCGGTTTCGCGCGCTGCGTTTACAGCAAGGACGAAAAATGCCGCGATTA  
CCAAGCTGTTGCGCATCGTGAACCGGAAGATTAAATCAAAATTCGCGCTGATTCCGGAATTAATCGGACGTTTCCCGGTGATTGCAACTTTAGAAGAACTGGATGAGGACGCGCTGATTAA  
TATTTTAAACGAGCGGAAAAACGCTTTGGTCAAGCAGTATCAAGCCTTGTTCGGCATAGAAAACTGCGGTTTGAATTTGAAGAAGGCGCATTCGCTTCATCGCGCGGACGCAATGGAA  
CGCAAAACCGCGCGCGCGCTGCGTTCCATCGTGAACCGCTGCTGCTGATACGATGACCGCTGCCGATTGCAAGGCTTGAAGAAAGTGGTGGTGGCAAGGCGAGTCAATCGAAG  
AGGCGAGGGAACCGGAATGGTGTTCGAGTCC

## SEQ ID 4316

MSNEWRTCSFGKSKSHAKHLIEGKNAYICDECVANCLEILYEGDNGGTPPENAGGEPESGLPTPAEIVANLDDYVIGQQAQKALAVAVYNHYKRLRHPKADGGVELSKSNILLIGPT  
GSGKTLIAQSLARKLDVFPVMAATFLTEAGYVGEDVEQIIITKLKCDPVEKARHGIYVYIDEIDKISRKSNPISITRUVSGEGVQALLKLIEGTVASVPPQGGRRKHPNQEPIINVZAN  
ILPICGGAFAGLEKVRIRTEKGGIGFASVHSDENAGITKLFIVGPEDLIKPLIPELIGRLPVIAITLEELDEDALINILTEPKNALVKQYQALFGIENVGLFEPEGALRSIARQAE  
RRTGARGLRISIVERCLLDTHYRLPDLQGLKVVVGKAVIEGREGPELVFES

## SEQ ID 4317

ATGCACAGCTGTGGCAGATTTCATATATACGACGCGCGCGCGCGAGGAATTCGCGCAAAAAATGGTGAAACACAGTTTTTTCGCGACAGGTTTTTTCTGCAACTCGGGCGCGGAAG  
CGAATGAGGCGCGGTTAAAGCTGGCAAGGAAATATCGCGCGGACCGTTTCGCGGAGGCAAAAGCGAAATGCTGCGCTGATCAACAGTTTCCAGGACGACGCTGTTTACCGTGTCCGT  
GCGCGGACAGCGCAATACAGTAAGGATTATGACCCGCTGCGCAAGGCAATACGACAGTTTCGCGTTCAACGATATTGCGCGCGCTGGAAGCTGCGGTGCGGGAACAGAGCTCGCGGTCACT  
ATCGAGCGGATACAGGCGGAAAGCGGCATCTGCCCGCCACTCGGGAATATTTCAGGCGCGCGCGCTGCTGCGACCGGCAATGCGTGTGATTGTTGAGCAAGATTCAACCGGGA  
TGGGCGATACGGCGAGCTGTTTGCCTATGAACATTACCGCGTTGTTCCCGATATTTGAGTTTCGCGCAAAAGCTTGGGCTCGCGCTTTCGATCGGACAGATGCTGCGGACAGAAAGAT  
TGCGCGCGCTTCCACCGCGGACGACGCGCTGCACTTTCGCGCGCAACCGGATGGCGGTGCGGCTGCGGACGCGCGCTTCGATCATCATCAACCGCGCGGAACTTGCACACGCTCCGC  
AGTCAGGCGCAGAACTTCAGACGCGATTCGTTGATTTCGGCAGGAAACAGGCTTGTCTCAGGTTTCGCGGATGGGCTGCTGCTCGGCTGCGCGTTGCACACGCTTATCGCGGAC



GCTCATCCGAAATCGCCGCTACCTCCTTGAACACGGCGTGATGATCTTAGTTGGGGTCCGGACSTATTGCGTTTCGCGCCTTCGCTGCTGTGAACGATGAGGATATTGCGGAAGGTTT  
CGCGCGTTTGGAAACAGTCTGCTGACGGAATTTGCCCGCCAAACCCCCC

SEQ ID 4318

CGCGCGTTTGGAAACAGTGTCTGACGGGAATTTCGCGCGCAAAACGCGG  
EQ ID 4318  
MHKLWHISNIYTTTPRAQELAQKLKXHSFADKVPFCNSGAEANEAAALKLARKYARDRFGGKSEIVACINSFPHGRTLFTVSVGGQPKYSKDYAPLPQGHITVHPNDIAALEAAVGEQTCVAVI  
IETIQGESGILPATAEYLQAARRLCDRHNAALLDEVQTCMGHFGRLPAYEHGVVDPDILSSAKALCGCGPPIGTMLATEKIAAAPQPGTHGSTPGGNPMACAVGSRAPDIIINAPETLHNVR  
SQGQKLTALLDLGRKTLGFLFSQVRGMLLIGCALDTPYGRSSSELAATSLEKHGVMLVAGADVLRFPASLLINDEDIABGLRRLEHLVTFEFAANRP  
CGCGCGGCTTGGAAACAGTGTCTGACGGGAATTTCGCGCGCAAAACGCGG

SEQ ID 4319

SEQ ID 4319  
TTGAAATATTTAGGTTTATTTTACCACCTGCCCCGATATGTGCGCAATTCCCTTTATCCGCCCTTGAAAAACGGTGCATAATCCCGAACAAAACCGCAATCAGGAGCAATTATGCAAAAC  
TATCTGACCCCCAATTTCGCCCTTGTCCCGGATGATTCCCGAACGGCTTCAGGCAGCCGGTTTGGGATACGGAAGGGCG

**SEQ ID 4320**

SEQ ID 4320  
 ...KIDP...TAYCROFPFIRLEKRCIIIPNKTAIRSNYAKLSDPQFRLCPDDSRTRFRQPRILGYGRA

SEQ ID 4321

SEQ ID 4321  
ATGCTTGAGGCGCGGCAGCGTTTGAATTAGAACTCCCCAATATTTTATCTTCGGACGGCATTTTCATCATGCAAGGCCAAAACGTTTACAACCGCTTACTGCTATTGGTACCACACAGAC  
GTGCGGTGCTTTTGGCGCTTGCT

SEQ ID 4322

SEQ ID 4322  
MLEARQRFDLSPQYFYLR TAFH HARQNVYNRL LLLVPHRRAVLFALA

SEQ ID 4323

EQ ID 4323  
GTGGTACCAATAGCAGCTAAGCGGTTGTAAACGTTTTCGCTTGCATGATGAAATGCCGTCCGAGATAAAAAATATTGGGGAGATTCTAAATCAAAACGCTGCCGGCCCTCAAGCATTTATATC  
GAAATTTTTTTGTTTTTTTCAGCTATCCGGTTGAAAAATATT

SEQ ID 4324

SEQ ID 4324  
VVPIAVSGCKRFALHDEMPSEDKNIGBILNQNAAPQALYRNPFVFFSYFVENT

SEQ ID 4325

VPVIAVSGCKRFLAHDEMPSEKDKNI GEILNQAAAFVADIRKPFVTFSTVLE  
EQ ID 4325  
ATGAACAACGGCGCGGCCGCTTCCGACAAATCAAAACAGCCTGACCGCGGCCGCGCGGCCCTCTGTACGCAAGATTGTGGCTGAATGAAAACCTCGCCGACTTCGTGCGCGAAGTCA  
TCCCGCGAAGCCCGTATGCAACGCCAAAGGTTTCGGCGCGCTTCGGTACGTTTACCGTAACACAGCATCACCAAAATACACCCGCGCCAAAATTTTCAGCGAAGTCGGCAAAAAACCGAGAT  
TTTCGCGCCGTTTACCACCGTGGCAGCGGAGCGCGCGGCGAGCCGATGCGGAACCGGCATACCGCGGTTTTCGGTTGAAATTTCTATACCGAAGAAGGCACTGGGATGTGGTCGCAACAC  
ACGCCCGTGTTCCTTCCTGCGCGAACCCGCGCAAATTTCCCGGACCTGAAACAAAGCCGTCAACCGCGATTCGCGCACCAATATCGCTTCCGCGCAAAACAACTGGGACTTCTGGACGCTGTCTG  
CCGAAGCCCTGCACCAAGTTACCATCTGTATGAGCGACCCCGGTATTTCCGCGCAGTACCGCCATATGCACGGCTTCGGTTCGCATACCTACAGCTTCTGGAACGAAGCGGCGCAACGTTT  
TTGGGTTGAAATTTCTTCGCGCGCAGCAAGGGAATTAACAACTGACCAACGAAGAAGCTGCAAAAATCATCTCGCCGACGCGCGGAAAGCCCTGACCTGACCAAGTTTGGCGGAAAAAGACTATCCGCTGA  
CGCGCGGAGTTTCCCGAATGGACGATGTACATCCAAGTCATGCTGAAGCCGATTCGCGAAAAAGTCGCTTATCATCTCGTTGACCTTACCTGACCAAGTTTGGCGGAAAAAGACTATCCGCTGA  
TTGAAGTGGCGGAATTCGAGTTGAACCCGCAATCCCGAAAATCTTCTTCGCGGATGTGGAACATTCGCGCAATCCCGCTCAATCTGTCGCGTTCGCCCTGTTTCACAGCAACCGCGCGACCGCAACGG  
GCAAGCCCGTTTGTCAATTACGCCGACCGCAACGTTACCGCTTCGGTGTGAACTTTCGCGCAATCCCGCTCAATCTGTCGCGTTCGCCCTGTTTCACAGCAACCGCGCGACCGCAACGG  
CGCGCGACCGCAACTACCGCAGCTTCGCGCATACGAAACCAACAGCTTTCGCGCAATGGCAGCAACCAACCGACTTCGCGCAACCGCCCTTTGAAATCAACGGCGCAACCGCGCATCGG  
ACTACCGCAAGCATGACGACTTTCAGCAACCGCGCGCTTGTTCACCTGATGAACGCGCGCAGAAACAGGCTTGTGTTGACAAACCGCGCGCATGGCGGATGGCGCGATCGCGCGA  
CTTCATCAATAACCGCCATATCCGCAACTGTACTCGTTGCGACCCGCGCATCGGTGAAGCGGTAGCCAAAGCCCTCGGACTGACCTCGAAGACGCACAAGCCGTCGCGCGACCGCATCC  
GCACTGGGTGACGCGGTTTGCTG

SEQ ID 4326

GCACCTGGGTCAAGGCCGGTTTGTCTG  
**SEQ ID 4326**  
 MNGAPVADNQNLSLTAGRPGLLTQDLWLNEKLADFVREVIPERRMHAKGSGAFTPTVTHDITKYTRAKIFSEVGGKKTMPARFTTVAGERGAADAERDINGALKFYTTBEGNWDVVGNN  
 TPVFFLEDRPKFPDLINKAVKRDPTNMRSATNNWDFTWLLPEALHQVTTVMDSRGIPTASYRHMHGFGSHSTYSFWNEAGERFWPKFPHFRSQQIGKNLTNEEAKIITADDRSHQRDLYEAE  
 RGEFPKWTMYIQVMPEDAEEKVYPHPDILTQVWPKDYPLIEVGEFELMRNPFENFADVEQSAPFASNLVPGIGASPDKMLQARLFNYADAQRYRLGVNFRQIPVNRPRCPVSHNRDQGG  
 RADGNYSGLRPHYEPNSFGQWQQQPDFAEPLPKINGDAAHWDYRQDDDDYSQPRALFNLMDNDAQKQALFDINTAAAMGDAPDFIKYRHIRNCRCDPAYGEGVAKALGLTVEDAQAVRATDP  
 ALGQAGLL

SEQ ID 4327

ALQAGLL  
SEQ ID 4327  
GTGTACAGGCAGGCAGGGTTTCCCGCGAAGGATAATAAAATTTTTTCCCATCGGCTGCCGTCCGAAACCGGTTTGCCGATTTTATCCAAAGAGTGTGTATGTGCAGACGAAAATATG  
AACAACAACCGCTTGAGCCGTCGTTCTGTTCTTAGTACGCGCCGCGCTTCCCGTGCAGGTATTGCCGGTCCGGGCTGTGGGTTTGGCGGGTTGCTCTAAAGACGCGGAACAGGCTGCCGC  
TAACGCTTCCGCGCGGCTCCCGTCCGCAAGCGCGAAGGGGAATCAAACCCGCGCAACTGTCTTCCGAAGTCCGGTCCGGGCGAACTCGATCAATATTACGGTTTCCCTTCCCGCGGCCAG  
TCCGGCGAGATGCGCTGATCGGCTTCCCTTCTATGCGCGAACTGATGCGTATCCCGGTGCTACCTACCACCAGCGGACCTTGCACCAACCGCACTCTGCTTTACCGCAAACTTATGACGCGCGCTATGC  
GCAATATTACCGAGAAACCCGTAAATCTTAAAGACGACGCGGCTGCGCTGTACCTACCACCAGCGGACCTTGCACCAACCGCACTCTGCTTTACCGCAAACTTATGACGCGCGCTATGC  
CTATGCCAACGCAAGGCAACCAACCGGCTGCGCGGTGCGTTTGGATGTGATGAAGCCGACAAAATCATCGCATCCCTAATGATTACAGTATTCACGGTCTCGGTCGCCAAGCTTATGC  
CCGAAACCGGTTATGTTTGTGCAACCGCGGAACACATTACCCCTGTACGCGGTGTAGGCAAACTGGATGATGCGAAAACCTGGAATGCAAGTATACACCGCATCGACGCGGAAACCATGG  
AGATCGCATCCGAGTAATTTGGTTGACGGTAACTTGGACAACGCGGATGCCGACTATCAAGGCAAAATTTCTTTTGCCACCTGCTTACAACCTCCGAGCGCGCTGACCGTACAAGTGGCTC  
TTCCAACGAGCAGGACTGGTGGCTGTTTTCGACTGAAAGCCATCGAAGAAGCCATCAAAGCCGCTGACGGTAAATACATCATGCCCAACCGTAACTGCCTCAACCGTTACCGTATTGGATGTCA  
TCCAATAACACCGGTTATATCCCTGTGCGCAACTCTCTCACGGCTGTAAACCGCTGACGGTAAATACATCATGCCCAACCGTAACTGCCTCAACCGTTACCGTATTGGATGTCA  
GCAACTCGGACGATTTGTTTCGCGGCAAAATCAAAGCGCGGATGTGGTCTAGCCGAACCGCAACTGGGTCTCGGCCGCTTACACACTGCATTGACGCGTCCGGCAATGCTTTATACGAC  
ATTGTTTATCGACAGCCAAATGAGTGAATATTGACGATGCGATCAAAGCTTACAAGGCGAGAAAAATCGATCCGATCAACAAAACTGCAGCTTCACTATCAACCGGTCACAAC  
CATACGACCATGGGCGAAACCAAGGAAGCCGACGGTCAATGGCTGGTGTCTTGAACAAATTTCTCCAAGACCGCTTCTTGAATGCCGTCCTTTGAAACCGGAGTGGCGACCAATTGATCG  
GCATCTTCGCGCGACGAAATGCGTCTGTTACACGCAACCCGACTTTTGCGCAACCGCACGACTTGTGTTTGGTTGCCGCTCCAAACTGGAACCGGGCAAACTTGGGACGCGCAAGACCC  
GATGCTC

SEQ ID 4328

GTGGTTC  
SEQ ID 4328  
VSGRQGPGRRIKFFSHRLAVRKFVPCRLSKBCCMSDEKLBQNGLSRRSPFGTAAASGAGIAGAGLLGLAGCSKDGEBQAAANASGAAPVAKAQGSEKPGQLSSEVGPGLDQTYGYFLSGGQ  
SGEMRLIGLPSARELMRIPVFNMDSATGWGRTNESLKVNGNITESTRKLKDSGLRCYPNGDLHHPHLSPTDQTYDGYATANDKANRRVCRVRLDVMKADKIIDI PNDSGIHGLRQRY  
PKTYGVFANGEHITFPVSGVGKLDDAKTWNAVYTAIDGETMELANQVLVDGNLNGDADYQGYKSYFATCYNSEKALTVQGASSNEQDWCVVFDLKATEBGIKAGDFKEVNGVMLDGREA  
SKYTRYIPVPPNSPHGCNASPDGKYTIMENCKLPPTVTVVLVDKLLDLFAGKIKERDVVVAEPQLGLGFLPHTAFDGRGNAYTTFLDSQMVKWNIDDAIKAYKGEKIDPIKQKLDVHYQPCHN  
HTTMTGETKADQGNVLVSLNKP SKDRFLNAGPLKPECDQLIGISGDEMRVLHNDPTPAEPHDLCLVAASKLNPCKTWDKDKPWF

SEQ ID 4329

[illegible]

SEQ ID 4330

MNPSFVPLFLVTLILLGVVSNNSITVSATILLMLQQTALVQFVPLVEKEGLNLGIILLTIGVLSPLVSGRAQVPPVAEFLNFKMLISAVFIGIFVANLAGCGVPLMGROQFVLVTGLLIGTV  
 IGVAFMGGGIPVGPLIAADILLSFVAGKV

SEQ ID 4331

ATGGTCATTTCCTGATTCTGTCGTGTGTTGCCGAATCGGGCGACCTGTGTGAAGGTAACAAAAAGCCGCCCGTTTTCGAGCGGCTGTTTTGCGTATGGGATGGATTTCAAGCAAGCG  
CAAAAAGCAGCCGACGCTGTGTGGTACCAAPAGCAGTAAGCGGTTG

SEQ ID 4332

MVIFLILSCVABSGDLCEGNKKAAPFSSGLFCVWDGFOASAKSTARLCGTNSSKRL

**SEQ ID 4333**

ATGACCATGGATGCAATGCCCAAAACGCGGTACAAAAAGAAAACCTGCACACTTGCAGCACTTATTGTGATGATGCGCAGGATTTTTCGCCCATGCTTCTCGATGCAGGGCGGGAGCACA  
CGCTCATACAGGAATCGATGATTTCCGAAATCCGCAACCGTTCGCGCCCTGATAGCCGCGCAAGCGGCAGCACTTCAGCGCAGCAGCCGCCGCGAGTTTACCGATGCCGCCGATTTTTCG  
CGCACGGATTCTCGTATTGGCGTGCAGACGCTTCCATCTGGACGTATCGTGCTTCAGATTTTGA AAAACCGCAAAACAGCGCGCTCGCGCTTTGCCGAAAAACACCGCCTGTTTTCACA  
CCGCAACAGCCGAATTTGACGCTGAACAAACACAAAACCGCGCGCTCTGCACATAGAAACCGAACACGAAGTCGAAACAAAGGCACACCTGTGCCCAACAGCCTCGCATTTGTGCCCA  
AAGTCACACCCCTACCCCTG

**SEQ ID 4334**

HTMDAMPQTAVCNENLHTCSIIVDDAQDFSPMLLDAGRDPTLISESMPIQRTVAALIAAERHDFSRSSPAEFTDAADFPAARILVLGVRFFHLVLSLLQILKTANKRACRFABKRLRFFTPAQAEISLNKHKNRRLLTETEHEVENKGNPVANSIAFVRKLTLEPL

**SEQ ID 4335**

ATGCTTGCCAAAATTCCCGACGGCGATACATACAAACGGATTFTCCACCCGAACAGGACACACATGAAAAAATCATCGCTTCGGGCTTATCGCAACATTGCGACTCACCGCTGCCAAG  
ACGACACGCGAGGCGCGGCTCGAACGGCAGCAGAAACAGATTGAAGCCCTGCAACAGCAGCTCGCAGCAGGCAGACGATACGGTTTACCAACTGACTCCCGAAGCAGTCAAAGACACCAAT  
TCTTGCCACGGCGCAGGCAAAACGGCAACACGGTCAGCCCGTTACCGGCAAAAGACGGGCAGCAGTATATTACGACCAATCGACAGGAAGCTGGCTGCTGCAAAACCTGATTGGCGCGGG  
GCAGGCGCGTTTATCGGCAACGCGCTGGCAAAACAATTACACGGGCGGGCAACCAAGACAGCCCGTCGCCGCTGCGCGCGTGTGCTTACCATCAGTTCGACGCGCCCAATGCGGCA  
CCAGCAGGGATTGGAACACGCGCAGCCTTCGTCGCAAAACAACAGGCGCGCAGGCGCAGCTGTACCGCCGACAAACGCGCCGCGCGTCAATTACGCGCGTCCCGCTATGCGCGGTTTCGG  
CAGCAAGCGGG

**SEQ ID 4336**

HLAKIPDGTGQIPFHPRNTHMKKIIASALATTFALACQDDTQARLERQOQKQIEALQQLLAQADDTVYQLTPRAVKDTIPAAQAQANGMNGQFVTGKDGQQYITYDQSTGSWLLQSLIGAA  
AGAFIGNALANKFTAGNODSPVARRARAAYHOSARPNA RTSRLNTRSLRAKQAAQAORYRPTTRPPVNYRRPAMRGFGRRR

**SEQ ID 4337**

ATGCCCTTAACAAATACAAAATGCGGTCGTGAAGAGCCCTTCAGACGGCATTGACGCGCGGGGTTTACCGCCTTCTGCCGAACACCGGCATAGCGGGACGGCGGTAATTGACGGGCGGGCGC  
GTGTGCGGGCGGTAAACGCTGCGCCTGCGCCGCTGTGTTGTTTGCACGGAGCGTCGCGGTGTTCAATACCTTCGCTGTGTGCGCGCAATGGGGCGCTGCGGCACTGATGTGTAGGCAGACACCGCGC  
GACGGGCGACGGGCTGTCTTGGTTGCCCCCGCGCTGTGAATTTGTTTGCAAGCGCGTGTGCCGATAAACCGCGCTGCCCGCCGCGCAATCAGGCTTTTGACGAGCCAGCTTCTCTGTCGATTG  
GTCGTAATAATACTGCTGCCCGCTCTTTGCCGGTAACGGGCTGACCGTGTGTGCGCTTTTGCTCGCGCTGGGAGCAAAATGGTGTCTTTTGACGCTGCTTCGGGAGTCAAGTTGGTAACCGTATCG  
TCTGCTGCTGTGCGAGCTGCTGTGTGCGAGGCTTCAATCTGTTGTTGCTGCGCTTCGAGCGCGCGCTGCGTGTGCTGTCTGCGAGCGCGGTGAGTGCGCAATGTGCGCAATAGCGCGGAGCGCA  
TCAATTTTTCATGCGTACCTGTTTCGGGTGAAATACGGTTGTATTGTATGTCGCCCTCGGGAAATTTGGCAAGCATTTCTGCCGCGCAATCG

**SEQ ID 4338**

MFLTNTKMPSESSEPSDGDIDAPGLPPSAETAHSGTAVIDGRARCRAVTLRLRLFLFC<sup>2</sup>TEAA<sup>3</sup>R<sup>4</sup>VQ<sup>5</sup>I<sup>6</sup>PAGARIGACGLMVGSGTRATGDGAVLVARPCEFWQ<sup>7</sup>Q<sup>8</sup>RVADK<sup>9</sup>ACRRANQALQQ<sup>10</sup>PASCR<sup>11</sup>L  
 VVNILLV<sup>12</sup>FPAGNGLTVVAVCLRLGRNGVDFDCFGSLQVNRIVCLLC<sup>13</sup>ELLQGFN<sup>14</sup>IFLL<sup>15</sup>PFEPRLRVVL<sup>16</sup>AGGCECCDKRGGD<sup>17</sup>DFHVC<sup>18</sup>PRVVENRL<sup>19</sup>YCI<sup>20</sup>AVGN<sup>21</sup>FGKHSAGKS<sup>22</sup>

**SEQ ID 4339**

GTGCAAAACAACAGCGGGCGCAGGCGCAGCGTTACGCGCCGACAACGCGCCGCGCGTCAATTACCGCGTCCCGCTATGCGCGGTTTCGGCAGAGCGGTAACCCGCGCGCTCAATGC  
CGTCTGAAGGGCTTTCAGACGGCATTTTGTATTGTTAGGGGCGATTGTTATGTTGCCGTTTGATTTTCAGACGGCATTTTGTTCACAGCGTTTGATGTCGGGATGCAATTCTGATCTA  
CGTGGCTTGGCAGGGCGGCATTGTCATACCGCGCTTGGGTTTTCAGACGGCATCATATCGAACCGTCAAGCGG

**SEQ ID 4340**

VONNRERRRSVTARORARPSITAVPLCAVSAEGGKPGASMPSEGLSDGIFVVRGIVMLPFDFOAFPCFOAFDVGMAILIYVRWQGGIVIPPLGFOQTASYRTVKP

SEQ ID 4341

TTGGCAACGATGTGAAAAATTTCCGTAAATTCAAATATCTAGATTCCCTTCCTCGCGTGGGAATGACGCAGAAGGGTTTCAGATGCAGGATGGACATTCCTGCCCTACCCAATCTCGCCCTACGGC  
CTGACGGTTCGATA

**SEQ ID 4342**

LAT IENFRKFKYLD SFLRGND AEGFOMQDGH SCLPNLALRLDGSI

**SEQ ID 4343**

ATGTCGGCGCCGAATCAGCGGCCGACAGGGATACCGCCCAATAATGCCACCCCGATGACCGTACCGATCAGCAAGCCCGTTACCAATACCGGCTGCCGTCCCAATCAAGGCCACGCCGAATC  
CGCCAGCCAGCCAGCAAAATACCGATAAAACGCGGGATATCATTTTAAAAATTCAAAAATTCGGCAACAGGAGGAACCTGCGCCTTTCTGTAAACCAACGGACTCAAAACCCCTATGGT  
CAAAAGAATGATACCGAGGTTCAACCCGTGCTTCTCGACCAACGGGACAAACTGTACCAATGCCGTCTGCTGCATCAGCAGCAATATGGTTGCCGAGACGGTAATCGAATTGTTGTGCTG  
ACCAACCCCAACAGAAATCAGCGTAACAGAAACAGGGGAACAAACTGAAATTATCGGTTACGACACCTGACCAAGATTCCTTGCCGAGC

SEQ ID 4344

MSAALISGGTGI PPINATPMTVPISKVTTTCGRPIKGTTHPASQATRIPIKTADIILKFKNSATGGTCAFPETNGLKTPHVKRMIPFPNCPSTNGTACTNAVCCISSNMVAETVIELLLL  
TTPNRISVSTNRCGKILKPIGYD/TLTKDSFAS

**SEQ ID 4345**

ATPACGAAATCTTGGCGTATAATCGCATCCATAGTTTTTTCGCAAAAGGAAATAAAATGTCGATTCAAGAAATTTATTACAATCAAGAAACCGGTTACGAATACGCTTTCCGCCAAATCGT  
ACTGTAAAGCGTTTGGCCCCCATTTGACCAACCTGAGAAAAGGAAACAAGAGCGATGACTACCTCCAATGCCCGTAACCCACTGTGACCATGAACAACGGCGCGCCCGTTGCCGACAATCA  
AAACAGCCTGACCGCGCGCGCGCGGCCCCCTGCTGACGCAAGATTGTGGCTGAATGAAAACTCGCGACTCTGTGTGGCGAAGTATCCCCGAAGCGGTATGACGCGCAAGGTTTC  
GGCGGTTTCGGTACGTTTACCGTAACACAGACATCACCAAATACACCGCGCCAAAATTTTCAGCGAAGTGGCGAAAAAACCAGAGATGTTTCGCCCGTTTACCAACGCTGGCAGGCGAGC  
GCGGCGCAGCGGATCGGAAACGCGACATCCGCGGTTTTCGCTTGAAATCTATACCGAAGAAGGCACTGGGATGTGTGTCGGCAACAACACGCCCCGTCTTCTCTGCGCGACCCGCGCAA  
ATTCCCCGACCTGAACAAAGCCGTCAAAACGCGATCCGCGCACCAATATGCGTTCCGCCCAAAACAACCTGGGACTTCTGGACGCTGCTGCCGAAGCCCTGCACCAAGTTACATCGTGATG  
AGCGACCCCGGTATCCCGCCAGCTACCGCCATATGCACGGCTTCGTTTCGCATACCTACAGCTTCTGGAACGAAGCGCGGCGCAACGCTTTTGGGTGAAATTCCTATTTCCGCAAGCGCAGCAAG  
GGATTA AAAACCTGACCAACGAAGAAGCTGCAAAATCATCTGCCAGCAGCCGCGAAAGCCATCAGCGCGCACTGTACGAAGCCATCGAGCGCGCGAGTTCGCCGAAATGGACGATGTACAT  
CCAAGTATGCTGGAAGCGATGCGCAAAAGATGCTTTCATCATCGGTTTGACTTGACTGCAACAAAGTTTGCGCGCGAAAAAAGACTATCCGCTGATTGAAGTGGGCGGAATTCGAGTTGAACCGC  
CCGCAAAACTCTTTCGCGGATTTGGGAAACCAACCGCCCTTTCACGCGCAACTCTGCTTCCCGGTTATCGCGCGAGCCCGGATAAAATGTTGCAAGCCCGTTTGTTCATTTACGCGCAGCGCGC  
AACGTTACCGCTTCTGCGGCTGAACTTTCGCCCAATCCCCGTCAATCGTTCGCGCTTGCCTGTTCACAGCAACACGCGCGCAGCAAGGCCCGCGCGCAGCGCAACTACGCGACGCTTCGCGCA

CTACGAACCCACAGCTTCGGCCAATGGCAGCAACACCGACTTCGCCGAACCGCTTTGAAATCAACGGCGACGCGGCACACTGGGACTACCGCAAGACGATGACGACTTCTCAGC  
CAACCGCGCGCTTGTTCAACCTGATGAACGACGCGCAGAACAGGCTTTGTTGACAACACCGCGCAGCCATGGGCGATGCGCCGACTTCATCAATACCGCCATATCCGCAACTGCT  
ACCGTTGCGACCGCGCATACGCTGAGGCGTAGCAAGCCCTCGGACTGACCGTGAAGACGCACAAGCGTCCGCGCAGCCGATCCGCGACTGGGTCAGGCGGTTTGTGTAAGGGG  
CATATGTGTGATGGAATGAAGAAATCTGTCCCGCGCTCCGATACCGGAATAACCGGGCATAAATGCGCTGAAACGTCGTTGACCGTTTCAGACGCGAT

## SEQ ID 4346

ITKILAYNRHSFCKRKIKCRFKFITIKKPVNTLSAKSYCKPFAHLTLNRKGTTRAMTTSKCFVTHLTMNAGPVDNQNLSLTAGPRGPLLITQDLMLNEKLADFVREVI PERRMHAKGS  
GAGGTTTVDHITKYTRAKIFSEVGGKTEMPARFTTVAGERGAADAERDIRGALKFYTEBGNWDVVGNNTPVFFLRDPKRPDLNAKVRDPRTNMRSTANNWDFTWLLPEALHQVTIVM  
SDRGIPASYRHHMFGSHTYSPWNEAGERFWKPHFRSQOGIKNLITNEEAAKI IADRESHQRLDYEAERGEFPKWTMYIQVPEADAEKVPYHPDLTKVWPKDYPLIEVGEFELNRN  
PENFFADVEQSAFAPSNLVPGIGASPDKMLQARLFNYADAQRYRLGVNFRQIPVNRPRCPVHSNQRDGGRADGNYGSLPHYEPNSFGWQQQPDFAEPLIKINGDAAHWDYRQDDYFS  
QPRALFNLMDAQKQALFDNTAAAMGDAPDFIKYRHIRNCTRCDPAYGEGVAKALGIVTEDAQAVRATDPAIGQAGILL\*GGIMMETERILSRAYRYK\*PGIKMPSSETSPDRFRH

## SEQ ID 4347

ATGCTATTAAATTTGCGGATTTGAACCTTGATAAAACATTTGTCCGCGCTCAGCAGCGAGGTTACGAAAGCCGACGCGGATTACGCGCAAGCTATTCGCTTTGCTTTGGAAGGCT  
GGGACATCATGGCTTCGCGCAACCGGCTCCGGAACACCGGCTTCCTGTTTACCGACTTTCAGCGACTTGACCAACCGCAGCGAAAAACCGGCAAGGCGCGCGCTGCTGCT  
GGCACCAGCCCGCAAGTGGCGCGCAAGTCGAGAAAAACGCACTGGCGTATGCCAAAAATATGCGCTGCTTCGCGACCGTCAAGCATGCTCGCGCGCAGCTGCTTCGCTACCAACACCGC  
GCCCTGAGCAACCGGCTGCTGTTGTTGCTGCCACTCCGCGCGCTGACGACCTGATGCAAGCGCAAGTGTGATTGTAACGCTTTGGAAGTGTGATTGTTGGAAGCGCGGACCGTA  
TGTGTGATATGGGCTTTATGACGACATCGAAACCATCGTGAAGCCACCGCGCGACCGTCAAGCTTTATGTTCTCCGCCACTTGGGACGGCGCAGTCCGCAACCTGCGCGCAACCT  
GACCAAGACTCTGAAATTTATCGAAGTCGAACCGCTGGAGCGCAAGGCAAAATCGAAGAGCAGTGTGTGATGCGACGATATGCGCCACAAAAACCGCTGCTGACCAACCTGCTCGCG  
GATGCAACATCGACCAATGTGTGATTTCACGTCACCAAGCGATGACCGAAGTCATCGCGGATGAAATGTACGAAAAAGGTTTCGCGCGCAACTGCTGACCAACCTGCTCGCG  
GCTGGCGCAACCGCAGCTGACGATTGCTGTAAGCGCGCTGCAAAATTTGTTGTCACCGGACGCTGCGCGCAGCGGCTATTGCGATTACGTTTCCGCAAGTGAACGAATACCTCAAGTCCAAAAATCGAAAA  
GCCGAACAGCGCGAAGACTGCTCCACCGCATCGGGCGCAGCGCGCGCAGCGGCTATTGCGATTACGTTTCCGCAAGTGAACGAATACCTCAAGTCCAAAAATCGAAAA  
TACATTAAACCGCAACTGCGCGAAGTACCATCGAAGCGATGAGCGCGCGCAAGCTGCGCAAGCGCGCAAGCGCAAGCGCAAGCGCGCGCTGCGCGGATAGGAAATCGCGCGCG  
GGCGCGGATATAAACCGCGCAAGAGGCTTCCGCGCGCAAGCGCGCGCGGAGGTTTCAAGAAAGAGCGTTTCAAGAAAGAGCGTTTCAAAAAACCGCGCAAGGCTTCAAGGCA  
ACGCAAGCGCGGACTCTTTGCGCGCAAGCGCAAGCGCGCTTCAAGGCA

## SEQ ID 4348

MSIKFADMLDKNLISAVSSEGYESPPIQAQIPFALBGCDIMASQTSKGTAAFLIPTLQRLTKRSEKPGKPRALVLAAPTRELAAQVEKNALAYAKNRWFRFVSIVGGTSFGYQTR  
ALSKPVDLIVATPGRILDLMSGKVDFERLEVLILDEADRLMDGFIIDIEITVEATPADRQTLILSATWDGAVGKLARKLTKDSEIIEVERVDGQKIEBOLLYCDMDRHNRLDLILR  
DANIDQCVITFTSTKAMTEVIADLEYKGFANCLHGDMPQWRNRLTDLRKGKRLILVATVAARGIDVPTITHVINYLDPKAEDYVHRIGRTGRAGRTGIAITFAEVNEYVKVHKIEK  
YINRKLPELITTEGMEPARKRKSGAGKPKGKGWGDRLSGRRGDHKGKKGPGKTRGEGFKKKGKDSFKKTGEGFKGKRKAGDSFAGKSERYRDR

## SEQ ID 4349

TTGATCTTGCAGAGCTATCTGTGCGAGTTGCGCTCGATGTAAACCAAGCAAGCGCGCTTGCAGCAACCTGTAACTTCACATTCCCGTATCGTTACCTTCCCTGCTTCAGCGCGT

## SEQ ID 4350

LILQSVSVQVADVNMHQAACDNFVTSHPYRPSLQAV

## SEQ ID 4351

ATGGCTTCGTATGACGATATAAGCGGAGATGATAGGGTTTGGCCGAAAGGTCAGCAATCGGGCTTAATTACAGTAAATTTCCGTTTTCCTTTATCTGCTGAAATCAATGA  
CCGACATCAACCGTTTCCCAACCGCTTGGGCAAAAACATCAACACCTTATGAAATGGGCGAAACGCAACCGCATCGAAGCCTGGCGCATTTACGACCGGACATCCCCCAATTCCTTT  
TGCGCGTGTATGTTACGGCGATCGAATCCACTTCAGGAATACGATACCGGCTGGCTGATGCGGCGCGGAGAAATACGAAGCGTGGCTTGGCGAAGTATGGAAGCGCGCTTCGTTTAC  
GGTTTGAACCGCAACAAATCCGCTCTCAACCGCGGCAAGCGCAAAAGGTTTGCAGCAGTACGAGAAACCGCGCAAGCGCGGCGGAGATTTCGTCATTGCCGAAACCGCGCGCAAGTTT  
GGTCAACCTCGCAAAATCTCGACACCGGCTTCTTCTCGATCAACGCAACCGCGCAAAAGTTCGCGAAACCGCGCGGCGGCAAGCTTTTGAACCTGTTTCTTACACCGCGCAG  
CTTACCGCTTATGCGCGCACCGCGCGCGGCGGATCCAGCGAAACCGTTCGATTGTTCAACACTTATCTCGATGCGCGGAGGCGCAATTTGAAATTGAACGGCATGATATGGAACCGCAC  
AAATCGTTCGCGCGGCGGCTTCCAAATCTTCAGACCGCATATGGGCAAGCGAGGCGATTCGACCTCATTGTGATGAGACCGCGCGGAGTTTTCACACGCAAGAAATCGCGCGCATCC  
TCGACATCCAGCGGACCATCAAAACTCATAGACGGCGCGGTAACCTGCTCGCTTCAGACGGCATTTGTATTTTCAACAACCTGCGGAGCTTGTGTTGAGCATTGCGGTATCGGA  
ACAATACCGCGTGAAGACATTTCACAAACATCCGTTCCGGAAGATTTCGCAACAAAAATCCACCGGTTTGGGAAATCCGCGCAACATCT

## SEQ ID 4352

MASYDDISGEYRVCPRSSNRALITVKFPSTFLCLKSMTDITPFANRLGKNIKHLMKMAKRNIGIARWRIYDRDIPQPPFAADVYGDRIHQEYDFWMLMRPGEYEAWLAEVLEAVPVT  
GFPEQIRLKRERQKGLQYKRTGKAGDFVIAENGRKFWNLDKYLDTGFFLDHRNRTRKVGETAAGKRFNLNFSYTGSGFTVYAATGGAASSETVDSNTYLDWARRNFELNGIDMERH  
KIVRADVPYQLQYAYEGRQFDLIVMDPPSPNSKMPGILDIQRDHQKLIDGAVNLLASDGLILYNNLRSFVLDSVSEYAVDKISKQSVPEDFRNKIHRCWEIRKHS

## SEQ ID 4353

ATGCCCAAGCCCTATCTGCACGCTATCGTGCGAATCCCAACCGAAAGGAAAAATATGAGCAGCGAATTAATCGTACACACCGGCGATGCGCGCTTCGAGCAAGATGTTTGAATCCG  
ACCTCCCGCTCTGCTGGAATTTTGGGCTCGGTGCTCGGCGCTCGCAAAATGATTCGCCCGATTTTGGAGCAGATTCGCGCGCAATTTGAAGCGCTCTGAAAGTAGTCAAAATCAACAT  
CGACGCAACGAAAGCACCCCGTCCGCTTTCGCGTGCAGCGCATTCGACCTGATGCTGTTCAAAACCGCGAAGTCTGCGCACCAAGTTCGCGCAAGGTCAGCTGACC  
GCTTTGTCGAGGCTCCATCGCC

## SEQ ID 4354

MFKPYPARYRANPRKKGKIMSSELIIVHTGDAEFQDVLKSDLPVLLDFMFWCPCPKMIAPIILDDIAAEFEGRLKVKINIDNENATPSRFVGRGILPTLMVFKNGEVVATKVGALAKGLT  
APVEASIA

## SEQ ID 4355

GTGGCGCGCGGGAATAAGTTTTCTGTACGCGCCCAATCGCTTTGCAANTCTAAAAACCGGTCGACAGTATTTATTTTGAATAATTACTTTATATCAAGTA

## SEQ ID 4356

VGGDRNSFSPVPSQLILKNGSDSILFLKITPILK

## SEQ ID 4357

TTGGTTTGAACATTCATCTTAAAGATCTATTTAAACGGAGCATACACCGCGCGCGCTTCTGTACAGCCTCAAAACATTCCTTATCTTTGATAATAAAGTAATTTTCAAAAA  
AAATACTGTCCGACCGTTTGTAGAAATTCGAAAGCGGATTTGGGCGGTACAGAAAAATATTATCCCGCGCGCCACT

## SEQ ID 4358

LVLNHTLRIYINGAYTARAFYLSLKNIPYTLIKVIFKNILSEPPFRICKDGGTEKLSRPPT

## SEQ ID 4359

ATGACTGATTTTCGTTTGGGAAGCTGCTCCCTTGGCGCAACCGTTGATCATATCTGCAACCGTACCAACATGTCCACCGCGCAATTTGAAGAAATGGTGCCGCTGGCGCAGAAAG  
TGGCCCAAGTCCATGCCGATACCTTTCGCGGAAATTCGCGGCTGCTTGGCGATATGCGGGACGAGCTGCTGATGTCATATGATGAAGGAGAGCGGATGCTGTTTCCGATGATTATCA  
GGGTGTCGAGCGGCTGCGCGATGCCATCAGCGTATGATGACGAAACATGAAGAACACGACCGCGCATTCGACCGGCTCAAGAGCTGACCGGTAATTTCCAGCAGCCGGAAGGGCT  
TGGCAAGTTGAGCGCGCTTACGCGCTGGCAAGAAATGGCGGAGATTGAACGACCAATTCATTGGAAGAACGATATCTGTTTGGCGCGTACTCGATTCT

## SEQ ID 4360

MTDFSVWEAAPPFGATVDHILQRYHNHRAQFELVPLAQKVAQVHADTFPAETAGLLADMRDELIMHMKERMLFPMINQVGRGAAMPISVMHHEHEHRAIARLKEITGNFHAPEGA  
CGSWRLYALAKEMADDLNDHIHLENDILFARVLD

## SEQ ID 4361

ATGCCGCTCGAAATACGGTTTTTCCGTTTCAGACGGCATTTTCATGTTTCAGCCAGCAATTCGGGCGGAATCGGCGACACAGGAATCGGGTTGATTTGTCTGCATCGCGCGGTGAAGC  
CGCGTATAGATTTCCAGAACTTCGCGCGCGCGCTCTTCAAAATCTTCGGGTTTCGCGCTGCGCGTACACGCCCATTCGCCACTCCAGTTGCGGCCATCTGCTCTCTCGTCCG  
TGCCTTCCTATCCACAGGCGCGTCCGTCGCGCGGCTTTTGAATCGCCTGCTCCACGCCCAATGCTTCGGCAAGCGGTAAACCTGCGTTTGGTTCAGGTCGGAATCGGCGTATGTC  
CAGCGCGCGCTCGCGCTATTGGTAAAAAACCACGCGGAATCTCAACCTTATTACCTGTCCCGTAACCCAGCAGTCCGCTATCTGCGCGTGTAGTACAGGGTCAGCATACGCAGG  
CGGCTTCTGGCGTTGGCGAGCGAAAGCGGCTGATTGCAAAATGCCCTCTGATGAACGCCGAGGTTTGTTCAAAGGTCTGGAAGGTGTCGGTCAGATTGCGCGTTTTCGCGCTTACATTTG  
CATATTGCCCTTGCAGATTGCGGATGTCGCGCTTGCCTGCTCAAGCTGCGCGGGGTGTCGGGTATCGGCATATCCAGAAGCAGCGTGGTCCGCGCGGTGCGCGCGCGGAGCGTGGAGAC  
GACGCGGAATCGATCGCGCGGAACGCCCTACGACGAATCTTTTGCATTTGCTGAGCGCGGTATTCTGCCAACCATCGGACAATATGTGTGATAACTGCTGCGTATCCATTTTCTCT  
CCTGTCGAAAATATCCGATCATAGCTTCCGCGCGGTGCAATTTGAA

## SEQ ID 4362

MPSEIRFPFRFRHVSQAQFGRNAHRNRVDFVLRHAVKPRIDFQNPAPPSPFKIPGFARAVHAHCLPQFGLACHLFLVGAFRIPQAVGRRGFLNRLVHAQCPGKPVNLRFGQVGNRADV  
HAAVAVFGKTHARIFNLITCPRNQSVYLPVVQGGHTQAASGVGERKRLIGKRLMNDGLFKGLEVGQIGRLRAYTIGILPLQIADVPFCLKLAGVLAIRHIQKQGAAGAGGERGD  
DGGIDAAGNAYDESPCICLSGVFVQPSDNMCDNCLRIHPSCKRYPHHSLPAVQFE

## SEQ ID 4363

ATGGATACGCGAGCTTATCACACATATTGTCGGATGGTTGGACGAATACGCGCTCAGGCAATGCAAAAGATTGCTGCTAGGCGTTTCGCGCGCATCGATTTCGCGCGTCTCTCCA  
CGCTCGCGCGCGCACCGCGCGCTGCTTCTGGATATGCGGATACGCCAACACCCCGCGGAGCTTGAGCGGCAAGGCGGCACATCCGCAATCTGCAAGGGCAATATGCCAATGT  
AAGCGCGCAACCGGCAATCTGACCGACACTTCCAGACCTTTGAACAAACCGTCCGCGTTCATCAGACGGCATTGCCAATCAGCGCGTTTCGCTCGCCAAAGCGGAGAGCGCGCTGCGT  
ATGCTGACCTGCTACTACTACGGGAGATACAGGACTGCTGTTACGGGACAGGTAATAAGGTTGAAGATTTCGCGGTGGTTTTCACAAATACGGCGAGCGCGGTCGAGATCA  
GCCGATTTCGCGACTGACCAACGAGGTTTACCGGCTTGCAGGCAATGGGCGTGAGCAGGCGATTCAAAAGCCCGCGGACCGGCGCTGTGGGATACGGAACGACCGGAGCA  
GGAACAGATGGCGCGAAGCTATCCGAACTGAGTGGGCAATGGCGGTGACGGCAGCGCAACCCGAGATTGGAAGGAGCGCGCGGCAAGTTCTGGAATCTATACCGCGCTTAC  
CGCGGATGCGACACAAATCAACCGATCTCTGTGCGCGCATTCGCGCGCAATTCGCGCGGATTCGCGG

## SEQ ID 4364

MDTQAVITHVRLHDEYAAQANAKGVVGVSGDISAVVSTLAARTGRTLLLLDMPQIRHPQGLERARRHRNLQGGYANVSAQTNLTDTQTFEQTVGVHTAFANQPLSLANARSRLR  
MLFLYYGQIHLLVIGTGKGVDFGVGFPTKYDGGVDISPLADLTQTVYRLAEALGVDEATQKAPPTDGLMDTERTDEBQMGASYPELEWAMGVGTGRKPEDEBGRREVRLEIYTRHL  
RANQKINPIVCRIPPELLG

## SEQ ID 4365

TTGTTAATCCACTATAAACGCAAAATATCCCGTCATCCCGCACCATCCCCACCGGTTCAAACCGGCACGAAACTTTTCCGCGTCATTCGCGGAAAGTGGGAATCCGGAACG

## SEQ ID 4366

LLIHYKRIKSRHSRTIPTGSRNHNFSASFPRKWSGT

## SEQ ID 4367

TTGAAGCCCAAGCGGCATCGTGCCGCTAAATGTGCAACATATATTAACACGCGCATCTTGCCGCCAGCGCTTTCTCTATATGACTTTTTTAAGCGGGGAATGGGAAAATATTCATCA  
ACCCGCGCTCAATCTATTCAAATGCAACGCGCGGAGGCTA

## SEQ ID 4368

LKPKAASCRNLNQYINRHLAASFLYDFFKRGMKIFINPPSIYSNCTAGRL

## SEQ ID 4369

ATGCCGCTTGGGCTTCAAAACATATTCATATTTTATTATTGATTGATTCGATGCTGATTTTTCATCTGACGCTGTGTCGCTTTCGAGTTGAACGCAATTCGCCAAAAGTATTT  
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CAAGGGTCGCGCGCGCGCTTTGGCGCAACCTTTGAAGAAGCGGACCATGCAAGTGCGCGGCAAAATCAGTATTTACGAGCGCGCGGCAATTTACAGTTACCGTAAACGAAGTACGG  
CTCAAGGTTTGGGCGCTTTACGAAGCTACGAGCGGTTGAAGCGGAGTTCAGGCGGGAAGCGCGCTTTCGCGGGAACGCAAAACCTTTGCCGCTCGCTCCGCAATGTATCGGCA  
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CCAACCGCAAGATCACTGCAACGCGCTGTCGAAGCCCAAGCGCGCTGGAACCGCTTTTGGAGCAAGCTATTTGATGCGCGCAAAACCTGAGTGGCTCGCGCGCAAAATCCGCCA  
CCGCGCGCAAAACTTGACGAGCAGCGCGCTTCAATCGGCAAGCTGCGCAACCGCTGCTTACTCGATGACGCAAAACCTTCGCGCGCGCGCACGCGCGCTTTGAACGCAAAACCGGAGCG  
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CGCATGCTCGAAGCGCTTTCGCGCGCAGCATCTGGAACGCGCTTCTCGGTTGCAAAATACACGCGGACAAGTATCGTAAACGCTGATGTTTGAAGCAGGCGCAGAAGCTGCA  
CATTACCTTTCGCGCGGCAACCGCATGCGCTAAGCAAGAACAGGCGCAGCAGGATTGTTGATGTCATT

## SEQ ID 4370

MPWASKHIHIFYYLIDSMDFPHSDVLSVSELNAFAKSIENHLAGLWLAGVSNLTRAASGHYYPSLKDSRAQVRCANFKGAAARLAQPLKEGDHIEVAGKISIEYARGEFTITVNEVR  
LKGGLQLYBAYERLKAQQAEGAPFAERKKPLVPRPQICIGVPTSLAAALRDVVTTLKRRAPETPVIVYPAAVQAGSGFQIAQAKTASQRAECDVLIIVCRGGGSIEDLRAFNEEPVRA  
IETCTLPVSVGVGHETDPTLADFPVADVRAPTTGAELVSPNRQESLRLVQAQGRILKTVLEQRYFDASQRLDMLARQIRHPRQKLBQRAISIGKLAQTLYSMTQNLRAHTARFERQTQA  
LQHCPRFVSVYQDIVRLQALPAAPSRLLARRQSLTAQAALLEAVSPQHILERGFVVKWTRGQVIRNADVLKQQLHTTSPDGETDVRVSKQGGQDLFDICI

## SEQ ID 4371

TTGTTATATAATTTCTGTAACTTTGAATTTTCAGGCATCTTCAATAAATATTCGAAACGTATCAATCGTCATTCGCGCGAGCGGGAATCCGTTTTCGAGTTTCAGTCAATTC

## SEQ ID 4372

LFINFCNFEQFSSINYNVIVIPAQAGIRFLSFSEF

## SEQ ID 4373

TTGAAACCGCGCTGCAATGCTTGCTCACGCTTAAAACTTCATAACATCTCTTCTGTCAGTTGAAAAATAAAATTCATTTGCCCAATGGAACCTTATTAATAATATATAAAAA  
TATCGGGTTGGGTTTTATCCGCGCAAGATCGCGCTGAAACATTTCCGGTGTGCGGAGAGGTTCTGTTTTTCCGCAAAATCTTCGCGCTTCCGCTTCCGGAATTCGCGCTTTTT  
AGGACTCGGATTCGCTTTCGCGGAA

## SEQ ID 4374

LKPLGLAMLASRKNFTSSFCQLKNKISFAQNKLIKNYKKISGVVPIRPMRRLKHPGCAERFLFPTNSCGPLPDSRFLGTGFPFSRE

## SEQ ID 4375

GTGCGCGCGCAGCATTAGCGGTGCACCTTGCCATCGGGCAGATTACGCTTATTCGATTCACAGCGCGCGTGACCAAACTTATCGGCATAACCGAATCGGCGCGCGGAGATTGGAAGC  
TGACGACCGTAGGTGGATTTCAGTATCGCACTCGCGATGCTGGCGCGCTCGCGCGCTGTTCCGCACATGATGGAACGGGTAGGCGCGCGCAAGCCATATTTCCGCGCGCGCTGCTG



[illegible]

**SEQ ID 4376**

EQ ID 4376  
VPPAALAVHLAIGQIYYSVFNAPITKLIGITESAAGDWKLTIVGWIPSTIALANLGAASALPGTMMERVGPRAKIPAAACCFSLGFPVSFAVGVRTHNLFLLYLGNVGIGVGLGLGYIGPV  
STLKMFPDKPGMATGLAIMGFGGAGMLASPLSVSLNAPSNAAASVGVAETFAVLGLPYLALMFGAPTIRVPADGWKPEGYTVPKTKNQKPVSSNNHVNVSQAMKTPQFWLLFWVLCLNVT  
GIGVLQASVMIQELFSETSAGRQAAVGAAGAVSLLSLFLNMGRFLWSSVSDIKRKNTYTIFFVLGSLLYFAVPSIGEGGSKALPIGFCVIIISHWGGGFAAIPAYLKDLFGTYQVG  
AIIHGRILLAWSTAAVIGPVLVNYIRQSQIDSGIPAAQAYSVTMYIMAGLLTVGLLCLNAVKSVEHKKHEKDITKAARSGNPDETAISDAYLVEKVKSGDGI5VWNRWALAVIPLAYGVVM  
VFVKALDLFS

SEQ ID 4377

EQ ID 4377  
TTGCACAACTTTGTCCCCAAGCCGAGCGACGATTTCATCCGCAAACCGCCGCATCAGGTACAATATCGAACCGTCCGACCGAGGACGGCATTTTATCAACCCGTCCTGCCGCACACG  
CCGCAGAAGAACC GCCCTTATCAGGCGAGT

**SEQ ID 4378**

LHKLCPQSRSDDFIRKTAASGTISNRPTEDGILSTRPAHAHAERPYPYQAS

**SEQ ID 4379**

EQ ID 4379

TTGATGGTTACAGCGGCTCTGAGTGTGAACGATAAAGCCTTCGTTACCGCCGATTTGGATTACGAACATGCCCAAGCTTTATTACGTCGATGATCCTAAAGCGCGCCCGTAGAAATCAGCG  
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TCATCTCTGTGGCTGTTACGGCTGCAACCATGCTGCTGTGGAA CAGGGGGACGTTTTGCGCTGGTTGTGTCCGTTCCGGCTCATTACAGGAATGTGACTAACCGCATGCCCCAAAAATCGGG  
TGTGAAACAGATTACCGTACCCGATATGCTGTCATACCCGTTTGAACGTCATAAAAATACCTGATTTTATCGGTTTATTTGGCAATTTCCGCTGATGATTTGGGTATGGGTACGCGCGAATAATTTGCC  
GAAGTGGAAACCGTTCAAAACTGCGATTATCTTGAAATTCATGTGCGGATTGTGTGCTTTGTGCGCTTTTCCGCTGGGCACTTTTGATGTGGCGGGGCTGTTTATCGAACGCTTCTTCTCGCGTTATC  
TGTGTCTTTTGGGTCGGGCACTCCGCTGTCGGCGGAGATTCCGCGCTTTGACTGTGCTGCGCGCTACAAAATGTGCGGCAACCCCTGCCAAATCTGTAGCAGCAAGTGCCTCGTTACAGC  
AATCGCGCCCTCGAGGGCGACATTCGATCCGAACGAATGTATCCAGTGCCCTGCACTGCCAAGTGATGTACCAACCAGGATACGCGCTGTGCGCAAGTGTGGCGGAAAATAAGAAAAACAAAA  
CAGGCTGCTGCCAAATCAGGGGAATTGAAAAATGTCTCTAAGCAGCCCGAGGAACAGGTGCTGCGTTTGTGTCAACCCGAAACGGCGCAATCTGAAAAA

**SEQ ID 4380**

SEQ ID 4380  
LMVQRVLSVNDKAFVTADLDYELPQAYIVDDPKAPPVETSAFVEAPVAAASDITASDGIADAASAENGVSQNLWKQIWKAKQGGIVVVGIALTILLLVLPQDWTIVRYEKWYDRFRFAFLT  
TLFYIGWYQAQQLSVVNTLTPLSAILTFPHWEFFLMDDPIVILMLPTAATMLMNRGTPCGWLCPFGSLQELTNRIAKKLVGKQITVPHMLHTRIAVIKYILPGFLAISLYLDLSTAEKFA  
EVEPFTAJILKFKMCDWVFVAFAVALLIAGLPFERFFCRYLCPLGAGIALPGRFVFDWLRRYKMGNGNQCQICTHECPVQAIAPBGDIHPNECIQLCHCQVMYHEDTRCPQVVAENKKQK  
QAAAKSGELENVSKQPOQBVVRFVVKPETAQSEK

SEQ ID 4381

SEQ ID 4381

ATGCTCGAGAAATCTGCCCTATTTCACGCGACATCTGCCCTGAAGACCTTGCCTAAAGTCAATGAAGTCATCAACCGTGCAGTCAATCCGATGTGCGCACTGATTTCGCAAAATCGGTACATATA  
TCATCAGCGCGGGCGGCAAAACCGCTCGCTCCGATTATGACGATTTTGGCGGGTAAGCGCGTTCGGTTATGATGACGAGAACTGTATTTCGCTGGCAGCGATGGTTCGAGTTTATCCACACTTC  
CACACTCTCTCGACGACGATGCTGCTGATGAAGAAGCGATTTCGCGCGTGGCGGGCAACGGCAAACTCTGTTCGGCAATCGCGCGCAGTGTGTGGTGGGCGACTTTTATATACCGGTGCA  
TTTCAACTGATGGTTGCCCTCGGGCAGTATGCGCGCTTTTGGAAAGTGATGCGCGGATGCGACCAACTCATTTGCGAGGGAGAGAGTCATGCGAGCTGATGAACATCGGCAATACGGACATTACCG  
AAGAACAATATATCCGAGTCATCCAAATATAAAACGGCAAAATGTTTGAAGCTCGCCGCTCAAGTCGCGCGCAATTTTGGGCAAACTTCCCGCGGACAGAACAGCCCTTTGAAAGCATACGG  
TATGTACGCTCGGTACGGCAATCCAGATTTATGACGATGTGCTGGATTATCTCGGGGAAACCGGAAGAAACAGGTAAAAACCTGCGCGAGCATTTTGGCGGAAGGAAAAACGACCCCTGCCCTTTG  
ATTATCTGATGCGTCAGGCTTCGGAACAGGTTGCCAACGATGTCGCTCGCTTTGGAAATCGAGATCGGGCTATTTTGAAAAATCCGCGATTATGTGTCGCTCGGTTCGAGTGCCTTTGG  
CATATTCGATAGGCGAGGCGGCAAGCAGTCGATTGTGCCGTGCGCGCTGCGCTGTCCGACAGCGAAGTGAAGGATGCTATGATTACAGTGGCGAAGGAATCTTTGTGTCAGGCT  
GTCTG

**SEQ ID 4382**

SEQ ID 4382

MLENLPYFQRHLPELAKVNEVINRAVQSDVALISQIGTYIISAGGKRLRPIMTL LAGKAVGYDDEKLYSLAAWVEFIHTSTLLHDDVVDESILRRGRATANLFGNAAAVLVGDFLYTRA  
FQLMVASGSMRVLEVADATWIIAEGVEVQLMNTIGNFDITEEQYIRVIQYKTAKLF EAAAQVGAILGRASPGHEQALNDYGMVGTAFQIILDDVLYSGETEETGKNVGGDLAEGKPTLPL  
TYLMROGSEQVANDVTALEVADRGYFKIRIDYVVRSDALAYSIGEARKAVIDCAVALDALSDEVKDAMIQLAKESLVRVS

SEQ ID 4383

SEQ ID 4383

TTGTGCAAAATCCATTACCGCTCCTCTTTATCATTTGAAAGATTCTACTCCCGCACGCAAAACGAGTTTCAACCGTTGCACAAACTTTGTGCCCAAAGCCGACGAGCATTTTCATCGCAAA  
ACCGCCGATCAGGTACAATATCTGAACCGTCCGACGCGAGGACGCGATTATTATCAACCCGTCCTGCCGCACACGCGCAGAGAAGACCGCCTTATCAGCGGAGTTAGGAAAAATGATGTCCAA  
GCAACCCACCGAAGCGCAATGGCGGACGAGCGGCGCAGCCCGCTCTGCCAAGAAAACCGCCAAACCTTTCAAAGCAAGACCCGTCCTCCAAAGACGAACCGCGCAAAACCCGCCGCCAAGCT  
TACGGCAATAAAGCTTCAGACGGCATCAAGCTGCAAAACGCCGCCCAACACGCGCGCCGCAAGCGCAAAAGCAAAACCTCGTCGTCGCGCAATCCCAACCAAAAAATTTATGGAACACGCGCGCGGATT  
TGAAAGAACGCGCGCAGCACTGTGCGGTATGGAACCCGAACGCGCTGCAAAAGTGTCTGACGCTTCGGCGCTCGGCTCGCGCCGCGAATGGAAGANTGGAATCAACACCGCTGGGTATC  
GGTCAACGCGCAAAACCGCGCAACTGTGGCGACAAAGTTACCCCGCAGCAGCACGTTACCGTCAAAGGCAGCATCATCAAATCAAATGGCGCGACCGCTCGCGCGCATCTGCTGATTATC  
AAACAGAGAGGCGAATATCGTTTCCGCGACGACCCGCAAGGCCGCTCAGCATATTCAGCCCGCTGCCGCGCGCAGCGCGCTGGGTGCGCATCGCGAGCGCTTGGAACATCAACACCA  
CGCGACTTCTGATTCTCATTCTCCGGCGAATCTGCTCAAGCTTTGCCGCCGCCAGCTTCGAGATCGAAGCGGAATACCGCGTGGCGGTACTGGGCGGCGTACTACCGAACAATGCG  
CAGTCTCACCGAAGAAGCGGTGATGCTCGCAAGCGGCTTGGCAAAAGTCGAACGCAATCAGCAACAAGCGCGGCGAAGCGCAAAACAATGGTACAACATCGTGATTAAAGAAGCGCGCAAC  
CGCGAATGTCGCGCATATTCGAAAGCAAGGCTTCAGTTCAGCGCGCTCGTGGCGGTGCGCTTCCGCCCATCGGACTGCCCAACCGCTCAACCGCGGACAGTTCTACGAACTCAAC  
CGCGCGAAGTCGCAACATCTTCAAATGGCGGATATGCTGCTGCCGGGCGAAGCGCGCGCAAAAGCC

**SEQ ID 4384**

SEQ ID 4384  
LCKSTYSSYHLKDDSTPARKPLSTVAQTLSPKPQRRPHQRRIRYNIEPSURGRHFINPSCRTRRRRTALSGELGKMMSKQPTSKRQWRDGAAPSAKKTAKPFSKARPKDETRKTAQA  
YGKASDGKIQONAPKORAAKAKKLVRNPNQKIMEHARDLKERRSOLSRMEPERLQKVLAAAGVGSRRMEEWNNQWTVNGKTAQLGDKVTPDQHVTVKSGSIKILKWADRLPRIILY



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KQEGEIVSRDDPQGRVSIIDRLPQAASSRWVAIGRLDINTSGLLILITSGELVQRFAPSPFEVEREYAVRVLGLITTEQMRSLTEBGMLEBDGLAKVERITYBQGGEGANKWYNIVIKEGRN  
REVRRIFESQGLTVSRILVRVAFGPILGNRLKRGQFYELNPAEVANILKHAMLLPGERRRKKA

## SEQ ID 4385

ATGGATTGACACATATTCGGGAAGATTACAGCAAAACGGGAATTGTCGGAAGCCGATTGCGCCGATAATCCGATCGAGCAGTTCGAGCGGTGGTGGACGAGGCGGTACGCGCGGAGGTCA  
ACGAGCCGACGCGCGTCAATGTGGCGCGGTGACGCGGCGGGAGGCCAACAGCCGATATGCTGCTTTGAAGGAGGTTAATTCAGAAAGGTTTGTGTTTTCAGAAATACACAGCCG  
CAAGGGCGTTCGCTGGAACCAATCCGTTTCCGCGGATGACGCTTTTTCGCGGAGCTGGAGCGTTCAGGTGCGCGTGGAAAGGCGGTGTCGGAAGGCTGGCGGAGAGTTGTGCGACGAA  
TATTTTGAAGAGTCGCGCTATCAGAGCCGTTTGGGTGCGTGGGCAAGCGCGCAGAGCGAGGTGATTCCGAACAAGCGGTATTGCTGGCAAAGCGCGCGCGGTGCGGACTCAACATCCTT  
TGCACGTGCGCGCTCCCGCCATTGGGGCGGCTATATGTTGATTCCCGATTGATTGAGTTTGGCAGGCGAGCGCGAGCGCTGCACGACCGCATCAATACCGTTTGTGATGCGCG  
CTGGATACGCGAGCGGTGTCGCT

## SEQ ID 4386

MDLHNTREDYSKRELSEADCANPIEQFERWLEAVRAEVNEPTAVNVAVDGRGRPNRMVLLKEVNSEGVFFFTWYHSRGRSLLELNPFAAMTFWPELERQVRVBRVGRLEKLSDB  
YFESRPYQSLRAGANASQSEVIPKRAVLVAKAAVGLKHLVFRPPHGGYIVIPDLIEFWQGRSRSLHRIQYRLLDGGWIRERLSP

## SEQ ID 4387

TTGAACAGGAAAAACATATGCGCTGTAAGAACCGGAATCAGGTTTCAGACGGCATTTTTTCAGGGGAAAAATACGGACGGGAAGTTTTCGTTGTCGGAACGGAAGCCCGAATCCTCTT  
TATACCGAGGAATFATGATCGGACGGG

## SEQ ID 4388

LNKKHMPSENINQVSDGIFSRKYGREVFCVPNGKPESLSYRIGIMRTA

## SEQ ID 4389

ATGAACCAACCGTTACCTGCGCCGACAAACCACTTTGCGCGCGGCGGAGCGGAAACCGTTTTCGCGCTGCGCGCCGTCAAAACCTCAATCTGCCCCATTCTCGCAAAACCGGTGTCT  
GCGGACATGCAAGCGCAATGCGGACGCGCGGATATCAAAATGGCGGACACTCGGAACAGGCTTATCCGAAGCAGAAAAGCGCAAGGCAAGATTTCGATGTCGCGCACCAACCGCGCA  
AAGCGATATCAATCAATCAATCCCGGCTGCAAGCGGATGCGCTACCGCTCGCGACCTGCGCGCAGCATCGAAAGTATGTTTCAAAACAGCATGTCGCTTCTGAACTTCGCGCTG  
CCCAAGGCCCCCGCTTTGCTTCTACGCGCGCAATACATGATTATCTGCTGCGCGGCAACGTCAGCGCGAGCTACTCCATCGCCCAATTGCGCGACCAAGAAGCAATTTTGGAACTAC  
ACATCCGACGGCGGAAACCGGTGTCTGCTCGGAAATGATTTCGCGCAGCAACCAAGTCAAGAAAAAGGCAATGTCGCGCTTAAAGCGCGCTCGGTTCGTTTACCTTCGAGGAAGA  
CAGCGCAACCGCTCATCTGCGCGCAACGACACAGGCTACGCGCCCATCCGCGCATCTGCTCGACCTTATCCGCAAAACAGCAGCGCGCTGCCCATTTCTACTGGCGCGCGCT  
CATCAAGATGATTGTTATGCTTCGAAAGACCAAGCGGTGGCATGCGCTCGAAACACCTGCTTACCCCGCTATTGTCGCGCGGAGAGGCTGGCAGGGAAGAAAGGCCACG  
TACAAGACATGCGCGCAAGACACCCCGACCTGTCGGAATACGAAGTGTTCGCTGCGGCTCTCGGCTATGACCGAACAGCAAAATCTGTTGTGCAACAGCATAAGCTGCGCGA  
AACTGTTTTCGCGACGCAATTCAGCGCTCGCATCA

## SEQ ID 4390

MNHTVTLDPQTFAAGDGTVLAAAARQNLPHSKCNVCGQCKAELASGDIQMGHSEQALSEAKAQGKILMCRITTAQSDININIPGCKADALFVRLTPARIESMVPKHDVAFIKIAL  
FKAPPPAFYAGQYIDLLPGNVSRYSIANSFDPQEGILELHRRRENGVCSMTFGESEPKVKEGIVRVKGLSGFTLQEDSGKPVILPATDTGYAPIRSILLDLIRQNSSRAAHFYWGAR  
HQDDLYALEBAQGLACRLKNTCTFVLSRPGEWQGRKHVQDIAAQDHPDLSEYFVACGSPAMTQAKNLFVQHKLPENLFFSDAFTFSAS

## SEQ ID 4391

ATGACTTGGGAACTGTAATCGCTTGGAAATCCAGTCCAATTGAACACCAAAATCCAAATCTTACGCGGTGATCGACCGCATTCGCGCGCAGAACCAACGCGCAGCGAGGTAGTGG  
AATGCGCGCTGCGCGCGGTACTGCGGTAAATGAACCGCAAGTCTGTAAGAACCCATCAAAATAGGTTTGGCTTGGATGCAAAATTAACCGGAAAGAGGTGTCGACCGCAAAACTA  
CTTCTATCCGACTTGGCGAAAGGCTATCAATCAGCCAGTTGGATTGCGGATTGTCGAACACCGCAAAATGGAATCTGTTGTCGCGCGGTGTAAGAACCATCAAGTAAACCGCGC  
CATATGGAAGAACGACGAGCAATCCGTGACGAGGCTTGAACGCGCGCAGCGCATCGACTGAACCGCGCGCGCAGCGCGCTGTTGGAAGTGGTATCCGAACCGGAAATCGCTCG  
CGCGCAAGCGCTTGCCTACCGCAAGGCTTACACAGCTTGTGTAACCTGCTGGACATTTGCGACGCAATATGGCGGAAGGTTCGTTCCGCTATGATGCAACGTTATCGCTTCCCGGAA  
AGGCCAAGCGGAATTCGCGACGCGCGCGGAAATTAACCACTCAATTCCTTCCGTTTTCGATCAGCGGATTAATACGAAGCGCAAGCGCAATTCGAGATTTCGGAAGACGCGCGCA  
GTTTCAGCAGCGGACGATGCTGTTGCGACCGGAAAGCGGAAACCGCGGTGATGCGCTGAAAGAACGCGCGCAGCATACGCGCTACTTCCCGATCCCGATTTCGTCGCGCTCATCTT  
CAGATGCCCAATGCAAAAGCGCAAGATGCGCGAGCTGCGGAAAGAAATGCGCGCGGTTCGTTGCGCGATTACGCGGTGTCGGAATACGACGCGCGCGCTGCTACCGCCAGCG  
CGTGCAGGCTGCTTATTTGAAGAGCGCGCAAGAGAGCGGACAGGCAAGCGGACTGCCAAGTGAAGCGGAACTTCCGCTTACGCTGAACGAAGAGGATGGAATTCGCGGAC  
AGCGGATTACCGCGCCACGCTTGGCGCGCTGTTGGGCAAAATTCGCGATGCGACATTAAGCGCGCAAACTTGGCGAAAGAGCTTGAAGCCATGTTGGCGGAAACCGGAAACAGCATG  
CCGAATCATCGAAAAACAGTTTGAACAGATGACCGATACCGCGCGGTGGAAGCGATGTTGAGCAAGTCTGCGCAACACGCGCAAGCGGTGGAACAGTTTAAATCCGCGCAACGA  
AAAAGCCCTGAATCGATTGTTGGGCGCAAGTATGAAGACAGCAAGGCAAGCCATCCGCTCAGTTCAGGAGTTGATTAAAGCGCAACTTGCC

## SEQ ID 4392

MTWETVIGLETHVQLNTRKSFSGASTAFGAEPNAHSAVVECALPGVLPMNREVVEKAIKLGALDAKINRNVFDRKNYFYPDLPGYQISQLDLPIVEHGLEIVVGGDVKTINVTRA  
HMEEDAGKSVHEGLNGATGIDINRAGTLPLEVVSEPEMRSAAEAVAYAKALHSLVTLWDICDGNMABGSFRIDANVSVRPGQAEFGTFRRIKUNLNSFRPLDQAINYEAEQIEILEDGGT  
VQQAHLFDPEKGETFVNRLEDAHDYGYFPDPLLPVITSDAQMQKAKAEMPELPKEMARFVADYGVSEYDARLLTASRVQAAFYEEAAKESGQKPTAMNMNGELAATLNKESMELAD  
SPITAPRLAALVGIADGTLGKLAKEFAMWAEPESTIAEILEKHSLLQMTDGTGAVEAMVDEVLANNAKAVEQFKSGNEKALNAIVGVNKTSGKANPAQVQELIKALIA

## SEQ ID 4393

ATGAACGAGAACCGCACCTTTACCTTCCCGGATTTCGACCGGTTTACAGCTATGCGCTTTATATCGGCTGCAACATTTAAATATACATATGCGAAATTTTCGGAAGAAAGAAATTT  
ACGCTTCGAGCAGTTTGTCAACGCTCCCTATCCGTAGGGGCTGTTCTCCACTGCGCGCAGGATGCTATCCGCTGTCGCGGAAATTTGTGACAGCGTTTAACTGCAACCGCG  
TTTATAGTCGATGACGCGCAGATTTCCTATGCGGAAAGAACTTTCGCGCAGACGTTCTGTGCAAAATGGAAGACTGCGGCTTCCATCTGCTGTCGCGACCTTTTCAGACGCGCATCAGC  
TTGTGGCTCAACCGCAACGACAACTGCGTGAAGAGGCGCGTGTCTTTATCTTTCGCGGATGAGCAGGCAACCGGCTGTATATGCGGACCTTCGCTTTCGCGCACACCTGCTGA  
CAGCTTCGTTACAAGGGCGCTCAGGTGAAGAGGCAAGACACCGTCCGCGCATTAACCAAACTTCACGCTTACGTCCTCAACAACTGATGTTAACCGCACTGCAATTTTCGCGC  
CGCATTAATATGACGCGCGCATGAGCATTCGACAAAAACATCAAGTCAAAATACGCTGGAACCTTAAAGAGCGCGTCAAAATGAATTAACGACGATTCGCGAGGAATACGCGCAAGT  
TTGGAACGCGACGCTTATGTCATCTTCCCAAAACCGCGCGCAAGAGCTTTCGCGCATCGAAAGCAAAAGCGTTTCGATGATCCGCAAGCGTTATGAAATGCTGAGCATATGTTG  
CAAGATGAAGGACAGTCTGAAACAGAGCAGCGGCGATTTCAGACGCGATCCAAACGGAAGAACCGCTCCGCGGACAGTC

## SEQ ID 4394

MKQNRITFFPDPFTVSYAPLYRLQHLKYTLRKFPGKEIYAFEPQVNASPIRQGLFLHCPQDAYPILLREFVDRFRNCKRRLDAMTDFLMAEKLFGTDVLCQMEDCRPHLVLAHLSDGIS  
LWLNRRDNCVEBAGWSLSLRDEAGNRLYMATFAPVGTLLHTASVQGPSGEAKDVTTRITKQLHGLRPQQLHVTALQYFAAALKLDGAIGIAQKHQVKLEWKLKRRVKNYDAPQBYGAS  
LERDGYWHLPTQPKDLADIESKKRSMYRKRYEMLDVMVAKMDSLTETARGISDGTQTEKPLRRTV

## SEQ ID 4395

ATGACCAATACACATTGAACAGGACGAGCGCTGTTGCGATCCAAACAGATTTCGCGCTGCAACTGGCAAGCGCATACCTTCCGCGCATTCGCGAAAAAATCCGCGCTCAACGCGT  
ATATCACCATCGACCAAGATAAAACCTTGCAGAAAGCGCTGCGCGGACGAAACGCTGCGCGAGGCAAGCTTTCGCGACTTACCGCGGTTCGCGCTGCTACAAAGACATTTTCGCA  
AACCGCTGCGCGAGCGCTGCGCTTCCAAATGCTCGCAACTTCATCTTCCCTTACACCGCGACCGCTTCCAAACCTGCTCGACGAAGGTATGGTAACGCTGCGCGCACCAACATG  
GACGAGTTCGCTATGGGTTCGACCAATGAAAACCTATCTTACGCGCGCGGCAAAACCGGTGAATCCGGAACAGTACCGCGCGGTTCGTCAGCGGTTCGCGCGCGCTGCTGCGCGC  
GCTTCGCGCTGCGCGCTTCGTCGACACGCGCGCTTATCCGCAACCGCATCGCATGCGCGCATTAACGCGATCAAACTTACCTACGCGACGTTTCCGCTTCGCTATGTTGCTC

CTACGCCCTCCAGCTTCGATCAAGCGCGCCGATGGCGCAAAACGCCGAAGATGCGCGATTCTGTGAAATGCAATGGCAGGTTTTCGACCCCAAGACTCCACCAGCTTCGAACGCCGAAAA  
 GAAGACTACACCCCGGATTTGGACAAACCGCTCAAGGCGTGAAATCGGCTGCCCAAGAACTACTTCAGCGAAGGCAACAGCAGCCGATGTCAGAGCGGATTCGAAACACCACTTGATT  
 TGCTGAAAGCACAAGCGCGGAAGTGGTCGAAGTTTCCCTGCCGCAAAACAGCTGTCATCCCGCCCTACTACGCTCCGCTCCGAGAACGCCGCAACCACTTTACGTTACGACGG  
 CGTACGTTACGGAACCGCTGCGCCCAATTCGCGGATTTGGAAGAAATGTACGGCAAAACCCGCGCGGAAGGTTTGGCAGCGAAGTCAAAAGCCGCAATCATGATCGGCATCTACGTTACG  
 TCGCAGCGCTACTACGATGCTATTATCTCAAAGCCCAAAACCTGCGCGCCCTGTTGCCGATGACTTTAGACGCGCATTTGACAGCGCTGCGACCTCATCTCCGCGCGACCGCACCTCCG  
 CCGCACCCCAAAATCGGAGCGGATCTCTCCGGTTGAAACCTACTTGAGCGGACATTTACACCATCGCCGCTCAACCTCGCGGACTGCCCGCATTTGACCTGCCCGCAGGCTTCAGCGCGG  
 CGGACTGCCCGTGGTGATCAGCTTGTGCGCACTACTTCGCCGAAGCAAAATCTCGSTGCGCGCATCAAACTCAACAGCGATTGCGCAGCGCAAAACGACCGCAA

**SEQ ID 4396**

MTQYTLKQAGSLQSKQISAVELASAYLAALAEKNPALNGYTTIDQDKTLEAARAADERIAQGNASALTGPVAYKIDIFCTGWRASACSKMLDNFIPPTATVQNLDEGMVTLGRNM  
 DEFAMGSTNENSYGAANKPWNPEHVPGGSSGGSAVVAARLAPALGSDTGGSIQRPASHCGITGKPTTYGTVSRFGMVAAYASSFDQAGPNAQTAECAIILNAMAGFDPKDSTSFEREK  
 EDYTRDLKPLKGVKIGLPEYFSEGNSTDVQALQNTIDLLKAQGAELVEVSLPQTKLSIPAYYVLAASAEAGTNLSRYDGVRYGHRAAQFGDLEMYGKTRABGFGSEVKRRIMIGTYVL  
 SHGYDAYYLKAQKRLRLVADDPQAFARCDLILAPTAPSAAPKIGADTSPVETYSIDYTTIAVNLAGLPALFLPAGFSGGGLPVGVQLVGNYPARAKILGAHQIQLNSDMHGRPE

**SEQ ID 4397**

TTGGGTCATAAATCTCCATCTTAAAGGGCTTCGGGCGGTATGCTGATGCCGCTGAAGCGTATTTCGGATTATCTTCGATAACTTCGCGGTACGATGTACAGGCGGTTGCGCTACTTCGG  
 GCGAACGGCTTGGTATTCGGCGCGCGGTCGGTTTCGGTTACTTCGTTTCAGCAGCGCGAGGGCGACCTTCGTCGGGTGCGCATCGGCTCGATCGCGCTGTGTGTGATGTCTCGCAT  
 CTGTCGACCATAGTGAAAAATGCTGTTAATCT

**SEQ ID 4398**

LGHKSSILKGLRAVLLMPSEAYSDYSSITCGTMYRRLTSGATANYSAARSVSVTSSRRRRRATSCGCAIGSNPVLMPFCSTIVKMSFNS

**SEQ ID 4399**

ATGAGTCTTTACGCTTTGCTCTTGGTTGCGCTGGGAATGTGATGGATGCGGTTTCCGCTGCGCTGGCAAAAGGGCGCGGCTCAGGATGCCCGCGCAAAATTCAGCAACGGCTTTGG  
 TGTTCGGTACGGTTGAAGCGTTTCATGCCGCTGGCGGGCTGGTAGCGGTTTATATGCCAAGCCGTTTATCAGCGAATGGGACCATTTGGGTGGCTTTTGTCTGTTGGCGGACTGGGCT  
 GAAATGATGCGCGCAAGGGTTGTCGGCGAGCGGAGATGTGCGCGAAGCAAAACAGGAAGCCATGATGATGACGTTTGTGACTGCTTTTGAACCAAGTATTTGATTCATGATGCTCGCGG  
 GTGGGCTTGGCGTTTATGAGGTAACATCGCTTTGCCCGCCCGCTAATCGGTATGCGCGCTACGGTAATGGTTACCATCGGGCTGACGGCGGGAAGGCTTTTGGCGTATTTGTCGCA  
 GCGGTGCGGAATTTGCCGAGGTTTGGTGTGATTGCCATCGGTACATGACGCTCTTATCGCATTTGGGTTTGTATCA

**SEQ ID 4400**

MSLYALLLVALLGHSNDAPAVALAKGAARMPKRIATAALVFGTVEAFMLAGWVGFPYKPISEMDHWAFVLLGLGLKMMREGLSGEAEVRESKQESLWMTVLTPAGTSDSMIVG  
 VGLAFNEVNIAFAAVIGMAATVMVTIGLTAGKAFGVLFGRRAEFAGGLVLIAGTWTLLSHLGLIQ

**SEQ ID 4401**

ATGCTTTTCATGGCACTGACACTTGCCGACGTAGACAAATCGCCGACTCTCCCGACTGCACTGACTGCGGAAGAAAAAGAAAAATCGTTCAAGAATTAAACGACATTTTCACTATGG  
 TCGAACAGATGCGAGAACATCAACACAGCGCATCGAGCCGATGGCGCACCCCGCAGAGGTGCGCTCCGCTCGCTGAGACGAAAGTAACGAAACCGACCGCGCCGCAATACCAAGC  
 CGTGGCGCGGAAGTACGCAACCGCTGTACATCGTACCAGTAATTCAGGA

**SEQ ID 4402**

MLFMALTLADVDKIALRLSLQLTAREKEKSLQRLNDIPTMVEQMQNINTDGIEMAHPEVALRLREDEVETEDRAAEYQAVAPEVRNRLYIVPQVIEE

**SEQ ID 4403**

TTGCTTGGATTTTAAATATAACGGAATAATCCGTTGCGCGCGCAATTTGCGAGCATCGGATGCTGCCGACGGGTTTGAAGAGGGGAAATATGGGATTGGGTATGGAAATCGGCAAGC  
 TGATTGTGGCTTTTGTGGTCTGATCAATTCGTTTAGCGCGTTGCTGCTTTACCTTGACCTGACCAACGAGCAGACAGCAAGAGCGCAGGAAGGTGCGCGGACCGCCCGCTCGCGCT  
 GTTTCGCTGATTGCGGTATTTGCGCTGATCGCGGTCGCTATTGAAGGTTTGGGATCAGCGTGGTTGCTTTCAGGTGCGCGCGGGATTTTGGTGTGCTGATGCCATTTTCGATG  
 ATGAACCGCAACGACAATCCGCAAGCAGAAATCTCGCGCGCAGCGGAAACGGGCAAGCGCGCCCGCCGCAATGACGGGCGGATTCGCTGCTGCCCATGCCATACCGATACCA  
 TCGGTCCGGCGGTATTTTCGACTGTGATTATTTATGCTTCGCGAGCAAAACGTACAGCGATATCGCGCTGATTATCGCGCGCGGTTTGGTGTGATGCGGATTTGTTATGCCATTTTAAAT  
 CGTTGCCCGGAAGGTACCGCGCTGCTGCGCGCGCAGCGGCTGACGATTTTAAACCGCATTTATGGGTATGATGCTGCGCGCGGTATCGGTGGAGATTTGTTGTGCGGACTGAAACGATA  
 TTCCCGCAACTGCGAGT

**SEQ ID 4404**

LLGLIITEKSVAAACISIGLPHGPERGEIMGLMEIKLIVAFVLINPFSALSLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFIIGGALLKVLIGISVGSFQVGGILVLLIAISM  
 MNGNDNPAKQNLGAQPETGQARPARNAGAIAVVPPIAIPITIPGGISTVITIASAARTYSIALIILAAGLVVSAICYALLIVAGKVSRLIGATGLFILNRMGMLAAVSVELIVSGLKTI  
 FFQLAG

**SEQ ID 4405**

ATGTTTCACAGTGCAATGTATTACGGGCGAAACGCTTACCGCGCCCGGATCAAGATTATCGGAGTTTGAACGGCGCTGCGGAGTTTGAATAACGCGAGGCGCTTCGCGCAAT  
 TGGGCGTAACCGAACGTGCGCGCGCTGCAAAAATTTGCGCGCGCTTGGAGGCGGAAAAAGAGCGTTTTCGCGAAATGGTGTGCGAAGAGTTCGACGCTGCTGCAAGTACCGGTG  
 CGAAATCGTCAAGTCTATCGAATGATACGCTATTACCGCGCGCTTGCCTCCGAACTGCTTGCACAAAAACCATTCGACGCGAGCGAGTTTGAAGTACAGTGGCTTCGAGCCTTTGGG  
 GTGGTGTTCGCGTCAFGCTTGAACATCCGCTGTCGCGGATTTGCGTTTCGCGCTTCCGCTATGTCGCGCGGCAACGCGTCCGCTCAAAACCGCGCCGCGGCTGCGACGCTCA  
 GTCCGCGGTTGTTGATTTGGCTTCAGACGATTTCTCTGCGAGCGCGCTGGCTGGATGAGGCGGACACGCTCAAGGCACTCGAAGATACCGATGCGATGGCGTTTACCGGTTTCAGCGCA  
 TACGGGCGGCTTCTTGGCGCATGCGCGCGCAAACTCAAGAAAACTGTTGAGCTCGCGCGGCAACGCTTTATCGTATGCCCGATGCGGATTTGGAACGCGCGCGCGGAGAA  
 GCTGTTATTTCCGCTTCCGCGATGCGGCGCAATCGTTAACCGCGCAAGCGCATCATCTAACCGAAGCGCGAGCGGCTTATTCAGCTGTTTTCGCGGATGCGCCAAATTTGA  
 AATGGGAGACCGCAACATCCGATACCGCTTGCACCGCTGCACCGGAGATTTGCGGAGCGGCTTACGGGCGAGTTGAAGATGCGCTTCAACAGCGCGCGGTGTCCTGACCGG  
 AGGCAAGTTTCACAGGGTTCGGGTGCTTTTACCTGCGACGCTTTAGACAGGTAATCTGCTGCGCGCTGAGAGAGAAAGTATTCGCGCGCGCTGCGGCTGCTGCTGCTGCGCGG  
 GAAACGAGAAACACGCCATCTGCTTGCATGATTTCCCGCTGCGGCTCGGTGCTGCTGCTTATACCGCGGATCTGAACGCGCTGCGGCTTTCGCGAAAAATACAGCGCGGATCGG  
 TGTATTACCAACCGCATACAGCAGCGATTTGCGCTGCTTTCGCGGAGTCAAGATTCGCGTACGGGCGGAACTGTCGCAATTCGGGTGTACGAGTTGCTCAACGCTCAAAACCTA  
 CTGGCAGAAA

**SEQ ID 4406**

NFHSNVNFTGETLYRRPDQDYAEFERRIADLKMHGRAFAQLGVTERAARLQKFAGRLEAEKERFAEMVCEEVGRCLHECRAETVKSIELIRYARLAPKLLAHKTIATQASLSQVRFEPLG  
 VVFAVMPNPNYVQVLRFAVPAACAGNACAVKPAFVARVSRALFDLSDGIPLAGAMLDEADTLKAVEZTDAMAPTGSTHTGRILAAHAGANLKTIVLELGGSNFIVMPDADLERAAAE  
 ACYSRFRDAGQSCNAKRIIVTEAADRFIQLFLAECARKMGDPKHPDITLAPLHREDLRHVQGVEDAVSNGAVLCTGCKVPGSGWFTPATVLDVNPACRVVREEVFPVALILRA  
 ENEHAICLANDSPFLGACIYTADTERANRFAEKIQAGSVFINRHTSSDLRLFPFGVKDSGYGRLESEFGLIYEFVNVKTYWQX

**SEQ ID 4407**

ATGAACCTTTGCTTTATCGCTCATCATATTACCTCGCCTCTTCTCGCCCTGCCGCTGCCGGAACCCGCTCTTACTTGGAAAGACGGCGCGGCAACAGCTATTTCGATGTGCGGA  
 AACAGCTTCATCCGACGAGCAAACTCTCAACCTCGGAGCGCTCAAAACCAACCGCGGCTCAAGCCCAACCTGCGCTCGATACGAATCGGACAGTGCAGAGGAAACGAAAGGA  
 TATCGCGGAGAAAAACGGGACGCTTGAAGAGAAAGAAAAATTCGCGAAACCGAAGCGGAGCAACAAAGAGAAACTGCGCGGATTTCAAAATGAACCTGAAGCGGCTGGGAACTCA  
 AATGCGAAAAACAGGATGATTTGATCCGTAATACAAATACCGCGTAACAACTACTGCGCT

## SEQ ID 4408

MFALSVITFTLASFLPVPAGTAVFTWKDGGNSYSDVPKQLHPDQSQILNRLTLQTKPAVKPKPAVDINADSAKENEKDIAEKNGQLEEEKKKIABTERQNKKEENCRISKMNKAVGNS  
NAKNKDLIRKYNNAVNYCR

## SEQ ID 4409

GTGATGACGGATAAAGCAAAGTTCATTAGGGTTTCCTTGATGGCTGACTGCCCGGGCAGAAATCGGGATTGGTTCGGGCGGTGTCTTTTCGGGTTCCGGTCAAGGCAGGGAAGACACTCCG  
CCTTAATATGGTCTTTATATATTGGGGTAAACAGATTCCAAAAATATCATTTGGAATATGGTATGCTACCGTATATTTGGCAAAGAAAAGAAATTCAGGCAGGCGCGTA

## SEQ ID 4410

VMTDKAFIRVSLMADCPGRIGISGGVFSFGFSRQGRHSALINCFIYWKITDSQKYHMMVHLPYILAKKKKIAGRNV

## SEQ ID 4411

ATGATGTCGGAATAAATGCGGTCTGAAGCTTTACCGGTTTCAGACGGCATTTTGTAAACTTTGATTCTCTATCGGTATTATTGTGTAAAGCTATTGAAAAATAAATAT

## SEQ ID 4412

MSENKMPSEALFVSDGILLNLILYRYCVKLLIKY

## SEQ ID 4413

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TCCGCCAGCCCGAGCGTGGCGCGGGGACATCATCAGCGTCCGACTGTACACTGATGGTGGTTAACGACAGCATCCAGCGTTCGACAAAGTTCATGCAACCAATACCGTTCGGGT  
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GCCGGAGAGGCGCTTATCTTGGAAAGGTTTCGGCTATGTGCGCGCGGTATTTTCGACCGTATCGAGATGATTTCAGGGGAGAACAGCTTCGTTTACCGATGCCCAACAGAACGCG  
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## SEQ ID 4414

MVARVYKGEQIGLVYITTDVAVNTRGYSSKPIDTLMALANDGTIAGAKLVHHEPIMLIGIPQSRVDFIDKYIGLNFINKNPPTSPVAPGDIISGATVTLMVNDISQSYKVLNQTRLG  
SDKALQTASASDVREAPASETRPRMANPDQDILSWDELLKQKAVGHLHITLDQINKLFEGKGAGVADHABQGDPTDITDLYVALVSQPSIGKSLLEDGWAHLQKRLKPGQAVLV  
AGEGRYSWKSGSYRGGIPDRIEMIQGENSFRTDAQHERVVELSAADAPRKEVSWPTIPBGVAFDGAEPRL

## SEQ ID 4415

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CGCGTTCGACACTATCAAAAATCAGTACCGCGCTGCGCGCTCGCAGCGCGCAGCGCGCAAGAGCGCAGCTCGCGCGCTGGTTCTCGCGAGAAGTACCAACATCAGCCAAATCAAGAC  
CTGCTTGATGAAGAAGAAACAGAGTTTTCGCGCAATTTGAAAGCCGTAACACCGAGTTTTCAGACGGCTGAANTACCGCGCAGAAATTCGCGCAATGGCTGGTGAACAACTGCAGCAGC  
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CCGAATTTGAACCGCTCAACTGCGCGCACTGCTGCAAACTGAAGGTCGATTGGATACCGCAAAATACCTGCGCTCGATTCCGCGCGACACCAACCGCGCTTCTTCGCGCGCT  
ATTGCAACGCAAA

## SEQ ID 4416

MSAGRLLRNRTTYEGRKLPFTNFKRTHYIMNAQLDHTAKVLAEMLTFKQPADAVLSAYFRKHKILGRQDRHEIAETFAALRHYQKISTALRRPFAQPRKAALALVIGRSTNISQIKD  
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QLLALLVAGKRGELIVDFCAGAGKTLAVGAQMANKRIYAFDIAEKRLANLKPMTWRAGLNTIHPERIGSEHDTIARLAGKADRVLDVAPCSGLTLRRNPDLKRYQSAETVAKLLEBQ  
HSILDAASKLVKPGCLVYATCSVLPEENELQIKRFLSEHPEFEPVNCBELLQNLKVDLDTGKYLRILDSARHQTDGFFAAVLQRK

## SEQ ID 4417

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GCTGGCTTTTGGTTTACCAACGCAACCGCACCAAACTGCACGATATATCTGACCGTTTTCAGACGGCAAACTTTAGCGCGCGCGGATTTCGCTTTTCCCTCAACCAACGCGCC  
TATCATATCAGAGCTGGCGTGTAAATACTACGGCGGAGACCAAGTCAGAACCTGCGCGGTCTCAATCCAAAGACACGCTGACGGCAAAAGCGCAATTTGGTGGTGGTTCAGCAATTCAGCTGG  
TGCATACGTCGCAAGGCAAGCAACCTTAGCGCGCAAGACCTGCGCGGAAATCCACTTCCTGCTTCCATCGTGGCGCGCATCGGATTTTTCACAAAGGTTTCCATGCTTTTGAAGCGCC  
GCTTAATCCATACGGCTGGCGCGCATCTATATTCAAGATTGGCGGGAATACGGTTTGAACGCCAAGAGCGCGCTATCACCTGCTGACCGCATGCTATCTCGCGCTGCGCGCTGCT  
GCCGAAACCGCAACATTAACGCAACCGGAAATCGCGCATCGACCAAGCTTGATTGCGGTTTGAATGTCGCGCGGACGCGCTTTGGCAGCAATCGAAGCTATTATGAAGCGCGCTC

## SEQ ID 4418

MNYALDALWKLFSQPVRLDLSLITAPPLWQSGCELSVRELLGERGFRYLLALDADPAPLTDYLAQRAPFDHRLGIYAEELLAFWFTNAPHFKLHAYNLVFSFGQTLGAADFVWSLWQOP  
YHIELACKYGGDQVONLRGLNPKDTLTDKAAKLVQPPQLVHTSQKATLAQDLFENPLPASIVRGIGFFPQGFHAFEPPLNPFYGHGTYIQDWAIEYGFERQEARHLLDRMVLYAPRV  
ABETELNATEIRLDGLIADLECRPDGFWHEIERIKAV

## SEQ ID 4419

ATGACTGCTCTCAACCCGCGCTGCCGACTACCTCGGCAACATCCGCATCATCTCACACGCCACGACCCCGCCCAACATCGGCTCTGCCGACGCGGATGAAACGATGGGTCTGC  
ACAGCTGACCATGCTCACCCTCAATCTGATGGCAACGCGGATGACGGAATATCCGCGCTTTTAAATCCCGATGACGTGCAAGTTTTCGACTGCTGAAGAGTTTCATCTCTCGCTTC  
CGGCGCGCGGAGCTATTGCACACGCGCAATCGTCCGACATCGGACGAAGCCCTTGGCGACACCACTCGCTGCGCGCTGACGAGCGCGCGCGGAAATACCGCGCGCGCTGCA  
ACCCGCGCGGATTGGTGGCGCAATTAATGACAGCGCGCAACCGCGCGGAGAAAGTGGCGTGGTCTTCGCGCAACGAGACTTTCGCGCAACGAGACTTTCGCGCTGAGCATCGAAGAGTTCGAGCGTGCACCGAC  
TGATGACCATCAACGCAACCCGACTATTTCTCGCTCAACCTGCGCGCGGAGGAGTGGTGTGCTGCGCAACGAGACTTTCGCGCAACCGAGTTTCAGCCAAACCGATTGCGCGCATGCCATCTTCAACAGGAAGA  
CCAGCGCGCAACCGACGACCAATCAAGGCGATGCTCGCGCATGGAAGCGTGATGGACGACATCGGCTTTTCAACCGCGCAACCGCGAGCGTCTGATGCGCGCTATGACAGCGCTG  
TTCGACGCGCGCAACGCAACCGGAGACATCGACATCTCGCGGTTTTCATACCGTCAGCCCGCTATCCATAAAAAGAC

## SEQ ID 4420

MTALKPALPDVILGNIRIILTRTSHPANIGSAARAMKTGMLHRLTIVTFNLMAFPMTENPVPVFPDDVQSFALPESFILASGAADVHNAEIVATLDEALDTTICALPSRRREITAPLQ  
TPRDLVPELLQANRGEKVALVFGNETPGLSIEVRACNRILNTINGNEDYFSLNLAQAVQVVCYELFSQTDSPFHLQEDHAATHEDQIKGMLAFMESVEDDGGFNNRNGERLMRRHQSL  
PGRANTQTEDIDILRGFPNTVSHRIKKD

## SEQ ID 4421

GTGCACTCTTCGGAGCGGCAAAATCGGAGTTTATCTGGTTGGGGCAAACCTGCCAAATCGGGTAAATACCGCTGACCGGTGCTGCTTCAGCGCAACGTTAAATTTCCGACGTTGT  
TAAAGAACAAGTTTCAGACGGCATTTACCGTCCGACGAAAGACGGCGCATTTATACCTATTCCATTCCGACGCAAAACCGAACA

## SEQ ID 4422

VQSPGAARSEFIWLGQTLFNRVKYRLTRVCFRRNVKFPFLKNSSDGISPSERRRRRIIPYSIPTENRT

## SEQ ID 4423

TTGCCAGTACTTTGGGATTGGCAGCCACAATATCGCCGCTTTCCAAACCAAGCGTCTCACCGACATATCGGTAAACGATCCGCGCTGCTTCTTGGACAATCAATGCACCGCGCGCAATG  
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AAATCGCCAGATATTGTTCCATCATGCTTTGATCGACAACAGGGAAGCCGATACCGATCAGGACGCGGTTCAATTCGATCGCGTTGGAGACACGGATGCGCGGCTGTTAAGCAACGCGCC  
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TTTAAAGGCTGATTCAAAACCGGATTCATCAGATTTCTTAAAGGTGGCATACCGCGGTTTCGACGTGTCAGTCTTCGAGCGGCAAAATCGGAGTTTATCTGGTTGGGGCAAACCTG  
CCAAATCGGCTAAATACCGCTGACCGGTGCTGCTTCAGCGCAACGT

## SEQ ID 4424

LRQYFGIGSHNIAAFQPSVLTRHIGNDAACFLDNQCTGNGVPRFEVELEKAVKTSCTCYGAQIQRSRAFAAASGGFCQKVFQNRQIFVHIALIDNREAGTDQAAVQFDAVGDVDAVVQRRA  
PTARSHVHVVTGVBHQSLQHAFFVQQCHRDGLGMVKEIGRPVERIDNPFVLGCSFAVEAAFFASDFVMRLSPFQSLAQDDPGIADVNIKNIVBGFVGFPGIEVTCGANHILGTAGG  
FKGCIQKRIHQISLRVAYRRFGRVLRSGKIGVYLVGANPAKSGKIPDACLQQR

## SEQ ID 4425

ATGAATCCGTTTGAATACAGCCTTAAAGCCGCGCGCGTCCGCGTCAGATGATGATTTCGCGCGCAGGTAACTCGATGCGCTCAAAACCGACAGCAAGCCTTCAACGATTTGTTT  
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GATTATCGATCCGCTCGACGGGACGACCAATTTCTTACCGGCATCCCAATACGCCATCTCTATGGCAGTCTGTCACAAAGCGCTGTTGACGAGAGCTTTGGTGTACGCCCCGAACTG  
AACGACGTGTACATGGCTTCGCGCGTAAAGCGCGTGTCTTAAAGACCGCCGATCCGTCCTCAACCGCATCGAATGAACCGCTGCTGATCGGTACCGGCTTCCCTGTGTCTGATC  
AAAGCATGATGACAAATATCTGCGGATTTTGAAGAGCTTTTGGCAAAACCGCGGAGCGCGCGCTTCTTTGGATTGTCGCGCGTAGCAACAGGACGTTTTCAGCG  
CTTTTCGAGTTCAACCTCAAACCGTGGGACATTCGCGCGGTGCAATGATTGTCTCAAGAAGCAGCGCGCATCTTACCGATATGTCGGGTGAGGACGCTTGGTTGAAGCGCGGATATT  
GTGGCTGCCAATCCCAAGTACTGGCGCAATGTAAATCATTTCCGACACGTT

## SEQ ID 4426

MNPFINTAPKARRAGQMIMRAAGNLDAVKTDKAFNDFVSDVRNSEILVEALKEAYPHKHTCEESGPHGKATAEYEWIIDPLDGTINFLHGHPOVAISMLLHKVQLQALVYAPER  
NDVYMASRKGALLANDRIIRVSNRIELNRCLIGTFPVVDQSMMDKYLAILKDFLAKTAGGRREGAASLDLCAVATGRFDGFFFNLPWDIAAGALIVQEGGIVTMSGEDANLRSGLDI  
VAANPKVLAQMLKIIISAHV

## SEQ ID 4427

GTCCCGATATTTCAGACGGCATTTTATTGGCGCGGGGCGAGGAGCGGAAACGGTCAATGCCGAAATTCGCGGAATGGAATCCGATATCTGGTTAAACGGGAGAACCTGTGCAATT  
TGTCCTTTCTTCAATTGTTTAAAGCGGCTTGTCTGGAATCTAATCGGCTGTGCGAGAAACAGACACCGGGGAATAAAAACAAAGGCTCTGTACCAGATTAGCAGATATGTTACCTT  
CGAATA

## SEQ ID 4428

VPFPTAFLLAAGQEGGNGQMPFIAGNGNPVLYKRRITLNLSPFLFKGGLLESKSAVAENRHRGINKNGLYQISRYVTLEI

## SEQ ID 4429

TCGCATTTCGGTTTGATTCAATGATGTCGGAATAAATAATGCCGTCTGAAGCTTTACCGGTTTCAGACGGCATTTTGTAAACTTGATTCTCTATCGGTATTATTGTGTAAAGCTATTGAA  
AATAAATATTGATTTCCGCA

## SEQ ID 4430

SHLGLIQ\*CRKIKRLKLYRFQAFCT\*PSIGIIV\*SY\*K\*NIDFPQ

## SEQ ID 4431

ATCGGATTTGTTTAAAGATTGTAATTTGATTTCGATCAAAATCGCGATAGATGATTATATATCAATATTAAGAGTATCGGTATATCGGGGATAGCTATGCTCTGTTTTC  
ATCCGGGTATGTCGCTTTCGGCGCGGATAACGGCGTTTTCACCGCTTTGCTCTTTTTCAGCGCGCAGTCCCGCTTATCGCGGAGCGCTGCT

## SEQ ID 4432

MRIGFKICKPDLHQSPIDDSYNINIKERYIGDSYVLFNPAYVCVSGADNGVFRYLCLFDGGTARLCGASA

## SEQ ID 4433

ATGGTTAATATCCGCACACCATTTGTCGAAATTTGGGCAATGTAATGTTATTGCTGTTTTCGCAAGTTTCGCGGTTTCGGCAATCATATGCCGTCTGAAAAGATGTACCTGATGGCT  
TTGCTGATATAATTCGCCGCTATTGTAATCAGCTTTCAAGCGGTATCTGCGGTTTCAGCGAAACG

## SEQ ID 4434

MVNIRTPLEIGHCTIVICLPQSLRSGSNHMPSEKMYPDGFADIIARYLNQLSSGICRLTET

## SEQ ID 4435

GTGTTATCTTCATATTCGAGGGTAACATATCTGCTAATCTGTACAGACCTTGTTTTTATTTCCCGGTTCTGTTTTCTGCCACAGCCGATTAGATTCCAGCAAAACCGCTTTAAAC  
AATTGAAAGAAAAGGCAAAATTCACAGGCTTCCGTTTAAACAGATACGGATTTCATTCGCGCAATTCGGGCAATTCAGCGTTTCGCGCTTCTGCCCCGCGCGCA

## SEQ ID 4436

VLSSYFEGNISANLVQTLVFPYSPVSPCHSRVRFQQTAFKQLKEKGQIAQGSPPNQIRISIPGNFGLHVSFAFLPRRQ

## SEQ ID 4437

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ACCGGCTCGCGCGCGGAGGAAAGCGGTTGCTTCGGCATTCGAAACGCAACGGGCGGCGCTATACCGTTGCCGACAGCATGCCAGCTTGAAACGTTGCTCTTCCGCTCAAAAG  
AAATCATGCGGAGCGGATTTGTTTATGCGGATAGCCCGGACGCGCGGCAAGTCGACGCGGCGGCTTTACCGTTGCCGATCAACCGTTCCAGGAATTTGCAGACCGTTCGGAAC  
ACATTAACCGCATTTGGGAATTTTGAATCAGGCAAAACCGCTTTCGGAATACACCGAATCGATCGTAACCTTTCCCGCGGTTGTTGAGGGAATGCGAATTTGACATTAACCTTCG  
CACACCGTCCCGCAGCTAAATTCCTCGGGATCGGTGTGAAT

## SEQ ID 4438

MXITHCKLKEVQKEFLRSFVPEVARSADILGIHFDAAALFYRKIRTVANHLRALAADEVEFGPAGPGGSCFGRRRKRRRGRGAAGKAVVFGIPKRNRAYTVAAADAEPEILLPAVK  
KINPDGIVYADSPGSRGSDAGGFTRCRINRSKEFADRRNHINGIGNFNQAKRALRKYNGIDRKPFPPLLRCEFRINFGTPSRQLKILDRCGI



## SEQ ID 4439

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CGACCGTCCGTTCGCCCGGAGCGCGCTTGTAGCAATTCGTAAGGATTGAACTGTTTGCATTTTGCCTCTGCCGTTTTATATCCGAAATTAGCAACGCTCCACGCTCAAGCCT  
GAAATCTGTCGGGTTCGATATTTTGTATGTCGCGAATCTACCGCGATATTTATTTCCGCGAACCAGCGCGCATCCGTGTTTGGAAACCGCGAACACGAGGCTACACACCATGA  
AATACAGCGAAAGCGAAATCCGCGCATCGCCACGTCGGCTTCCAATCCGCGCAAGGCTTCCCATATGTATGTGGCAATGCCCGCATGCAACTCGTGGCGCGCCCAACAGTTTGAAGTGTTCACCGCGC  
CGAAATCTTTGAAGAAATCGGCAACATATCCGATGTCGAGCTTCCCATATGTATGTGGCAATGCCCGCATGCAACTCGTGGCGCGCCCAACAGTTTGAAGTGTTCACCGCGC  
AACATCTTCGGCGACATCTCTCCGACGAAGCTCCATGCTGACCGGCTCCATCGGTATGCTGCTTCCGCTTCTTTGGACGAAACCGCAAGGCTGTACGAACCGTCTCAGCGCTCCG  
CCCCGACATCGCGCGCAAAACAAAGCAACCGCTGCGCCACCATCTCTCGCTTGCATGCTGCTGCTTACAGCTGACGACGAGCGCGCGCAACAGTCAAAACTCCGCTCA  
AAAGTGTGCAACAGGCTTGCATCGCGCATATTTACGAAGAGCGCAAAACTCGTTCTGCTCCGAAATGGCGACGCGTACTCGCGCGCTTG

## SEQ ID 4440

MTKHAILRGDGIPEIVAETVRVLDKFLAQGLDADYEYAPLGGAYDEYGHYPFPTQNLCKRADAVLLGAVGSPQYDNLDRPLRPERGLLAIKRLDLNLFANLEPAVLYPELANASTLKP  
EIVAGLDILIVRELTDIYFGEPRGIRVLENGEHEGYNTMKYSEIEIRIAHVAFSAQKRKSKVCSVGKANVLETTLMREIFEEIGROYVDVLESHMYVDNAAMQIVRAFPQYDVITATG  
NIFGDILSDRSM/LTGSIGMLPSASLDENGKGLYEPESHGAPDIAGQNKANPLATILSLAMLLRYSLNDEARAQVENSVOXVLQGLRTGDIYEGTKIVCSSEMGDAVLAAL

## SEQ ID 4441

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CAGCAGAGAATTTGTGGAAGTAAAGCGCTTCAACCGAAATGCCCTGCCGCGTTTGTATATTCAGATTTTAAATGTATCTGTAGTAAATCATTCATAAGCCCTATATGCTGGATGTAGAT  
TATTTAATATTCGTTACGATATGAGCAGCAACGCGCAATGTAAACCATCAAGGATTATGCTGTTAAAAAGTATGGCAATTAACGAGCATGGATGGTGGGCAATTAATCTTCAAGTCA  
AAAAAGCGCTGTGTCATATAATCCGCGCGGTGTTTGGTACAGCATAATAAAAAAGAAATATGCTATGTTGATGCTTGGAGATTTTGTTCGCGCAATGAAGAAACCGTTTATCAAAA  
CCCCGCAACACGCGCATACCGCATCTTATGAAAAAGAAATTTAGGAAGCTTATAAAAAACATACACCGCATGATTTCATACCCCGTTGGCAGCAATTCACACAAATACAAAAAG  
AAA

## SEQ ID 4442

MIKLAQOQIPDKLLDEEKILSANGQIRFFLGVDIVKQKDVGNIIQEWLGLWRKREIEFDVSTNTQMPDPFFLNKDRSRELLEVKAFNRNACPFIDADFMYSDIEIHKPYMLDVO  
YLIFGYDMDNGNVITKDLMLKKVWQITRSMDSWAINLQVKKGVVHKIRPGVWVISINKKNMPPFCELEDFVSAIEETVYQNPATRHNASLWKKKFEAYKHYNRSISIPRWHLEAHKYYK  
K

## SEQ ID 4443

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AGATACACGGGGAACGCTTTCTTGTATGTGCAAGGATTTTAAAGGCAAAAAACCAAGAGTTTATTTTGGAAATGTGGAAGGATTGGTGACACAGATAGAAAGATTTCGACACAA  
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TGACAGCGCAGTTTGAATCCAAACCGGACTTATCTTTCGAAACAGCCCAAGTCCGAAATTAATAAATATTTTGGAATCGGGACTGCTACTGAAAGCAGCCCTTCATCAAAAAATGCT  
AAAAAATTTCCCGCTCGAAGCTGACGAAATCAGTAAAGCAACAGGGGAGGAAAAACATATTACAGTTGGGATATTGAATTAAGGCGCAGTAACCGCAAGAGAGAGCAAA  
TTGTTAAATATCTTCTTAAAGCAACGAGGAAAAAATGGGCTTCAGAAATCGGCATAGATTGGATGGATGGATGCTTTGACAAAGCGCAAAATTTCAACTTCTATAACACCCCG  
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TTCAGGTAAAAATCTTTTGAATCAATAAATATTAGATCCAAACGATGTTGCGCAACCTTGGTTCGAATGAGATATGAGACACCTTTTCGTCGTTGACAAACGCGGTTTGGTACACCT  
ACCGGAAAGAGGTTACGCTTATTCGCTATCCGCGCATTCGCGCATTTGATATTTCCAAAAAGACAGATGCGATTATTGGGTAATACCGTTGCCCTCCCTGTGATTAAAGCGGAT  
CTGAAAGACTTCTGCATACCTTA

## SEQ ID 4444

MSGIRKGFQACRQSVACECVFTSEIKPAALEVLKQNPDEVPYGDITKIETGDIPTDFDILLAGFPQAFSPAGKRLGFEDTRGLFFDVARILKAKPKRPFILNENVEGLVTHDRKDSIQ  
KIGRTLAVILETLEALGYVSWKVLNAKDFGIPQNRKRIYITGSLKSPDLSPFTSPSPKLNILLESGLPTSSPFIKLLKPPSELYGKSVKDRGGKRNINHSWIDELKAVTEEBEQ  
LLNILLKERRKKWASBEGIDMDGMLPTKAQISTFYKHPDLQNILDSLTDRGYLVLEHPEKQIGGQRIKDESLPKGYNIVSGKSPFINKILDPNDVAPFLVAMDMELFVVDNGGLRLT  
TKBGLRLFGYPDDYSFDIPFKDRCDLLGNVAVPVKAVSERILHLL

## SEQ ID 4445

ATGAAACAATTTATCGCCCTCTGTTTACATTAGCCGCGCAATATATGTTATCAGGAATGCCGTCTGAACAGCCTTCAGACGCATAGGTTTAAACCGT

## SEQ ID 4446

MRTIYRPSVILSRNMYLSGMPSEQPSDGIGFNR

## SEQ ID 4447

ATGAAAGCTTTACCAAAATCACGCCATCGTCCGCCGCTCGACCGCAGCAACGTCGATACCGATGCAATATCCCCAAACAAATTTCTGAAATCCATCAACGCGAGCGCTTCGCCCCCA  
ACGCTTTGACGAATGGCGTTACCTCGACCAACGCGGAGCGGCGATGGAACAGCGCAACGCGCGTTGAACCCGATTTTCCCTGAACAGCGCGCTTACCAAGGCGCGCAAAATCTGTT  
GACGCGTAAAAACTTCGGTTGCGGCTCTTACGCGAACATGCCCTTGGCGATTTGACGACTACGCTTCCGCGCATTATCGCCCCAGCTTCGCGGACATCTTCTTTAAACACTGCTAC  
AAAAACGCGCTTTTGGCCATCGTGTGACCGAAGAACAGTGCACCGGCTTTTCAAGAGAGTGAAGCAACGAGGCTATCGGCTCTCCATCGACCTTGGCGAGCAACCTGACCAAC  
CGGCGGCGAAACATTACATTCGACATTACGAAACCGCAACACTGCTCTTAAACGCGCTTGGACGAAATCGGACTGACCTGCAACACGCGCAAAATTAAGCCTTTTGAAGAAAA  
ACGCGCGCAAGCGCAGCTTGGCTGTTTAAACGCT

## SEQ ID 4448

MKAPTITAIIVAPLDRSNVDTAII PKQFLKSIKRSFGPNAPDEWRYLDHGEFGMDNGKRLNPNDFSLNQPRYQGAQILLTRKNPGCGSSREHAPWALDDYGFRAIIAPSPADIFFNNCY  
KNGLLPVITVEQVDRFLPKEVEANEGYRLSIDLBQTLTPPGSETFTFDITEHRKHLNGLDEIGLTLQHADKIKAPREKRRSQWPLFNG

## SEQ ID 4449

GTGCGGATATTAAACATAACCCCTTATGAGATTGAGTATGTACGCGGTCTGTAACAAACCGCGCGCAACAGTATAAGATTTCGCTCGCGCAAAATTTGAAGTAGAACAGATACGACCCCAAC  
TCGACAGCAAAATGCAACTGACCGAAGTTTGTATGATTGCTGACGCGGAATCTGTAAAGTTGGCGCACCTTTATCGAAGGTGCAAAAGTAAAGCTAGTGGCAGACGCGTCTGG  
CGAAAAAGTCCGATCTTCAAAATCGCGCGCGCAACACTACCAAAAAACGCGCAACGCGCAAAATTTACCCCAATCGAAATCGTGGCAATCGCC

## SEQ ID 4450

VRILITILMELSMYAVVKTGGKQYKVSUGEKLVQEIQAQLDSQIELTEVLMADGESVKVGAPFIEGAKVTAKVVAHGRGEKVRIFKRRRRKHQKRGHQRNFTQIEIVAIA

## SEQ ID 4451

TTGTGTAAGCTATTGAAAAATAAATATTGATTTTCCGCAAGATGGCTAAAGGTGCGATAGGTACTGAAGAAATAATCGGCAGAACAGGTTTGCTCCCGCTTTGAACAAATGATTTTA  
ACCTCCCATAGAAGATACAGATGCTTTTCAA

## SEQ ID 4452

LCKATENKILIFKRDG\*RCDRYTERIIGRTGLPAGLANDFNLPG\*GIHDVFO



**SEQ ID 4453**

SEQ ID 4453  
GTGCGGATACGGATTGCCCTCCTCGACCGGCAGCACAAAAATCTTGCCGTCGCGGATTTTGCCCGAAACGCCACCTCGACAAATCAGTCAATCGCGGTTCCAGCGCATCATCGCCAACA  
CCAACTCGATTTTGACCTTGGGCAGGAAATCGACGCGTATTTGCGCACCGCGA

**SEQ ID 4454**

VRIRIASSTGSKILPSPILPERATSTITSLARSTASSANTNSILTLGRKSTAYSAPR

**SEQ ID 4455**

SEQ ID 4455

TTTTCGAGGTTTGATGTTTGCTTACCCAACAGCGCACCGAGCGCAGGTCATTCGGTTCGCGCTGAAGGTTGCGCGCAATCTGTCTTTCATTTCGTCAAAAGAAGGCACCTTTCACCTCG  
CGGCTGTGTTGACATAAATAAACCGCGTAGAAATCGCCGTTTTCAGCGCGCTTGCCGTAAATTCGCCTTTTTCACAGTCCTTAATTGCTGTATAAAGCGGCGGAACACCTGTTCCAAAT  
CTTTCAGCGGCACATATTCGCTCCGGCGCGCGCGTTCGTTTGGTGCGGTCGTTGAGCGGATATGTTTCAAACCGGCATCAAAACCTTTTTCGCCTTCAAATCGGCAACCGCTTTTTCGCG  
ATTTTCCTCTTGTGCGGTGAGGATTCGCCCACTGGAATTCCTGCGTGCTTTATATAAAACCGCTGATATTGTGCTGAACCGCTTTTACTTCTGCTCGGAAACCGGTGGGTTTGGCG  
ATATGCAAGTCGATGCTTCGCCGCTTCAAGCATATTTTACCGCTGCCAAACGGTTTTGAAGGACGGTTTCTGTGCTGCGCCGACTTTTTCGCTTCGGCAGCGCAATTTGGCAAGCGCAT  
CTTTPAAACTCTGCGACACCGGTGAGTTTTCAGCGCTTTCCTTCTGTGCGCACCGGTTTGACCACTTCGTTTCCAGCAGGGATTGCGCGAGTTGCGCGGTGTCTTCGGCACCGCTGTT  
TTCGCGCAAGGATCGCGCAACCTGCGCATCGATGACGGAACGTGTCGATTTTCTGACCGTTAACGGTTGCCAGCGTTTGGGCAACAGCGTCCCGGAACAGGCAAGCAGCGCAACGGAAGTC  
AGGATTTTTGCTTTTCAT

**SEQ ID 4456**

SEQ ID 4456  
FCRCFVCLTQQRDTGTVNPFRLKVAGNLSFHFVKRRHFLAAVVDIINAVEIAYFQRRCKFAFFQVLNCLIKRRNTLQIQRHLSVRRAGPFGAVVERVLFGNGIKTFFRLQIGNRFFR  
IFFLVGQDFQLDFLRAFIKTADIVNGFYPLLGNRLFGDMQCVCLAVQAIFYRLNPGFEGFRLLVVARLRFPGTQPKRIFKLCRPVEFQAQPHFLCDHGVDEHFVQQGLAQLRRVFGTAV  
FRTECGNLRIDDGTVDLITVNGCQRLGKQAAGTCKQRNGSQDFCFH

SEQ ID 4457

SEQ ID 4457  
TGTGATTTTCAAATGCCGCCGAATGTGTTTCAGACGGCATCGGCTGTTTCGGCGGTTCTCCGGCGGCGTTTGGAGGTGGTAAGATTGTGCTGCCGGCGGGCTATCCGTCTCTTTCAATCCGG  
CGGTGATGCTGTTTGTGCGGACTGTCCTCGCGCGCGCGCGCGGTTTTCCAAATAGAAATGCTTTGCCCGCTTTTCGGCAGGGGCGGTTCAGACCGGTCGAATTTTGCTTACGA  
TGTTTTTATGTCGCGGACGTTTGAATGGCGGGCGGAACCCCGCGCGCGCTACTCGTTTCTTGCCCTGCTTTGCTCCGTTCGCTTATAAT

**SEQ ID 4458**

SEQ ID 4458  
LIPKCRPNVQTASAVSAFSGGVLEVRLCCRRLSVLNPFGVMLFVPDCPVGGAAGFFQYEMLCPLFRQGRLTQSNFAYDVFMSAGRLNGGRKPPRRLLVTLPCFAFLPYN

SEQ ID 4459

SEQ ID 4459  
ATGGGTTTGCGCTTCTGCTGACGATGCCGCTGAAACGGTTTCAGACGGCATCGCAATCGGTTATTCGGTGGCGTTTTCGATTTTTTGCCGAGATGGGAAATGCCGCTCCGACGGCA  
TTGCCGCCCTTTTTGACGGCTTCCTTTGGTTTTGTCCCAACTTTTTTCAGACGGCGTTCCTGTTTGTTCGGCGGCGCGTTCGGCGCGGCCCTGTGTTTTTGTCAAGGTTGCGGGCGGTGTCTT  
GTTTCGCGCCCTGCCAAGTCCCGGCGCAGCGCGACAAAGCGAGGGCGGACAGGGCGGTAACGAAAGTTTGTTCATGGT

SEQ ID 4460

SEQ ID 4460  
MGLRLVLTPSETVSDGIANLFGGVDFFAEMCNAA SDGIAAFFDGGFGVPTTFDGVACLFGGAPGGGLCFVKVAGGVLPFRALPSAGAGGQGGGGGKNEKPFVGG

SEQ ID 4461

[illegible]

**SEQ ID 4462**

SEQ ID 4462  
LITRPSEICFVRQKHLIFKPRSLTNNKLFVTALSALALSACAGTWQGAQDPTARNLDTKQAAAERAABQTGNAVEKGWMDKTKTKEAVKKGNGNAVGRGISHLGKKIENATE

SEQ ID 4463

SEQ ID 4463

ATGACGGCACAACCTCTACGCAAACTCTGGAACGCCACGCTGTCGCGAAGAAGAGACGGCACCGTCTCTGCTTTACATCGACGCCATCTGGTTACGAAGTAACACGCGCCGAG  
CGTTTGAAGGCTCTGAAAATGGCGGGCGCGCAAGCTGTGGCGCATCGACAGGTGGTCTCCACCGCGGACCAACAACCCCGACCGGCGATTGGGACAAAGGCATCCAAGACCCGATTTCCAA  
GCTGGAGTGCATACCTTGGATCAAAACATAAAGATTCTTGGCGCATCGCCTACTTCCGGTTTATGGACAAAGGCGAGGGCATCGTACACGTTATGGGCGCCGAACAAGGCGCGACCTG  
CCCGCAATGCAGCTCGTCTGCGCGGATTCGCACACTTCCACCCACGGCGCATTCGCGGCATCGGCACACGGCATCTCCGAAGTCGAACAACACGATGGGACGCCAGTGCATTACCG  
CGAAAAATCCAATCTATGCTGATTTGCCGCTGACGGCAATTAAGAAGCGGGCGTACCGCAAAAGACGTGGCGCTTACATCATCTGGGCAATCGGCACCGCGGGCGCACGGGTTACCG  
CGTCTGAGTTTCGGCGCGAAGCGCATTCGCGCACTTTCGATGGAAAGCAGGATGACCTGTGCAATTATGGGCAATTGAGCGAGGCGCGCGTTCGGGTATGGTTGCCGTGCATCAAACCACTC  
GACTATGTCAAAGGACAGCCCTTTCGACCCCAAGGGCGAAGCTTGGGACAAGCGCGTGCAGTACTGGCGCACGCTGGTGTCTGACGAAGGCGCGGTTTGTATAAAGATATACGTTTCAAAG  
TGCAAGACATCGACACCGAGCTTTACTTTGGGGCAGCTGCGCCGAAATGGTTTAAACATCGCGGCGAAAGTGCCGAATTCGCGCGAAGAAACCGATTCGGCTCAACCGCAGCGCGCATAGAGG  
CGCACTCGAATATATGGGTTTGAAGCGCGGTACGCGCTGAAACGAAATCCCTGTGCATATCGCTTCTATCGGCTTCTGCACCAACAGCGCATCGAGACATCTGCGGACAGCGCTGCTATC  
GCCAAGGCCATAAAAAAGCCGGCAACGTACAGCGGTGTTAATCGTCCCGGGCTCCGGTTTGGTTTAAGACAACGCGCAAAAAAGAGGCTTGGACAAAATTTTCATCGAAGCGGTTTTC  
AATGGCGCAACCGGGCTGTTGCATGTGCTTGCAGTAATCCGACGCCTCGCGCGAGGCAACGCTGCGCTCCACGTTCAACCGCAATTTTGAAGCGCGCAAGGCCAACGCGCGGG  
GCTTCACTCTGCTACGCCCTATGCGCGCGCGCGCGCGCGTACCAGGACACTTACCGACATCCGACAGATGGG

SEQ ID 4464

SEQ ID 4464  
MTAQTLYDKLWNSHVVRREEDGDTVLLYIDRHLVHEVTSPOAPEGLMAGRKLRWRIDSVVSTADHNTPTGDWDKIQDPI SKLQVDTLDQNIKEFGALAYFPFMDKGGQIVHVMGPEQGATL  
PGMFPVCGDSHTSTHGAFALAGALIGTSEVHEMTAQCI TAPKSKSMLIAADGKLKAGVPAKDVALYIIQQITAGGTGAYAVEFEGGEAIRLSLMBGRKTLTNNMATEAGARSGMVAVDQTTI  
DYVKGKFPAPGEANDKAVEYWRITLVSDEGAVPDKRYRPMADIEPQVTWTGTSPEMVLNTGGKVPNPAEETDPVKRSGIERALEYTMGLKAGTFLNKEIPVDIVF IGSCNSTRIEDLREAAAI  
AGHKHKAGNVQRVRLIVPGSLVLKEQAEKEGLDKIP IEAGFEWRPEGCSMCLAMNADRLAPRORCASTSNRNFEGRQNGGRTGLVSPAMAAAAAVTGHTFDIRMA

SEQ ID 4465

SEQ ID 4465  
TTGTTCAATTCGTATATCTAAAGAATGATTCGATACGAAAGAATACTTGTCTCATCTCTTCAAAGCATTATTATCTGTACCTTGTCAAAAACACGCAGAGGCAGACGAAAGATGAAA  
TTACCGGTATGTCGCCCGAACATTCGGCGCACTTCAGGCGTT

SEQ ID 4466

SEQ ID 4466  
LFISLYLNDKSIRKNTCRHSFKSIIICTLSKNTQRQTKDEITGYVARTFGATSGV

SEQ ID 4467

SEQ ID 4467

ATGAATTGTGTTTCGGGGCGGCTTCAATAATCTGAATCCGAATTTTATCCCGCTGGCGGGGGTTGCCGCGCAAGATGCGGTGCAACGCGCTGCGAAACGGAGAATCCGTATTGATTATTC  
CCGAAACCACACGCGCAATACGTTTACTCTGCAAAACGTTTACGCCCTCGCGAGATTTTCCGTTTCGGCAGGTTGTGAAGTCGCTTGGGCAAGCTGAAATCCGGAAGTAAACCGAACCGGC  
CGAATTTGAAACTGCAATTTGGGGGACAAAATCTGCTTGAGCCTTTTGCTGCGAACACCGGACGCGTCCACCTTGCACGAGCTTTTCGCGCTTGCCTGGTGTGTTTGTGAACAACGATTGTGCT  
GCGCGCATTTCCGACATTCTCAAAGGCATCGGCCAAACCGTTTTCGCCGCGCTGCACGCGGCTTGGACGACGCGCGGCAAAACAAATCAITTCGGCGCTTACAAACCAAGTTGCGCGCGAAT  
TTGCCAAGCTGATTGACATCGATGAAATGGCAGATCAACCCGATTTTGAAGAAATCGCGGGTTTGGACTTCCAAGGGCGCGAAGGTGAAGATCGCTGGCGGAAGCGGTAGAACCGCTGCT  
GGCGAAATTTCAAGCGAAATACGACGAATCGGGCATTTGCCGACAAACCTTTCTGTCATCGTCAAAGCCGATGCGCGCACTTACGGCATGGGTGTGATGAGCGTCAAATCTTCGACGAAAGT  
GCGCGCTTGAACCGCGCAAAACCGCAACAAATGGCGAAGGTGAAGAGGGCTTGAAGTTCAGCGAAGTGATTGTCCAAGAGGGGTTTATACCTATGAACCTTGAACGCGCGGTGTGCG  
AACCCGCTGCTATATGATGACCGCTTTCGTCATCGCGGCTTTTTCGCGGTACACGAAGGGCGGCTGCGGACGAAACCTCAACGCGCGGTATGGTGTGTTGTGCGCGCTGCCAACAG

CAFTCTACCGGTAACGGCGATAATTCGACAGAAGCTCCAGAAGCTGCAACCGGTAATTCGAACAATGGGATTTCGCTCGGTATGCCCGCTTCGAAAAAGACTCGGACGTGGACAACGAA  
CATAACCCCTCTACGTTTACGGCGTAATGGCAGCTCTGTCGCTTTTGGCGGCTTCAATCGAGTTGGAAGAAAACGGCG

**SEQ ID 4468**

MNLPFGGNNLNPFIPLAAVAADAVQACRCKTEKSVLIIPENHTRNTFYLVQVYALGEIFRSAGCEVRLGSLNPVTEPAEFETALGDKILLEPLRTRDRVHLADGFSPCVVLLANDLS  
 AGIPDILKIGIQTVLPPLHGGWYTRRKTNFPGAYNQVAEPAKLIDIDEMQINPYFEKIGGLDFQGREGEDALAEAVKVLAKIQAKYDESGIADKPPVIVKADAGTYGNGVMSVKSSDEV  
 RGLNRKNRNKMAVKKEGLEVSEVIVQEGVITYETLNGAVCEPVPVYMMDRFVIGGPFVRVHEGRGADENLWAGGMVFPVPLSNSIPTGNGDNSQEAPEACKRVFEQWDSLGMPSKDCQVDNE  
 HNRLYYVGVMARLSLLAASTLEETA.

## SEQ ID 4469

TTGAATACAGATGCCGCTGAAGCGGAAAAICCGGTTACAGCGCAATTTCCGATATTTGGCGTGTGGGAACATCTGTTTCAGACGCCAFTCTCAGACTATTTAAAAAGGGAAAAACATGAC  
ATCAAGCAATGGCCGGAAGGCGAAAGGCCAGGAAAAAGCTGTGGAACGCGGGCGCGCGCTTTGAGCGATGCCGAACTTTTGGCAATCCTTTTACGCGTCGGGACGCGCGGGATGAGCG  
CGGTCGATTTGGCGCGCTACCTATTTCAGGAGTTCGGCAGCTTGGGGAGGCTGATGAGCGCGGAGGTCGGCAAACTGTTCGGCATACAAGGGATGGGGACGGCAAGTTTCACACAGTTCGC  
CGTGGTCAGGAAATCGGGCGCGGATATTGGAGGAATATTCGACGAAGAAATTAACCTTATCCGATCCCGATACCGTTGCCGATTTATTACGCTTTCATTGGGGCAGGAAAAAGTCGAA  
GTCAGGTCGCGCTGCTGTTGAACGCCCAAACTGATTTGGCGGTACAGAGAGCTGTCGCGCGGTACGGTTCGGGAAAAACAGATTTACATCCGCGAAATCGTCAAACTGCCAFTGGAGCG  
AAATATCCGACAGCTGATTTATTCGCGCACAAACATCCGGCGCGCTCGCC

**SEQ ID 4470**

LKYRCRLKRKSGSDGLSDIWEVGTSSVSDGISDYLKKGKHEHQAMAGRRKAQKAVGTGGGGFERCRTFGNPFTRRDARDERGRFGALPLAGVRLGEADERGGRQTVGIQRDGDGKFHTVR  
 RGQGNRAADIGGRIAGRNLYLRSRYRCRLFTLSFGAGKSRSORRAAEPPKPTDCGQRAVARYCGCKHDLHPNRRQTGIGRICRQPDYRAQPSGRLA

**SEQ ID 4471**

ATGAGCATCAAGCAATGGCCGGAAGGCCAAGAGGCCAGGGAAAGCTGTGTGAACGCGGGGCGCGGCTTTGAGCGATGCCGAACCTTTTGGCAATCTCTTTTACCGTCGGGACCGCGGGA  
TGAGCGCGCTCGATTTTGGCGCGCTTACCTATTTCGACGAGTTCGGCAGCTTGGGGAGGCTGATGAGCGCGGAGGTTCGCAAACTGTTCGGCATACAAAGGATGGGGACGGCAAGTTTCACACA  
GTTTCGCCGTGTGTCAGGAAATTCGGGCGCGGATATTGGAGGAAGAATTGACGAAGAATACTCTTATCCGATCCCGATACCGTTGCCGATTATTTCACGCTTTCATTGGGGCAGGAAAAA  
TGCAAGTACGAGCTTCGCCCTGCTGTGAACGCCCAAACCACTGAITTCGGTTCAGAGAGCTGTGTCGCCGTTACCGTTTCGGGAAAAACAGATTTCATTCGGCAAAATGCTCAAATGGCAT  
TGCAGAAATATFGCCGACGCTGATTTATTCGCGACAACCAATCCGGCGGCTTCGCTGAACCTTCGCGAAGACATCATGTTTCAAGGCGCGCTGGCACAGGCCATGTCGCTGGTGTATGT  
TTGCTGCTTCGACCACTTTTATCGTTTACCTTCGCAAAACCGTCCGTTCTGCTTCAGGCAGCTCGGCGTATGATGCC

**SEQ ID 4472**

MSIQNPGEPERPREKLLERGAALSDAEALLLRLVGTGRMSAVDLARYLLQFSGSLGRLSAEVGLKSAYKMGTSFTSPQFAVVREIGRRILLEELQERITLSDPDVTADYLRFLHQEK  
VEVSVALLNLRNOLIAVRELSRGTVAEVTIYIREIVKLALDEYADSLIIAHNHPGSGSPESQEDINFTRRLAQAMSLVDVSLLDHFIIVTSOTVRSFROLGLMP

SEQ ID 4473

ATGGAACAACAAAACAACCTACCGTTACCGACATTGACCGCCCCATACCTGTCGCCGCCGGCGGCACATAAAAAAGTCTTGTGTCATTCTGCTGCGGCCCGGTGCACGGCGGAAGTGATGG  
AAGCCATTGCTTGCCTCCGGCATCGGCTACACCATTTATTTTTTACAATCCCAATATFCCATCCGCACAAGAGTATATGCTCCGAAAAGAGAGAAAACATGCGCTTTGCGGAAAAGTTCGCAT  
CCCTTTTCATCGATAAAGACGACGACTACGAAAACGACCGCAAGAATGTTTGCCAAAGCCAAAGGCATGGAGTTTGAGCCGGAACCGCGGCATCCGCTGCACCATATGTTTCGATATGCT  
TTTGAAAAGACGCGCAATACGCGCAGAACACGTTTTCCTCGCTTTACCGATTTCGCTGGGCATTTCACGCTGGAAAAAATTGGCGCAATACCGAGCATTCGGGACCCGTGCCCGCGC  
CTTACGATGATGTGGCCTATTGGGAGCTTCACTTGGCGCAAAAGGCGCGCGCGGCTGATGATGTAATACGACAAACCGGAAAACTTTCACGACGAGGAATATCGCGGCTGCGCCTATTTC  
TCTGCGCATATGACGACGCCCAACGCGCAATTCGACGGAGCGATCCCCGTCAAACCTCGGCGCTGCTGATATTCAGGCGACGAAATCGACACAAATACGAACCTGCACCCGTCGGAGTGGACAAA

SEQ ID 4474

METQNKPTVTDIDRPIILVPPGGHKVKVLLHSCAPCSGEVMEAMLSAGIGYTIYFYNPNTHPHKEYMLRKEENMRFAEKFGIPFIDKDDYENDRKWPAKAKGMEFEPEGRGIRCTACFDNR  
 FEKAAOYAEHHEGFPVFTSSLGISRWKNNIAQINDCGHRAAAPYDDVAYWDFNWRKGGGGARMTEISKRENFYOOEYCCGAYSLRDSNAHRKSGRIPVKLGVLTYGDESTOYEPAVPRVDK

SEQ ID 4475

ATGTCCTTTCAAACCTCCGTTACCTCGCATCAGTATTGGCATTGTCTTCACTGTTGGCGGCATGCGCGGTGAGAAAAGTCTGCGGCAGGCGATGCTTCTCTGCTTCCGAGACCGAAGCGG  
CTTCCCAAGTACAGGCCCTCGGAAGCGGTCTCTTCCGCTTCACTGGCTCTGCGCGAAGACCAAGACCTTTTGAAACGCGCGCAAGGGTGATTCCAACTCTTGCCGACTGTGCGAAGAAATGCA  
GAAAAATCCGTTCCGTTTACCGAAGAACAGGCTCAAACCTCGGACCAACCACTCTGTTATGAACCAACGCCCTTTCAAAGGCAATACCGTAAGCTGCAACTCTTGCCACAACTTGCCTTCGCGCGGT  
GTGGACCAAGTATGCGCAGCTCAGTCAAGGACCAAGGCGATTTCGGCGAGCTACCTGCCTACCGCATTTGAATGCTCCGCTGCTGGGACCGAGTTTGGGACGGAGCGCGCCGATTTG  
AAGAAACAGTGTGGCGGGCTTTTGTGTAATCCGCGTGAATATGGCGAATGATTGTCGAAGAGGCGCTGACGCAAAATTCGCGAAAGTCCCGAATATCAAGAAATGTTTAAAAAAGCTTTTTC  
TGAAGACGCGCGGTTTCTGTTTAAAAACATCACTACCGCATTTGGTGGCTTTGAGCGTACCTTCTGCTGACGCGGACCAAAATGGGACGAATACCTCAAAGGCAACGCTCAACGCCCTTGAGCGAA  
CAGGAACGAAAAGGCGTGGCGCGCTTCACTGGACAAAGGCTGTATTGCTGCGACAAACGGTGCAACCTTTGAGGACGACGACCTTCCAGAAATTCGGTCTGTTCCAGGGCGGTTATGGAAAT  
TCATTGAGATCCGAAACGCGACAAAGGCCGTGCTGACGTAAACAAAAAACCGAAGACGAATTTTCTCCGTGTTCCGGGTTGCGTAACGTGGCTAAAACCTTATCCGTATTTCACAA  
CGGCAGCGTGTGGGACGTGGTAATAGGCAATTACCATCACTGGGTAAAGCGCAATTGGTTAAAGACATTCGGAAGAGAATGTGGATTAACATCTCGTATCTCTGAAATGCATTTCCGGCAAT  
TCTTTCGAAATCAGGCGCACGATGCGGGAAGTCCGCTTACGCTGACGCAAGTGAATCTTAAGCGCGACCAAAA

SEQ ID 4476

MSFKLRYLAVSLIALSLLAACGGQEKSAAGDASPASETEAASQVQASEAVPSASSASPEDQLLKRAQGVFPQLPTVEHQKIRPPTTEBQVKLGHLWYEPRLSKGFTVSCNSCHNLASAG  
VDMPTSQGHKGQFGGRNSPTALNALIGSQFWDGRAADVEEQAGGLVNPVEMANDSQEAAAAKIAKVPEYQEMFKKAFPEDGAVSFKNITITALGAFERTLLTPTKWDEYLGKGNVNALSE  
QERKGVRAFMDNGCIACHNGVNLGGTTFKQKFLVQGPYKWFIEDPKRDKGRADVTKKTEDEFFFRVPGLRNVAKTYPYFHNGSVWELDKAVTIMGKQGLKDKPIDVDNIVVFLNALSGN  
VSESARTMPELPLTAPMSEKPDNK

SEQ ID 4477

ATGCGAAGTAAAAAGCAGGCGGCAGCACCCGCAACGGTCGCGATTTCAGAAGCCAAAGCGCTGGGCGTTAAAGCCTACGGCAACAGAGCTGATTCCCGCAGGTTCCCATCATCGTACGCCAAC  
GCGGTACCAAATTCCACGCGAGCGACACAGTAGGTATGGCCAAAGACACACATTGTTCGCCCCAAATTGACGGTTATGTGCAATTCAAAACCAAAGCGCGCTGAACCGTAAAACTGTTCAG  
CATCCGTCCTTACACCGGTTCTGAAGAA

SEQ ID 4478

MA SKKAGGSTRNGRDSEAKRLGVKAYGNELIPAGSTIVRORGTKFHA GDNVGMGKDHTLPAKIDGYVEFKFKGALNRKTVSTRPYTGSEE

SEQ ID 4479

[illegible]

CGAAAAGGTTGCCGAATTTGTCAGGCAGCACAGGGCAGGCAGAGCGTTCGGCTGATTAAGGCCCTTGCGGGACGAGGGCGAGAAAGCGCGCAAGCAGGTGTGTGAAAAATGCCGATGAACAG  
CTTCGCAAGAGGCGCAACGCGTGGCAAGAGGTTTGGAAACGGCTGTCGGTCCAACGACCAACAAGCTGCTGCATTGCGCAACTCAAACTTGAATAAGCGCGGGGAGAGATAAAGATTGG  
TTTCATCGCGTCGCGCAGATTTATCAATTGGACAAA

**SEQ ID 4480**

SEQ ID 4480  
MQLTAVGLNHQTAPLSTIREKLFAAAAALPEAVRNRLARSNAATEAVILSTCNRTLEYCVGVDEEIIIRWLADYHSLPIEIEIRFPLYLTLDMQETVRHAFKRVACGLDSMVLGEPQILGQIKDAVR  
AQDQESMGAKINLALPKQTFVSAKEVRTUTAVGENSVSMASAVKLABEQIPFDIGDLNVLFVIGAGEMTELVATYFAAKNPRIMTVANKRFLARAOELCDKLGVNAEPCLLSDLPAIHLHDYDV  
VVSSTASQLPTVIGKGMVERALKQRQSMPLFMILDIAVPRDIEAEVGLDNLDAYLITVDDMVNIIVSGKEARQKAAAAASTLVSEKVAEPVRQQGRQSVPLIKALRDESEKARKQVLENAKQ  
LAKGATAEEVLERLSVQLTNKLLHSPQTINKAGEEDKDLVHAVAQIYHLCK

**SEQ ID 4481**

SEQ ID 4481

TTGCCGCGTTCGGGAAGCGCGCATTTATGAAATCCCTTTTATTTGGCTGCTCTATTGGCGCTCGCGCGGACGGCGTTTCTACCATACCCAAAACCAATCCCTGCGCCGGGGGCAACTTGTCT  
ATCCGCTCCGACACCGCAAAATCAGGAGCGGGCGCATGCGCTGCACCTACCTTAACCGCATCCGCACAAATCGTTTGACACGCGCTGGCACACGCGCGGTTTGGAAAAATCCGCCGCGAG  
CAGCAGCACGCTATCTACGCTCAATCCCGAAGACGGACACGGCGAACCATCCCGACAATCCGCACCTACCCGACAAAAGCTGACCGAAGCGCACAGCGCTTGGCGGGTATCTCTACAC  
GGCGTGCAAGAAAATCATCAGCACGGAAGAGGAAGCGCGCAATCGTCCGACAGCGACATCCGACAGCAGCAACGCCAAGTGGACGCTTTGATGAGCGCAATCTACCAACCGCTTTGCTGTC  
TTGACCGCCATACCGACGAAGCAGGTGCGGCATTTGTGCGCGAAAACGGCAAAACGCTCCTCGTATTCAATCAGGGCAACGGCAGCTTCGAGCGCGCTGTGCAAAAAGGAAGCGCGCAG  
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CCTTATTTTACGGGGAACGTCCCGACCCCGTGGCGGAATATGAAATCAGCAGGCAATCTGCCAGCATTTATTTCCGAGGCGGACCGGACAAAATTCGATGATAAGAGTTTCAAGCTGTATC  
AGGGTAAAAACGAATCCGCCCTTCAGGTTTAAACCGCGGACACGACCTTAACGGCGAGCTGACCGCGCAACCAATTTCGCCCTTTTCCCGCTCAAACTTTGGAATACGCGACGCTTTA  
TACGGCGGTTATTCGATCTCCGACGAGCGACGCGAGCAGCGAATGCCAGTTTGAAGCCGAAAACCGGATTACCTTTATTTGAGGTAAACGGCGCGGAGACACTTGCGGTAGA  
AAGCGGCAAAAATATTATCTACCTGCGCGGACGCTGTTGTCTGGAAGCGGTGTAACCGTTATACCTACCGCGCGGAGTTCGGCAACAGCGTGTCTACTACTCCGGCAGAACGCGGCGGCA  
TTGTCTTCAGCGTACGGGAATGCGCGGAAGCGCAATCAGGCTTACTCCGGAAGACAGCCCGAACGCGGTGTAAACCTTTATTTGCGAGAT

**SEQ ID 4482**

SEQ ID 4482

LPRREGINKSLFTWLLLGSAAGVFYHTQNSLPAGELVYPSAPQIRDGGDALHYLNRITQIGLHALAHAPVLENSARRHARYLTLPEDGHHGSHDPNPHYTAQKLTERTRLAGLYN  
GVHENISTEEAARSSDSDIRTQQRQVDALMSATYHRLSLDLRITDEGAAFVRENGKTVLVFNQNGSFERACAKGRROPEAGRKYYRNACHGAAYADEAMPVTELLYTAYPVGGAL  
PYFYGERPDVPFVETITGNPISDITSEAAKGIAMKSFKLYQCKNEIRPVRVLTAGNDPNGRLTAHQFALFPLKPLEYGTLYTAVFDYVRNGRHAQAKWQFTRKRPDTPYFVNGGETLAVR  
PKGYPIHWRGRNCLACTRYTYRRQFQNSLSILRHEAGGIVFSVSGMAGSRILRTPEDSPERGVTLYLQD

**SEQ ID 4483**

[illegible]

SEQ ID 4484

SEQ ID 4484

LTVMSGRTGRNSATQAQPERVMLVGVMLDKDDTGSNAARLNGFQTALAEAVELVKAAGGDSVRVETAKRDRPHALFVGTGKAARLSEAVAADGIDLWVFNHELTPTQERNLEKILQCRVL  
DRVGLILAI FARPARTQEGRLQVELAQLSHLAGRLIRGYHLQSPRGIGMGKPGETKLETDRRLTAHRINALKKQLANLKKQRALRRKSRESGRIKTFALVGYTNVKGSSLPNRLTKSGI  
YAKDQLFATLDITARRLYSPACSIILTDTGVFVSDLPKHLISAFSATLEETVQADVLLHVVDAAARNSSQOI EDVENVLQBIHAHDIPCIKYNKTDLLPSEEQNTGIWRDAAGKLAAR  
ISVAENTGIDALREAIAYCAAAPNTDETETP

**SEQ ID 4485**

SEQ ID 4485

TTGTGCCGCCGACCAACACAGACGAAACCGAAATGGCATGAAAAAAACCTGTTTCCACTGCGGGCTGGACGTTCCCGAAAACTGCATCTGACCGTCCGCTACGAAGGCGAAGACCGCG  
AAACCTGTGCGTCCGCGTGTGAGCGAGTCGACAAAGCATCATCGATTCGGCGTTTGGCGAGTTATTATCAACAGCGCACCGCGGACGCGAAAAAACCGAATCGCCGCCCAAGAAATTCCT  
CGACCAATTCGCCGCTGTACGACCTGCCCGAAGTCCAATCCGACTTTGTGGAAACCCATAATGGCAGCGCACGAAGCAGTGTCTGATGCTCAGCGGCATTATCTGCGCGCGCTGCGCTCTGCGCTG  
ATCGAACAGCAGCTTTTGGCAGACAGCGCATCTGCTCCGCATCGAAGCTCAATATCAGCAGCGCACGCTGCCGCGTCTGTCTGGGACGACGCGCAAAATCCGCTCTCCGACATTCTGTTTGAAA  
TCCGGCAGACAGGTTACACCGCGCGACCTATGACGCGCAAAAAATCGAAGCGGCCAACCAAAAAAGAACGCAAAACAATACATCTGTCGCGCTTGCCGCTGCGCGGATGGGTATGATCGACAG  
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AGGGATGTATTTGGAATCCATFCGCGATGCTGCTGTTTCTCTGCTGGCGGACGCTTTATGGAACACATTGCCCGACGCAAGGCGAGCGATGCCCGCGAAAGGCTGGTGAACCTGATAAC  
CGGCTCTCGCGACCGGATGCCCGCTATCTCTCGCTACAGGATGTCGCGGAATCCGCGCTGCTGCTCAAACTCCAAAGCAGCGATATTTGTGATGTTCAACCCGCGCGAAACCATCCCGCTGTAC  
GGCAGGTTGCTGGAAGGAACAGTGCCTCAACGAATCTATGCTGACCGCGGAGAGCTGCCCGTGGCCAAATGCCGTCTGAAAAAGTAAACCGCAGGTACATCTAACCGCAAGGCCCT  
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TTTCATATTCGCGGAGCTCTGCTTTCGCGTCCCGGCTCTTCATCGGTTGGACGCTGTACGCGGACCGCCACACCGCATGTGTGATTACCGTGCCTGCTGGCTGCTTACCTTCAGCTTCGCCCTGGCG  
CTGTGCTTGGCAGCGGACCGCGCTGGCAGCTTCTACCGGTAAGCTGGCGCGGAAGATTTTAACTGCTGCGGAGCATGACCGAAGCCAAAGTGTCTGGCAGTGGCGCAAGTTTGGAAACAGCAGTCAGAACACCC  
ACAAAACCCGGCAGCTGACCCAAAGGCAATCCCGCGTCCGCGGATTTGAAGTGTCTGCGGAGCATGACCGAAGCCAAAGTGTCTGGCAGTGGCGCAAGTTTGGAAACAGCAGTCAGAACACCC  
GCTCGCGCGCGCATCTCTCAATCTCGCGCATTTTCAGGCGGCGAGCTGCCGGAATCCAAGTCGGACACCGCTCAACCGCATCGGGGAAGGCGTGGGTGCGCACTGACCGCTCAACGGCGAA  
ACACAGGTTTGGGCATTGGGAGGGCATCTTATGTTGCCGAAATTTCAAGTTAAAGAACCGCAACAGAAAGCGGCGGCGAGCGGTTTACCTCGGCGAGTCAAGCGCTGTTTCAAGCCGTGT  
TCTACCTGCAAGACCGCTCAAAGACAGCGCGCGGAGGAGTGTGCGGAGTGTGGCAGCGCAAAACCTGACGCTGCACATCTCTAGTGGCGGACCGGTGAAGAAGCAGTTGTTGAAACCGCGCG  
TGCTTGGGTATCGCGCACTACCGCGCCCAAGCAATGCCGGAAGACAAGCTGGAATAGCTCGAAGCCTTGC AAAAAGAAAGGAAAAAGGCTGATGATAGGCGAGCGGCATCAACGACGCG  
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AGGCGCGCGCGACCGCCATATCATCTCCGCAAACTGATATTTGGCGGCGGCTACATATCAATTTACGCTGACGCTGCGCTTTTGGGCTATGTCCAACCGTGGATAGCGCGACTGGGTAT  
GAGCTTACGTTGCTGCGGTTTTTGGGCAACGCCCTCGCGCTTCACAAACGGGGGAAATGCCGCTCGGAACA

SEQ ID 4486

SEQ ID 4486  
LCRRTRKRRNRNNAKKTCFHCGLDVPENLHLVTRYEGEDRETCCVCGQVAQSIIDSGLSYYTKRRTADAKKTELPPEQILDQIRLYDLPEVQSDPFVETHNGTHEAVMLSGITCAACVNL  
TEQQQLLRTDGIVRIDLNYSTRHCRVWDDGKIRLSDILLKIRQTFGYTAAPYDAQKIEAANQKERRQYIVRLAVAGLGMQMTMFALPTYLYGGDIEPDLQILHGGGFLMVLVVFVYCAVP  
FYQGAIRDLKNNRAGNDTPIAAALLMTFIFAGIYSLATNAGQGMYPFESIAMLFLFFLLGGRFMEIHARRKAGDAERLVKLIAPFCHRMGPYPAVDVRESAVVKLQAGDITVMVKGETIPVD  
GTVLGEENAVNESMLTGESLPVAKMPSEKVTAGTLNTQSPLIIRTRDTGGGTLSHIVRLDLRALAQKPKTAEABQYASSPFIPEGLLAVPVFIQNTLYDARTALMTVALLVITPCPA

LSLATPTALAASTGTLAREGILIGGKQAIETLSQTTDIIIFDRTGTLTQGNPAVRRIELIGSMTEAQLVAQSLQSEHPLARAILNCRISGGSVPEIQVQORLARIGBGVGAQLTFVME  
TQVWALGRASYVAEISGKEPQTEGGGSAYLGSQSGFQAVPYLQDPLKDSAAEAVRQLAGKNLTLHLISGDREBAVAETARALGLAHYRAQAMPKLEYVEALQKGGKVLIMIGDGINDA  
PVLQAQDVSAAVGSDIARDGADIVLLNEDLRTVAHLLDQARTRHILRQNLINWAGYNI LAFLAVLGYVQPHIALALGHSFSSLAVLGNALRLHKGKZPSEQ

## SEQ ID 4487

TTGATATATAAGAAAAATGTACAAATAAGAAAAGTTATGCAGAAAAATAAATGAAAGGATGGTTTCATTGAAAAATGGTTGTTCTGCCACCGTCATACACAGAGCCAGTATTTGGAAAA  
AAATAATCCATATGACATAATTATTCATTTGTCGA

## SEQ ID 4488

LIYKKNCHNKSIAENKMKRMVPIENGCSATVIHRASIWKKLIHIDIIPFVA

## SEQ ID 4489

ATGCCGTCTGAAGGTGACAGTTTCCTGTTGTCGACGGTTCCTGCGGACAAACGGGCGGTTTAATCCACTTCGCCCGCGTATTTGTTGCGGAGTACAGAGCGCGTGTAAATCGGAGGATG  
GCAGGTTTGATTTTGAAGAACCAGCTGCGCGGTAAGGGTGCCTGTTGGCGGTTTCGGCGCGCGCTGGCAAGTCATCGTTGACGGCAACGACTTCGCCCGCAATCGGCGCATACAGCTCG  
ATGCCGCTTTTACAGACTCAACCACACCGGACTGTTCTTCGGCGCGGAGGTTGCGCACCGACTTCGGGCGAGCTCGACAAACAGATGTCGCCAACAGCTCTTGCGCGTGATGGGTAATAC  
GACGGTAATGGTACCGTCTTCCTCAAGGCGGAGGATTCATGGCTGGCAACGATTTTCAGTTCGTGGGATGTTGTTGCTCATGTTGATTTCTCCATTGG

## SEQ ID 4490

MPSEGAIVSVCPTVAVGTGGLIHFAVLPGSQQAVVIGRIGRFDKEPACAVRVAVGGFRRANQVIVDGNDFARNRRIRHVGCGFYRLAHGTLFGGEVVRTDFGQLDKHDVAQQLLRVHGNT  
DNGTGVFFKAQPFMAGNVFQFCHDVVAHGLILHN

## SEQ ID 4491

GTGTATCAAAATCGGTATGGGTATGTAAAAAGCCGATCGTGAAGATGCGGCTTCAGGTATCGGTTGAATATTTCTTCAGAACCGGTGTAAGGACGGATGCTGACAGTTTTACGGTTC  
AGCGCGCTTTGGTTTTGAATTCGACATAACCGTCAATTTTGGCGAACAAGTGTGGCTTTTGGCCATACCTACGTTGTGCGCTGCCGTGGAAATTTGGTACCGGCTTGGCGTACGATGATG  
AACCTGCGGGAATCAGCTCGTTGCCGTAGGCTTTAACGCCAACGGTTTGGCTTC

## SEQ ID 4492

VYQIGYGVCKKPHREKMLQVSVLEFFETGVRTDADSPVQRAFGEFDITVNFGEQSVVFAHTTVVACVEFGTALAYDGTGCGQLVAVGPHQAQFGP

## SEQ ID 4493

GTGGATTTATCGGACAAATGGAATAATATGTCAATATGGATTATTTTTTCCAAATCTGGCTGTGTATGACGGTGGCAGAACCAACATTTTCAATGAAACCATCTTTTCATTTTA  
TTTTCTGCAATCTTTCTTATTTGTGACAATTTTCTTATATATCAATCACAATGATAAT

## SEQ ID 4494

VDLCKWNNYVNDYFPNTGSVIDGGRTTIFNENHPHFIPCIITFLIVTIFLIYQSHEN

## SEQ ID 4495

TTGGAATAAAGAGAAACCAAGCATATGGATTCCTACCTACGCGGAATGACGACGGTGTGTTTGGCGTAGCCAAAGCAGAAAAACATCCCTATTGTCTATTATCATGATAGGACAGCA  
GGATGTTAAAAATTAATATCATATATGATGATATA

## SEQ ID 4496

LEIKKPSIWIPTIAGHTTVFCRSQSRKPSLLSFYHDTARHLKINHYVIDI

## SEQ ID 4497

TTGAGCGCGCATTTGTGGATCAATAAGCGCTTGAATGCCGTCTGAACGGCATCAGCAATCAAAAACCCGATCTTGCCAATCAGGATTCGGGTTTTTA

## SEQ ID 4498

LSAHLWINKPLEMPSEHQQSKTPNLANDSSFL

## SEQ ID 4499

TTGTCCGTACACCACTGGACAGACGATATTTTACCTTTACCTGCATCCGCGACGAATCGTTGCGCTTTGAAAACGGACAGTTCGTGATGGTGGGCTGATGGCGGACGGCAAGCGCTGA  
TGGCGCATACAGGTCGCGCTCCGCCAATCGGGAAGAACACCTCGAATTTTTCAGCATTAAGTCCAAAGCGCGCCGCTGACAGCGCGCTGCAACACCTCAAGTTCGGGACGAGGATGTT  
AATCAGCAAAAAACCGACCGGAATCTGCTGCGCGGACCTGAATCCGGGCAACACCTTTACTTGTGAGCACCGGTACCGGCATCGCCCTTTCTTGAGCATCAACCAAGACCCCGAG  
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AAGAAAACTGATTACTACCGGATGTTTCCCGAGAGAAATCGAACACCGCGCGCCGCTGACCGACTGATGGTAAGCGGCAAACTGTTTGAAGACATCGGCTGCCCAAAATCAACCC  
GCAAGACGACCGCGGATGCTGTGCGGACGCCCGGATGCTGAAAGATACCTGCAAAAGTTTGGACGATTTGGTCTGACAGTCTCCCGAAAAACCGCGGTGCGCGGACTACCTGATT  
GAGCGCGCATTTGTGATCAA

## SEQ ID 4500

LSVHHWTDAYFTFTCIRDESLRFENGQFVWGLMADGKPLMRAYSVASANWEEHLEFSSIKVQDGLTSLRQLKVGDEVLISSKPTGTLVAGDLNPKHLYLLSTGTGIAPFLSITKDP  
IYEQFEKILLVHGVRYKDLAYYDRFTKELPEHYLGLDVKELIYPIVSREPEFHRGLTDLMSVSKLFDIGLKPINPDRAHLGSPAMLDKCKVLDGFLTVSPKTVRGDYLI  
ERAFVDQ

## SEQ ID 4501

GTGGGTACGCAATACTTTTTGGGTATGAATGCTGCCATTTGGGTTTCCGTGTCAGTAAAAAGAAATGGATAGTCTGTTGTCGGGACGTGCGGACAGTGGAAATGCTGCCCGATTCCG  
CA

## SEQ ID 4502

VVYGQYFLGIBCCHLGLSVKENDSACSGRAAEWKCLPDSG

## SEQ ID 4503

ATGACCTTACCTATGACAGGAAACCGGTTTTCTATACTGCTGGACGAATGGCGGCAAAACAGGAGGCAACCATCGCCCCCTAAGTCTGTTGCCGACGGGACCAAGGTATGGGTACGCAAG  
CAGGACGACCAATGCGCGATGGCGTTACCGCTGCTCGGTATGGTTGCCGATTTTGAAGTGGGGTGTGGAAGCGGTTCCAGCTCGGCGGAGGCTGCCATTGCAACCGGAAT  
AAAACGCGCTGACGAATTTGCGTTGCGGACGGATAGCGGTTCCCGAATTTGCTCGCCCTCCGGAATAAGTCCCTTATGTTGCGCAATTTGGAAGGCAATCCCGCTGATACGCAATCCGCA  
GAGCGGAGCGGAAAGCGGACGCTTGGCTTGGCGGTTTGAAGCCATTGCAACCGGTGCATAAAAACGGCAGTTCTTCAGTCAGGCGTTGCAAGAAATATGATGTGGGACGGAAAAA  
ACATCAGCTTTTTGGAATTTGAAGACGACCTTCCGAGGTCCTGACCATAGCCGAATGCCAAGCCCGGATTTGCTCTGCTACATCCATTGCAACCGGCTGATTTGAAAAACGGCGGACT  
GCTGGAAGCGGCTCGGAAAAATGGGCGCGGATTTGTCGGATCAGCTGCCGGAATACAAAAAGCTGATTGCCCGGACCGTCAAAACGATTCTCCGATACGACGCTGGAACACCCCGC  
TGGGACGCGGACCGCTCAGGCTGGCAGCTCGATTCTCTTAATTTCCCTCGCGGATATGCGCGG

## SEQ ID 4504

HTLPWQETRPSILLDELAQKQATIAFYLLADGTQVWVRKAGREHARWRYALLGMVARYLKLGLVLPVSLGGEPALATESKRLYZLSAGIAVPELLALAKNALMFGNLEGIPLDTQIRQ  
EAEAGKADAWLAGLEAIARVHKRQFLSQAFARNMMWDGNISFLDFEDDPSEVLTLAQQRDMLCYIHTALILKNGGLLEAAEKNGVLSQPAEIQKLIAGTVKPIPIRLLEHPR  
WGRDALRLAASISLISLADMP

## SEQ ID 4505

TTGTGCTGATTCGCCGCGAGCGGGAATCCAGACTTGTGCGGACAGAACTTATCGGTAACAAAGGTTTCTTCAATTTTATGTTCCGGATTCGCCGCTGCGCGGGGATAACGATTGAGTA  
TTTCTACATCGAATCCGCTTTTTATATCAAC



**SEQ ID 4506**

LSSEPRRRESRLVGTETYSVKRFLQFYVPDSRLRGDNDSGISTSNPLFIST

SEQ ID 4507

SEQ ID 4507

TTGATACACATTAAAGCTGAAAGTAAAAATCCGCATACACCCCTCCCTCGCATATTTCTTCAACAACAGGGTTTGATATAATCGCCTATCTGTTACAGATAGTTTCAACAGGCATTTCAACCCCTTACAAATCCCGCTTGAAATCATCGGCATCCGCCATATGCAAGAGATATTTATGAGTTTACACAGCGACATCCCTCGTCGTCGGCGCAGGCCCGCGGGTTTAAGTTTTCGACGCGCAACTTTCGGCAGCGGTGTGAAGTTTACTCTGTATGCGAAGCGAGCCCACTGACTGTTCTGCAAAATCTTCCCTATGACGGAGCGGAAATCGCCCTGACCCATTTTTCGCCGGAATCATGTCAGCGTTTGCGATGCGGACAAAATTTCCCGAAAACGAAATCTACCCCTTTCGCGCATGCGAAAGTGCTGAAACGGACGTTCCGACTTACAGCTTCCATTTTCCCCAAACGACTGAAGCGCGCGCGGAGCGCTGCCGACTGTTTGGGTATCTGATTTTCCAAACCAATATCCGCCGCGCGCGCTGAGAGTGCTTACCAACTTCGACATTCGACATCTGACCTTCTGACCATTTCTGACCGATCTGACCCGTTAAAGAAGTCAAACATCCCGACTGTTTGGGTATCTGATTTTCCAAACCAATATCCGCCGCGCGCGCTGAGAGTGCTTACCAACTTCGACATTCGACATCTGACCTTCTGACCATTTCTGACCGATCTGACCCGTTAAAGAAGTCAAACATCTGATATAATGAAGCGCAAGTCTTTTGGAAAATCGAGACATTTCAACCGCGGTCTTCCTTGTGAGCAGACAGCGCGTTCTCACAACCCCGCCGACACTCGGTATTTCTTCAGATATGCACGACTACGACCGCAACCATTTGCTGTCGCCGATGAACATCTACCTTTTCCAAACCAATATCCGCTTACGAATGCTTCCATTACGGACCGACCATCGCATGCTGCGCACTGGAAAGCGCTGACCAATACCGCTTATACAGTCGATACCGGATAAAATCAACAGCGTTTCAAAACCTTTTCGCCCGAAGAAATGGCGGGCAAGCGTAAAGAAGACAGCTTACGGCCAGGCTCGCGGACATGGAACTGTTCAGCAGCATCCACCATTACCCCTTTGTGCGCATGATTTGCCAAACGTTTCTACGGCAACCGCAGCGCGCTCGGATCGGCTGCGGATCGGCTTCTGTTGGTGGAAAAATACAGCAGCAACATATGCTGCACGCCCCCTCGGGCTTTTCAGCGCGGATATTTCTGGCAAACTGATACTCGAAGCCGAACCGCGCGCTTCAAGCATTCGATCGCGCGCTTCTGTTGGTGGAAAAATACAGCAGCAACATATGCTGCACGCCCCATCCGCTTTATCACGGCACCAATATGATGCTGAAACGTTTACCAACGAAACCGCGCGGCAAAACTGTTGCGCGGTTTGGTATTTACGACCGCGCAACACTTCCCGCGCTGAAAAAGCTGATTACCAAAACATGACCGGT.

**SEQ ID 4508**

SEQ ID 4508

LRIHLKKVKIRIHPPLHISSTGFDIIAYLLQIVQTAPKFLPMPSIIGIRLCKGYFMSLHSDILVVGAGPAGLSFAAELAGSGLKVTILERSPLTVLQNPFDGREIALTHFSREIMQRL  
GMWDKIPENETYPRLDAKVLNRSYDYLQHPPTFARGEPADCLGYLISNHNIRRAAYEVVSQLDNVISITDTAVKEVKTSDNEAQVPLENGDILTARLLLAADSRFSQTRRQLGISSDMH  
DYSRTMFCVRMKHITLSNQTATCYBHYGRTIALLPLEKRLTNVTIVTDDKINSVQNLSPFEELASVKQLKGRGLDMELVSSITHYPLVGMIAKRFYKRSALIGDAAVGMHPVTAHGFN  
IGLSSADILAKLILEABORGQDIGAASILEKYSKHEMLHAHPLVYHGTNMLKLPNTETAPAKLLGLVLRAAGNFPPLKKLITQQLTG

SEQ ID 4509

SEQ ID 4509  
GTGCAGATGCCGCTGAAAAATAACCCCTACCAATGGAGAATCAAACCATGAGCAACAACATCCCAACAGAACTGAAATACGTTGCCAGCCATGAATGGCTGCGCCTGAAGAAGACGGTA  
CCATTACCGTCGGTATTACCCATCACGCGCAAGAGCTGTGTGGCGACATCGTGTGTGTGAGCTGCCCGAAGTCGGTGCGAACCTCGCCGCCGAAGACAGTCCGGTGTGGTTGAGTCTGT  
AAAAGCCGCATCCGAGCGTGTATGCGCGGATTGCGGGCGAAGTCGTTGCGCTCAACGATGACTTGCAGGCGCGCGGAAACCGCCACAGCGACCCCTTACGGCGCAGGCTGGTTCTTCAA  
ATCAAACCTGCCAATCTGCCGATTACGACGCGCTGCTGACTGCCGAACAATA CGCGGGCGAAGTGGAT

SEQ ID 4510

SEQ ID 4510  
VQPMSENPLMEVQTMNNIPTELKYVASHENLRLEEDGTTTGGITHAQELLGDIVFVELPEVGANLAAEQSGVSVKAAADVYAPIAGEVVAWDDLPGAPETANSDFYAGWFFK  
IKPANPADYDGLLTABQYAGEVD

**SEQ ID 4511**

SEQ ID 4511

ATGCGGCTGTAATCCGTTTTCCTGCAATTTGCACAAACGAGAAAAATCATGAGATACATCAGCACGCCGCCGGCGAAACCGCACAAACCGTTTCAGCGAAGTTTATTGATGGGGCTTGACACCGACGCCGCCGATGATGCTGCGCGGAACATTATCCGCAAAATCGGGCGCGAAACCTTTGGACAAATGCGCGCGTTTGGCTTATCCGGAATTTGGCGTTTGAAATCATGTGCGCTGTTCTGTTACCGGATATTCGCGGACAGCATTTGAGCGCATTTCTGAGACCATTTCTGACATTCGACCGAAGCGCGTTTCGCTACTAAGGAATCACCCCGTCGCGACGCTTTCAGAGCGGCATCAAAATCCAAGCCTTGTC AACGCCCGGACGCTGGCGTTCAAAGATATGGCGATGCAGTTTTTGGGCAATCGCTTTGAATATGTTTAAACAAGAAGCGAAAAAAGCTCAATATCTTGGGCGCAACCAGCGCGGATACGG GTTCGGCTGCGGAATATGCCTTGCGCGGCAAAAAAGCGGTGAACGATATTATGTGTCGCGCGACGTTAAATGAGCGCGTTCCAAAGCGCGCAGATGTACAGCCTGCAAGACGGGAATAT GCACAAATATCGCCGTAAGAGGGAATGTTTGACGATGCCAGGACATTTGGAAGCGAGTCAGAACGATGCCGCGTTCAAGGAAAAATACCATATCGGTACGGTCAATTTCGATCAACTGGGG CCATCGCTGCGCGCAAGTGCGTTATTACTTTGCGCATTTTCAAGTGCACCTTCAAGCAATGACGAAACCGTCAGCTTTTGGCTACCGAGCGGCAACTTCGGCAAGCTTTGCGCGGGACACA CGCAACAAATAATGGGCTGCGCTGTCGCGCTGATTTGTCGCGACCAATGAAACGATGTGCTGGACGAGTTTTCACAAACCGCGCGCATACCGCCCGCGCAACAGCGCGCATCTTATGT AACCTCCAGCCGCTCTATGAGCAATTTCCAAAGCGTCCAACCTTCGAGCGTTTCGTGTTTCGACCTGATGATCGCATCTCTCAAGCAAGCTTCAATACGTGTGGGCGGAAGTTCGCGCGGACGAA GGCCTTGACCTGCGGTTTTCGCTTGGACAAAGTCGCGCGCAATACGGCTTTTACCTCCGCGCAAAATCTACCCACGCCGACCGGCTGCGCAAGCTTTCGATGCGACCAATACGCGGAAGC TCATTCGACCCGCATCTGCCAACGGCGTAAAGTCGCCCGCGAAGTGGCGAAGCGGGCAACGCGGTTTGTGTTGGAACCCGCGTTGGCGGCGAAATTCGATGCGACCAATACGCGGAAGC CGTCGCGCATGTGCGCATTTCCGCGCCCGCGCGCTGGAAGGTTTGGAAAACTGCGCGAGCGGTGCAACCGTGCCGAACAGTGCAGTTCGCGTAAAGGCATCATCGCAACAAACCTT GCT

SEQ ID 4512

SEQ ID 4512

NPSESVLQFRQTRKIMRYISTRGETAHKPFSEVLMLGLAFDGGMLPEHYPIQIGRETLDKWRGLAYPELAFEMCLFVTDIPEDLDRLILNRTTYEAFGTKEITFVRTLSGDIKIQALS  
NGPTLAFKIMAMQFLGNAFEYVLNKEGKKLNLGATSGDTGSAEYALRKGKGVNFMFLSPDGKMSAFQRAQMYSLQDGNHNLAVKGMPDDCQDIVKAVQNDAAFKEKYHIGTVNSIMWG  
RIVAQVYVYFAGYFNATSSNDETVPSCVPISGNFVNCAGHIAKMGFLPVRLCLVATNENDVLDEFFKTYATYPRNSAHTYTVTSSPSMDISKANSFERFVFDLMDRDPQIEHNLWAEVAAKG  
GFDLRFALDKVGKRYGPTSGKSTHADRLATIRQVYEQDKELIDPHTANGVKVAREVREAGETVVCLETLAAKFDTATIREAVGQVAI PRPAALBGLLENLPQRVQVTPNSADAVKGLIIEQTL  
A

SEQ ID 4513

SEQ ID 4513  
ATGTTGCCGGGCTCAACCGGATATTCAAACGGTTTGCTCCAACACTCGGAACCGGCGCATAAACCGCGCCCTTCGCGTTATCCGGAACGGGGCGGCTAATCAGATCTTATGCCCATAAAA  
GGCGGGGTTTCAACCGGAAAGGAATTGAGATGAATAAAACCTTGTCTATTTCGCGCGGGCAATCTTACTCGGCGGGTGCGCCGCGCGGGCAACACATTTCGCAGCTTAGACGGCGGCAC  
GGGTATGGGTGGCAGCATCGTCAAAATGACGGTAGAAAGCCAAATGCCGTGCGGAATTGGACAGGCGCAGCAATGGCGTTGACCGCGCTGGCGATGAGTGCCGAAACACAGGCGGAATGG  
GAAACACAGATTTCGGCTGCGCTACCGAAGAAGCACCTAACCGTGTACCGGCAACGATGTGATGCAGATGCTGAACAGTCCACGCGCAATCAGGCACCTTGCCGCGCTGACCGTCAAAA  
CGGTTTCCGCTGCTCAAACCGCTGTACCGC

**SEQ ID 4514**

SEQ ID 4514  
MLPGFNRIKRFAPTLGTAHKTPPFALSRGTGLRLRSYRHKRGFNKRGIEKNKTLNILPAAILGGCAAGNNTFGSLDGGTGMGGSTVKNVTVESQCRBELDRRSEWRILATALAMSAEKQAEW  
ENKICGCATEEAPNQLTGNDVQMQLNSTRNQALALTVKTVSACFKRLYR

**SEQ ID 4515**

SEQ ID 4515  
GTGTGGCGATGGGTGCGGTGCGGATGCTGCCCGTATCCCTCGGTTTTTGGAGCAGTTCAAATCTTTGGGCTAGGCTGAATCGAAATGCCGTCTGAACCGGTTTCAGACGGCATTTTTG  
CAACAGGCATAATGACGGCGCGCGGATTTTTTAATTTCCCGAT

SEQ ID 4516

SEQ ID 4516  
VWVWVSGCCPVSLRFWSSNLWARKSQMPSEPVS DGI FANRQNDGGGIFYPFD

SEQ ID 4517

SEQ ID 4517  
TTGACGATGCTGTTGGATAATTGGGCTTAATCGGCTGCAAGAACCAGCGCGCAATTAGGTTTTGTGCGACGAGTATTGATACCGGCAGTAGGTTCTTAATCTTGTGTGGCGATGG  
GTGGCGTCGGGATGCTGCCCGGTATCCCTCCGTTTTTGGAGCAGTTCAAATCTTTGGCC

SEQ ID 4518

SEQ ID 4518  
LTHLLDNLGLIGCKERSAQLGFVGRVLIPIAVGFLILCVANGAVGNLPGIPPFLEQFKSLG



## SEQ ID 4519

TTGCCGACGCGCAGAAATTTTTGGTGTCTTCCATTTCGGGTATGGCTGTGCAATGTGGTCGCCGATTTTTAGGACATCAAGTGTCCAAAAATCAGCTATCCGGAACCCG  
ATAAGGTATGTATGAATATAGACGACACCATGACAGTGTCTGTCTCGTCAAGCAGTGGGTCTATTTTAGGGGGTCAAAATTTTACCTCTCTTGGGGAACCTATATCGTCCGCGCATC  
GATTGCCAAACACCCCATCCGGGCGGTGCGGTTTAAACGCGGTTTATGTATTATCGCGGGTGTGGGCTATCCGATGGACTTGGCGATTTGGCAGCCGGTATGATCGTAGGCGTA  
TGCTTACCGCTTTTGAAGCGGCGATGGAATGACGCGCAAGGCAAAACACCACCAATCCCGCCCATCGTGGTGTCTCTTCCGCTGGTCAATCCGGTTTCCGCTGGGCGT

## SEQ ID 4520

LPTAESFLVFFPFAVLAVAMWSPDFLGHQVFKISYPEKTDKVLNIDDTHTSCSVQAVSILGGANFTSSHTYIVPASIAKEPIPGGAVLTAVLCIIAGLHGYPHDLAIWQPVILVGV  
CLPILLRAGMEMTRKGTQSAALVFFSSVNSIRFSAGR

## SEQ ID 4521

TTGAAACTGCCGAAATGCCGTCTGAAACGTTTCAGACGGCATTTTGTATATGAACCGTTTCCGCTTCCATATCCTTGGCAGACGGTTTGCAGCAGATTCCGATACGGCAGATGTTT  
CAAGCAGAAAGGAAACACAA

## SEQ ID 4522

LKTAEMPSFTFQTAFLYEPFCGPHLGRFPAADSHADVSSRKETQ

## SEQ ID 4523

TTGCCCTTCGTCGCCGCGAGCGCGGATGTATGTTTTTCGATACAGAAGGAAATCCCATCTGCAATATTTATGAAATCGTTGGCGGCAATGGAAGATTGCCGCGGAGGTGGTGATAG  
ACGGGGAATATGCTCTGTATATTGTCCGATGAATGATGATTGAGTATGCCGTGCAAGATAAAGGGTAGAAGCCGTGCTTCCGACCTGGAAGCATTTGTCGCAAGCGAAATCATTATAC  
CCTAATTGCGTTTCAGCGGTTATGCGGCGCAGTTGAAGTGGATAAAGTATCGGCTGTTACAGGCATTTGTGAGATTACCGCAGCAAGGCGCTGAAGGTTGCCGTTGCAGACAATATGAGG  
CCCAACAAGAAATCGTTGATTTCCGTGCAAGCGCGTAATGGCAAGTAATAAGCGCAAGATAAACGAAGCATATTTGGATTATCTGATCTCTAACTGCCCTCCGCCCAAAAGCAAG  
AATTGGAACAAGATAAAACAATATGATTGCGCTCCATTACGACGCTTGAAGAATTAATCGCAGAGGTATCTGCGTACCG

## SEQ ID 4524

LRFVAGERGLMFPDTEGKSHTAIFMKIVGGNGKLIAGEVVIDGEYALDIVRHNDLSIAVDNKRGRSRASDLALSOAKSPFLIAPSRVAGTVBVDKVSATVGCADYRSKGLKVAADNRH  
PKQEIIVVFRASGVMAKNRKLINBAYLDYSASSKLPSAQKQLEQDKNNMIAVHYGRLEELIARGICVR

## SEQ ID 4525

TTGGGCTGCTGACAGCTTTGTACTGGAATATGTCGCTATGAGCTTTTAATGCCGCCGCGTCTATCTTATTTGGTATCGGGCTTTTTCTGCCGCCGCCAACCTGCCCGGTACGCAGC  
GGCCGCTGATTCCGATGATTCCCATCGTTGTGTGCGGCGGCGGCGCATCTTTGGCGTTCGGCATTTTCGATTTCGGTTTAGGTCTGCTGATGGCTTTATTTCCGCGCGGCGATTTATGCG  
GAAGCTGACAAGCAACGGGTATGCGGCGGATTTACTCTATTTGGCTTTATCGGCAGCAGCGGCGAGTAAAAAATTTGTTTTCGTTGGCGAGCGGTTTAAATATGCCCTACATCGCT  
TTTACCGTCATTTATTAACGATTGTGATGATACGCTTTGTTGGAGCATTTGAAAAACCGCTGGTTGGCGCTGCCCTTTGGGATGCTTGATTGCCGCTGTGGCGGCATTGCAATGGGTGCGC  
CGTTTCAGTTTCACACCGCCCGCGCTGCCCTCAATGAGTCTGCTTATTTG

## SEQ ID 4526

LGLPDSFVLENVRYELLIAAASILLVSGFPLPGANLPQTHGLPIHPIVIVSAGGHPLAFGISIAVLGLLMLFRGGSINAKLTSNGVCGLLLYLIGFIGTGTQVKKLPSWAGGFNMPYIA  
FTVLIIVTIVMYALLEHKKRWLAAPLGLCLAGVAAPALGAPFEPHTAPGLPMPSPAYW

## SEQ ID 4527

TTGGGCTTTAATGGGTTACGGCTTCGGAACGAGCCCGTATCAAAAGAAAAGTACGCGCCCTTTTACGAGGCGGATATATAAGGAGGAAGGTTATGGAACATAATAGGACTT  
ATCGGATTTACACCGTCCGGCTTCGGAATTTGCGACGCGGGAAGATTTGGAACATGAATTCAGATTATGCAACCAAAACGCTGGCGGCCCAACCTGCGCTTCGCGGATTACCGCTT  
CGAGTGGGAGGATTTGATCTCCGCGATGGCGGAACGATTGGAAGTGGTGTGGGGGCGCGCGCGCTTTGCGCACCTTTGGGGCTGCG

## SEQ ID 4528

LGFWGYGFRTPQVSKRKMVRPFYEARYIRKVMKHNTRYDLHRPASEFATREYLEHLQIMQPKRWRPNLPFRDYRFWEEDLIAMAGTIKGVHVGGGVCRTFGAA

## SEQ ID 4529

ATGTATCCCTCTCTGTGCGGATGTTTTCTATATTTGTGCAATCGAAATCTTTTAGCGGATTTGTGCTGAAATTAACTTTTAATCAAGTGGTTGTAAATGTATCAGTTTTCCGATG  
ATGATTAT

## SEQ ID 4530

MYPSLCGFLYLGNRLILGGLLLKINFLIKHFNVCISFPDDDY

## SEQ ID 4531

ATGGATGCCGTACAAATAAAAATCATTTGTGCGCGTCGCGCACGAGGGCAACCTTACCACAAACGCCAAACGACTTTTCTTTCCAGCGCTGCCGTTTCCGCCAAATTAAGCCCTTTGAAG  
AATATGTGCGCACGCCGCTGTTCAGGAGCAGCGGGAAGGCGATGTTATGACGCGGCGGGCGAAATCTGTTGCCGGAAGCGGAATCCCTGCTGCAATACAAACACAAGTTGAGTATTT  
TGCCAAACCGCTGGCAGCGGATTTTCGGAAGAGACAGTTTGGGCATTATCCACCCCATCGATTTCGGCAAAACTCGTTCGCGCTGACGGAACAATATCGGTCAAAACAGCCCCCAAAACGCG  
CCTGCACATCCATACGGAATGAGCGCGCAATCTCTCGCGCATCCAACCAAAACCTGACGCGGCTTTTACTCGGCAACGCGGCCAAAGCGGCATCGCAGCGTATTCCTGCAA  
AACCTGACCTACGCGCTGATTTGCCCGCAAGCCAATATTCGCGGTGACCGCTCTCTTCGCGAGAGCTGCAAGAATGCGTATGATAGAAATGTGCGGCTGTGCGGGAAG

## SEQ ID 4532

MDAVQLKSPFAVAHEGNLTQAKRLFLSQPAVSAQIKALEEYVGTPLFRSTGKGMVLTRAGEILLPEASLIQYKHLEYFAKTLAGDYSEETSLGIHPIDSAKLVALTDNIQTAPQNA  
PAHPIRNERRNPLAHTQNPARRLYTRQRRRHPQRIPAKPDLRADLPKPIFPADPLPSAEPARMRDRNVGRVRK

## SEQ ID 4533

ATGAGCGGCGAAATCTCTCGCGCATCCACACAAAACCTGACGCGGCTTTATCTCGGCAACGCCGCCCAAGCGCGCATCCGAGCGTATTCCTGCAAAACCTGACCTAGCGCTGA  
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CAGCAACCGGCTCTCACCCAAAAACAGATTTGTGCGACTACCCCAAAACCTTATCGATTGTTGTTGCGCGGTATAGGTGTGGCAATGTTGCGAGGAAACAAAGCCGAGCGCGGCG  
AAAAGAAGCGCGGCGTGGCTATTATCGAATGTCGCCGACAGTATGCCGCTCAATTTTATTCGCGGAAGATACGAGGA

## SEQ ID 4534

MSGELLRIQKFLHGGFLLGNAAGGIRSVFLQNLTYALICPQSQYSRLTSLPQSLQBCVWIRMSGVSGSRKHLHQFWRSNRLSPKKTDIVRLFPNPFPGCRRYRCNGAGKQSRSGG  
KRRRGYAYRIVPYQAAPHLGRIRG

## SEQ ID 4535

TTGTGCGACTACCCCAAAACCTTATCGATTGTTGTCAGGCGGTATAGGTGTGGCAATGGTGCAGGAAACAAAGCCGAAAGCGCGGCGTGGCTATTATCGAAT  
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CGTTGCTCTCGGACAC

## SEQ ID 4536

LCDPQTLIDLWAGIGVAMVQGNKABAAKEGAGVAITESCRRHSMPLNFTYAREEYEDNPHVSLILLECEKVVGVQAVQPPVVSIN

## SEQ ID 4537

ATGAACCGTTTTCGGTTTCCATATCCTTGGCAGACGGTTTGCAGCAGATTCCGATACGGCAGATGTTTCAAGCAGAAAGGAAACACAATAAAAAATAAAAAGCCTCCGACAGTCCGAGG  
CTTTGCTTTCAAC



KDKIRKYLALYNTTQYIDKEGDETYIDNVLIKIGLRNRVIARNHMQLWGKGYNTLFSISTEYGRKFLDDDKLWRITPQVQLQYSYLRGTGYRIDNGINVLSHANSILIGRLGLDV  
VRKFDGKKLFYIKGNIPHEPLGSRSFKAPEKSHYAQK

## SEQ ID 4545

TTGAGAGTACAAGTTTAAAAAGGGGTATTGAAACGGCTTTTAAATCCAATACCGTATTAAACGGGAATAACAATAAAATATCCATCACCAGTGGGCGACGGCTTGGGATTGGCGTTAA  
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CAAGGGGAATAATGAAGTTGATTAAATGTAAAAAACCGCTCCGTAAAAAGGCATTTATCAGCTCGCATTTCTGCAAAAGCAACGCTTGAAGCGCAGGAGGATAATATTGTCGGGTAA  
AATCCGGACACCAAGACGGCTTTAATCAATGCTGGAAGAAAAATACCCCAATAATTGCCAGAACCATACAGGTTGGGGGTTCAATCCACGAT

## SEQ ID 4546

LRVQVFLRGIFETAFKSNVLTGNKKISITTEBDGLGLGVNGLQSNFSYSGHTTGTINNQPSTNTQPSLDGTSTIELKAVKGNNEVDLNVKNEASVKGIIITSHSAKATLEAEKDNIVRVK  
NPDFTALINAWKEKYFNNSPEFYRVGGSIDH

## SEQ ID 4547

TTGGAATTTATTACACCGGGGAAGGGCAGATGGAGACTTACTGGTCAACGGTCTTACGGCATCCGTCTTTGCGAGACTAAAAATGGAATACAAACCCGAATTATCGGTGAGAAGCA  
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AGATCCAACACACATCAAGAAAAGTTAGTGAACGATAACGCTTTAGTGGGTATGTCAACATATCACCCCTCCGATGAAAATGACAAAGGCAGCATATCTTCCATTCAAAACAGGC  
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## SEQ ID 4548

LELITTEGADGDLVNGSYGIRSPADLKLEYKPELSVRNHDIIFNNDQSVVDVQPSYSGNIHLVVGKIQFNLNVADKVTPTTHQEKLVMDNALVRYVNNITPSDENDKGSISSFHKTG  
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## SEQ ID 4549

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## SEQ ID 4550

MTDLFVREDAPIAERLRPHLDDVIGQHLIGEGKPLRVAVBEGKPHSMLLWGPVGKTTLARIQAQSFNAQFLPVSASFVSGVDIRGAIDKAEIALQQGRATILFVDEVHRFNKAQDD  
AFLPHVESGLLTFIATTENPSPFVNPALLSRAQVYVLQSLSSDDLKLLIARVLALPEYRDFPIEADVQELIVNTADGDARLLNLLEQLRAADTRRLKILITEFLADSLGAQIRRFDRG  
GESFYNIQISALHRSVRGSHPNALYWFPCRLMDGGTDPYRLARRIVRIAWEDIGLADPRAPQLANDAAATFERLGSPEGLALAQAIVLYLAAAANKSAGYKAYNQMRFPVKENASDEVFVHL  
RNAPTKLAKELGYGREYRYAHDEFNAYAGESYMPDGLDEPDPYQVPVPRGLEIKIGEKLAWSLDEALKAK

## SEQ ID 4551

TTGAGAACTGCTGCTGAAACACACCCGCTTTCATCAAGCCATCAAGATCGAGCGCGAAGCCCGTAGATTTTGCGCGCTGGGAACCTGCCATCCATTATGGTTCGCAATCGCGAAC  
ACGAAGCCGTCGCGACCGACGCGGCTATGTTTACGATATCCCATATGCTCGTTACCGAGCTGCTCGGAGCGAACGCCAAAGCCCTTTTCCGCAAAATGATGCGCAACGAGTTCGCAAACT  
CGCTTTTGTGCGCAAGCCCTTTATTCGCTTTGCTCAACGACACGCGCGGCTGATTGACGACTTGATCGTTTACCGCAACGAGCGCGCAACCCCAATACCGCATCGTGTCCAAACGCT  
CGGACCGCTGAAAGACACGCGCAATTTCCAAAGCTCGGACAGAGTTGCGGCTTGCCTTCAATCCGCGCTACGACCTCGGTATGCTTTCGCGTACAGGCTCTAAAGCCATTGAAAAAC  
TCCGACCGTCAACCCGCAATGGCGGGATGATTACGCGCTCAACCGTTTCCAAAGCGCGGATTGGGCAACGACTGGTTTGTGCGCGCTACAGGCTACACCGCGCAAGACGCGCTGCA  
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GAAACAATCTATCGCCATCGCCCGGTACCGAAGATTTTGACGCGGATACCGCAAGTCTGATTTCGCGCAAGAAAGCGGAGCTGCGGTACTGAAGCTGCCGTTCTGCGCCAGCGGT  
CAAAACAGTTTGTAT

## SEQ ID 4552

LRMTALKTTPFHQAQDAGAPVDFAWELPIHYGSQIAEHEAVRTDAGMFDVSHMLVTDVVCANAKAPFRKLIANDVAKLAFVKGALYSALLANDNGVDDILIVYRTNEATQYRIVSNG  
ATREKDTAQPHKVGQEFVAFNPYDLGLAVQGPKAIEKLLTVKPEWADVIHLKPFQGADLNDWVARTGYTGEDGVEVILPDTEAVAFKALQTAGVQPCGLGARDTLRMEAGMNLV  
GNDMDDTSPLEAGMGRVTDLKDERSDFVGKALLALKKEGVAVKQVGLLLEKGGILRAHMEVITDKKGGETTSGVFSPLKQSIALARVPKDFDGTAKVLIRGKEADVRLKLPFVRSG  
QKQFD

## SEQ ID 4553

ATCGCGATAAAATCAAACTGGAATCCGCTGACAGGTACTGGCCACTTCTACACCACTACCAAAATAAAGCAGCTATGCCCGCAAACTGGAATCAAAAAATTCGATCCGCTTCCCGCA  
AACAGTAGTGTACAAGAAACCAAACTGAAA

## SEQ ID 4554

MRDKIKLESGAGTGHFPTTKNKRTPGKLEIKFDPVARKHVYKTKLK

## SEQ ID 4555

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TTATTGAACAGGCGCAGCGCAATTTACTGCCGCGATTAGTGTGCTTACCATCGACAGCGCGAAGCCTTGTCTGCCGACATCAATCCGCCCAAACTTTGCAACCAACCGCAGCA





**SEQ ID 4566**

**SEQ ID 4567**

**SEQ ID 4568**

**SEQ ID 4569**

**SEQ ID 4570**

**SEQ ID 4571**

**SEQ ID 4572**

**SEQ ID 4573**

**SEQ ID 4574**

**SEQ ID 4575**

**SEQ ID 4576**

SEQ ID 4576  
 NLYICFTYCIISVQTKRTRSVGLDFAFFGPRVTSNSSFPRRRESGSSGFCVISDEFLNLFPPGFSLSGKERHKYFPNQTCKRLKGFQTAF



## SEQ ID 4577

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CACCATGTGCCATATTTCCCCCATCCCGAAATCTTAGCGGACATCAAGCGCGTAAATGGTCATCATCCGATGCCGAAGACCGGAAAAAGAGCGACCTGCTGATGGCGCGCAA  
TTCGTTACCCCGAAGCGCGTCAACTTTATGATCAACACGCGCGCGCTTAGTCTGCTTCGCTATGGAAGGTGCAATGGTTCGAAAACTCGGCTCTGGCGATGATGACCCAAAAAAGCGCG  
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CAACAGGCGGAAAGCGCGTCTCATCTCTCTGCAACACCGAAGACGCGCATCTCTGCTCGAAGCGACCTTACCAAGGCGCAAAACCAAGCTTCAAAATGGGACAGCAAAAGCTACG  
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AAAA

## SEQ ID 4578

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FVTPEAVNFMILKHARGLVCLPMEGAMVEKLGLPMTQKNGAQYQNTFVSLAAHGTITGISAADRALTIQAVSPAKPADIVQPHIPLRAQKGVLRAGHTBAGVDLAQMNGLIPA  
AVICEIINDDGTMRMPELMKFAEHLKI GTIADLIEYRSRTESLLEDMDAPVQPPWGEFQGHVIVDKLSGETHLALVKGTPSADTBTLVVRVHEPFSVMDFIQANPRHSWSLPAKLERV  
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## SEQ ID 4579

TGTGTTTTGCGCAATCGGATATTTCGCTTTTGTAAACAGATGCGGTTTGAAGCGGATTCGTGGCTTCAGACGCGATTGCCGCAACCCCGCGCGCGCGCGCTGTTCTTCCGCGAC  
GCTTC

## SEQ ID 4580

LFFAKSDYLPFGKMPFEAGFVADGIAATPPAGRLFLPARF

## SEQ ID 4581

GTGCGGGAAGAAACAGCCGCCCGCGCGGGGTGCGGCAATGCCGCTGGAAGCCAGAAATCCGGCTTCAACAGCGCATCTGTTTACCAAAAGGCAATAATCCGATTGGCGAAAAACAA  
ATTTGCTTTTGTAGTAATACGCGCTTACAATCCGTACATCCGATTCTTCAAAAGGATAAAACGA

## SEQ ID 4582

VREETAAPPAGLRQCRKPRIRLQTASVYQKANNP IWRKTNLLPSKYALTIRYIRFLQRIK

## SEQ ID 4583

TTGATTCCCGGGTACGCGATAGCGGTACGAGCAGGCGCAATACCGGCAATCTATGATGAATGCCGCTTCCCGATAAAAAACCGGAGGATGCGCTTTTACTTTCTACAAGTAACAGGGC  
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## SEQ ID 4584

LIAGYIGGTSRRNTGNMNAAPPIRTGRIAFYFLQVTGLFFARF

## SEQ ID 4585

ATGTTTGATGGCAAGTAGAAGCAGATGAAAGTTATTTTGGCGGACACCGCAAGGTAAATGCGGTGCGCGTGTCCCGGAAAGTCGAGTATTCAGGCTTCTCAACAGAAATGGCAAGG  
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GCTTCTGCGGTCGCGCGCGGCTCCGTATCATCAGCGCGCAACCGCTTTTTCATCCCTGCTTATCTTCCATGCTGCGAATCTCTCAAAACCGGCGAAAAAAGCCCTGTACTGTGATA  
AAG

## SEQ ID 4586

MFDGEVEADESYFGQRKGKCGRGAAGKVAVPRLKRNKVSFAVRYVRFTFEDFLNPARRFGRFTPLLDKGGKIRSGCRLPAVRRVRHHAGNRLFHPLLIIFHGANPQKRAKSPVTCR  
K

## SEQ ID 4587

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ACCGGAAAGAAAGGCGTTCCGCGCGGCAAGTATCATGACCGCTTTCGACGCGGCGCGCAAAATTCGACAAACACAGCTACAAATCTCCGCGCGCTGACGCGGTGGCGGTATCCGTGCT  
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AGGTTTGGCGAGATGAACCCCGAGCAGCTTTGGGAAACCAAGATGCGCGCTGCGCGCGCTGTTTGAAGTGGCATCGAAGATGCCATTCGCGCGGACGAGGTGCTGTTACCTG  
ATGCGCGACGAGGTGCAACCGCGCGCGCTTTATCGAAAAACTGCGCTGATTCGCGCAAAATATCGACGCA

## SEQ ID 4588

VAKRPFCHFAGKFRARTGRKCAARPFRRHDPADNAESGGEIGYNTQLYAPSRPLFPQGADCFGGIAKSFQNPAKNMTBQKHEEYGADSIQVLEGLAVRKRPMYIGDTQDGSGLHMFVE  
VLDAIDEALAGHCDKTTVTIADHSVSVADNCRGMPTEIHPKEGRSAEIVMTVLHAGGKFDNNYSIKSGELHGVGVSVVNLSDWVTLITTYRDKHEPVRVFRGETEELKIVGSDKK  
GTTVRFAGTETFTGNIEYSPDILAKRIRELSPLNNGVDIELTDERDGRHESFALSGGVAGFVQYMNRRKTPLEKIFYAFGEKDGMSVECANQWNSYQESVQCFNNIPQRDQTHLAL

RQVWTRTINSYIEANEVAKKAKVETAGDDMRGLTCVLSVKLPDPKPSSTQDKLVSGEIGFVVNEVINQALDPLFLENPNRAKIIITGKIVDAARAREARKAREITRRKGMVMDGLGLPGK  
LADQCEKDPALSELVYVEGDSAGGSAMQGRDRKFOAILPLKGLILNVEKARPEKMLASQEVATLITAGAGIGKEEFNPEKLYRHRIIIMTDADVDAHIRTLLITFFYRQMPLELVERGYI  
YIAOPPLYKAKYKQERYLKDELEKQWLLGLALEKAKIVSDGRPIEGAEADATQFLAKTVIEQESRPVDELVRAMLHASPIDLTSSENADKAVAEISGLLDEFEALERIIEGHEGH  
RFIKITRKLHGNVWVSYIEPKPLNSKAYQTLTQTAALKGLVGEKAKLYKGENEYDADSPETALDILMSVAQKMSIQRYKGLGEMNPEQLHETMTDPAVRRLILKVRIEDAIAADESVFVTL  
MGDEVEPRRAFIENNALIAQHIDA

## SEQ ID 4589

TTGCGCGGTGTCTGAATGGTGGTTACAGACGGCTTCTCCCTTCGGTGGACGTTATCTAACCGCGCTCTCCAGATTGTTTGTTCATGTGCAGTCCCTGATACCTGAGCGATTAAAGG  
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TCTGTTTTCACATGATTTCGGAACAAATTTGTCGGATGACGATATACTTTTATATGTTAATATGGTCTCCATCTATCGGATTCGCGCAACACACGGACAGACAATCCGAAT  
TCCTTAAACCGAACGCAATATGCCCCAATCACTTTAGACAAAACCGATATAAATCTTACAGGTCTCCAGGAAACCGGAGGTGACCAATGTCGAAGTCTCGAACGTGTGCAC  
TTTCGCTTCTCCGCTGCGCGCTCTGAAGCAGTTGGAAGATGCGGCGATCGTCCGCAATATGCGCGCTCTCTCCGGAATCCGTCACTTAGGTCTTCAGGCATTATCCGCT  
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ACCGATATGAACCGGTTTCCCATTTGTTTGGATACGCTTTATCCACCACGCGGTACAGGATGCGCAATCGAGCTTTGTTTAAAAGAAATCAACACACCCACTCCCTGCGGCTCA  
ACCACCTGCTGAAGAA

## SEQ ID 4590

LRGCLNGSGDGLLPFGGRYSNAALQIVCFNVQSLIPERFKGVCAFPGYTVVGCNTLLHLSRLCLESANWASRLKRDANRPPLFSHDFFPKTFVPDDGTYFYMLIWSPSMRILANTRTNDPN  
SLKRNANMPQLTLDKTDIKLQVLQENGRITNVLSERVALSPSCLRLRLKQLEDAGIVRQYAAILSPSVNLGLQAFIRVSIKAKDAREDFAAASVRKWPBVLSCFALTGETDYLLQAFP  
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## SEQ ID 4591

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CGCAGCGCAACAAACAAACAAACCGCGTTTTCGCCCACTTGCAATCAGCGCTTTTGGGTAGAAAGTGAAAACCGCTGGGTTCGCGCTGCGCGTTTCCAAACGCTGCATTCGCTATCCAT  
CGACAAAGTAGGCATTGATGCTGATTGGCTGATTTCGCTGCTCGCGCGCAAGCT

## SEQ ID 4592

LKRHCFSWYKSRFTILEVWRLIMARVCKVTGKRPMSGNVSHANNKTKRRFLPNLQSRFFWVESENVRVLEVSNAALRTIDKVGIDVVLADLRAGEA

## SEQ ID 4593

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CGGTGCCACTTTGACGACAGGCCAACCCGAATATCAAGCAGGAGACTTTAGCGGCTTTAAGATAAGGCAAGGCAATGCTGTAATCGCGGACAGCGTTTGGATGCCCGTGATACCGATTTC  
ACACGTATCTTGTATGCCAACAAATCACTTGATCAGTACGCGCGCAACAGCAGGCATTGC

## SEQ ID 4594

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VGNRGAILNNSRSNTQQLGGWIGQNPWLTREARVWVQINSSHPQLNGYIEVGGRRAEVLANPAGIAYNGGGFINASRATLTGQPYQAGDFSGPKIRQGNVIAHGHLARDTDF  
TRILVCCQNHLDQYGRSRS

## SEQ ID 4595

TTGTATCGTCCACTTCGTATTATCAATGACACCGTAGATTGCTGACCATCGTGAATAATCAGTTGTTGATTGGTTCGCTATTTCCGCCATTTTGTATGTTTCAGGCTGCC

## SEQ ID 4596

LYRAIRIINDNGRLITIVNQLLIGRYFALLIVQAA

## SEQ ID 4597

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## SEQ ID 4598

VIPISHVFLYANKITLISTAEQAGIRNQQLPASSGNVAIDANGRLVNSGTMAAANVQDMNNTAEHKVNIRSQAFENSQAVSQGTQIHSQSIQWIKLLSAGTEDLAVSGSLANQNGEI  
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## SEQ ID 4599

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## SEQ ID 4600

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## SEQ ID 4601

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## SEQ ID 4602

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## SEQ ID 4603

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## SEQ ID 4604

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## SEQ ID 4605

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CCGATAT

## SEQ ID 4606

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## SEQ ID 4607

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## SEQ ID 4608

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## SEQ ID 4609

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## SEQ ID 4610

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## SEQ ID 4611

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## SEQ ID 4612

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## SEQ ID 4613

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## SEQ ID 4614

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## SEQ ID 4615

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## SEQ ID 4616

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## SEQ ID 4617

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## SEQ ID 4618

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## SEQ ID 4619

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## SEQ ID 4620

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## SEQ ID 4621

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GGA

## SEQ ID 4622

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G

## SEQ ID 4623

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AATG

## SEQ ID 4624

VITYSPGGIILSYIIAGICPYCHEFQKMYNYSVIGSDSFTFFKGISPVPKIDYCSCKGKPLSPEAVNKVMNKTDZEM

## SEQ ID 4625

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## SEQ ID 4626

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## SEQ ID 4627

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## SEQ ID 4628

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## SEQ ID 4629

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**SEQ ID 4630**

LSLSFKFVFMFLTLFVSKILFKLPTFSVPNVFFEHYPAA

**SEQ ID 4631**

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AACGGTTTTGAAGACCGGTTTCTGTGCTGCGCGGACTTTTTGCTCTCGGACGCAATTTGGCAAGCGCATCTTAAACTCTGCGGACCGGCTCGAGTTTACGGCGTTTCACTTCTCTGTGCG  
ACCAAGGTGTGACCATCTCGTTTTCAGCAGGAGGATTTGGCGAGCTTGGCGCGTCTCGGCACCGGTGTTTTTCCGACGGAATGCGGCAACCTGCGCATGATGACGGAACCTGCGATT  
TCTGACCGCTTAACGGTTGCGCAGCTTTGGGAAACAGGCTGCGGAAACAGGACGAGCAGTCGCGCAACGGGAATTCAGGATTTTGTCTTCAATATCTTCTCTTAAATTTTAAATTTGAATAT  
TCAGGACCTTCATTTCAGTCTGCGGCTATTTGGAAATACTGTCGAGGGATGACCGCGCGGATGCCGAGCGGTGAATCATGCGCGC

**SEQ ID 4632**

MTFARI SRPPYLNVQCR LKRIQTASVSEMPRLFDTVFFQKGIIDPQAGFFLPQTLQVLVSDQLERLRVGVFPDRAEFQVIAFAQFDRIAGNVATVHTGKLBSQR LKGLLRHNEFVERLIVVR  
ITLHQPPKRPQFPEQELLRLTRLLFGCEADLLQFDHADLPLIKLTQCAPGNRFRFTQKTDVILG LKRRFGEDFKAVIDLILILIQTFLQCPVPQNFQSLQPADGLVSDCLPVRSLGLLRMPVCL  
LHDLRQRHRIHQSRVDFGCFGRKTCQHCSNNCGSGLFLFHGIPCPARRQNA CMNVLPYPYVFRFLPCRFDVCLTQORTDGTVNPFKRLVAGNLSFHFVKRRHFLAAVVDIINAVEIAVFP  
RCRKFAFPQVLNCLIKRRNTLFIQIFQRHISVRRA GPFQAVVERVLFPQNGIKTFRLQIGNRFFRLIFLVGQDFAQLDFLRAPIKTLVNVNPFYFLGLRIGDGMQCVCLVAQALFRLP  
NGFEGRLVLVARLFRPFGTQKRIFLKLCRPVEFQAPHFLCDHGVDHFVFEQGLAQLRVRVFGTAVFRTECGNLRILDDGTVDVDFLVNVCQRIGRQAAGTGKQRNGSQDFCFHNLSLNFKLKY  
SGRLHSVRRMEILVGRSPDAERVNHAA

**SEQ ID 4633**

TTGTATGTGTTGTGTCAAAGGAAATTTTATGAAAAAATCGAGGCGATTTGTCAAACCGTTCAAGCTCGACGAGCTGCGGAGGCGTTGACGGAAATCGCATTAACGGGCATGACCGTCAGCG  
AGGTCAAAGGGTTCCGCAGGCAGAGGGGCATACGGAANTCTATCGCGTTCGGGAATACGCGTCGATTTCTCGCCCAAGGTCAAATTCAGAGTTGGTGTGGCGGATGATGCCGTGGAACG  
CGCGATTGACGTGATTGTTCGAGGTGGCGCGTTTCGGGCAAAATCGCGCAGCGCAAGATTTTGTGCTGCCGTCGAGGAGGCAATCCGTATCCGCACGGCGCAACGTTTCGACGCGCGGTT

**SEQ ID 4634**

LYCLFKGNFMKKIEIVKPKLDDVREALTEIGITGMTVSEVKGFGRQKGTETIYRGAEYAVDFLPVKVIELVLADDAVERAIDVIVEVARSGKIGDGKIFVLPVBEAIRIRTGERSDAAV

**SEQ ID 4635**

ATGAAATTTGGGTCGTATTTTAGGCAGCGGGATAATGTTCAAATGGGACATTGGAACGGAAAAAGTCGGCAATTTAAAAAGGATTTTAGAAACAAAGAGGGCTCAAAAACATGAACACAAAC  
TTAAA

**SEQ ID 4636**

MNLGRILGSGIMFKWDIWNKSRQFKKDFRNKEGQKHEHKLK

SEQ ID 4637

TTGATATTAAATGAACACACCCCATCCOCTTCTCCGAACGGCTCATTCGCTGGCAAAAAACAACGGTGCACCACTCCCTTGGCAGGTCAAAAACCCCTATTGCGCTCGGCTTTCGGAAA  
TCATGCTCCAGCAAAACGCAAGTGCCTCCGCGTGTGGACACTATTCGCGCTTCTTGGAAAAATCCCGACCGCTTCAGACCGTTCCGCCGCCGCGCGCAAGACGAAGTGTGTGCTGTGGCG  
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AGAAGCAGCGCGCGCGCAATTTCGCTTGTCTTGTCTTCAACGACGAGAAACCAATCTGGACGGCAACCTCAAAACGGCTGTCTCGCGGTGTTTTCGCCAAGACGGCAATCCGCAAGATAAAA  
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TCTCCCTGACGATGGCGGATATTGGAGCAACAAACCGCCTGACCAACCGCCTTAACGCAACGGCTGCTGATGATPACGCCGCTTGAAGGGCAAGTCCGCGCTCGGAACCAATTACAGCGCAT  
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**SEQ ID 4638**

LILMLTPPIFSEERLIRWQKHRRHLPWQVKNPYCVWLSEIMLQOTQVAALVDYYPRFLKPPVTQVTLAAAPQDEVLSLMAGLGGYGRARNLHKAQQVTGQPGGTFPSEKDLIELCGVG  
 RSTAAAI SAFAPNRRREITLDGNVKRVL CRVFAQDGNPDQKPFENSLMTLAE SLMPSENADMPITYTGLMDLGATVCKRTPKLCRQCPMAIDCEAKQNRNATBLPRKKTALFVQTLPLYLWLI  
 VRNRDGAILLEKRTAKGTGGLYCVCFESLNLGLSDFAAKLSLTMADMEOTALTHRLTHRLMLTTPFEGQMPSEHSDGWIWKPHGLKDYGLFKPLLEYLNGNRLE

## SEQ ID 4639

ATGTTATTGTATAAAATTGTGAAATAATTCTTATTGACTTATTTTGTAGGGGCATATAACTCATATAAAGAACTTTATTGTGGTAT

**SEQ ID 4640**

MLLYKIVKIILIDLFFVGAYNSYKETLLNY

SEQ ID 4641

ATGAAAGCAATFGGTTTATCACGGCGCAAAACGACATCCGPTTTGAAGAAAAAACC CGCCCGCAGATTATCGATCCGACCGATGCGGTGGTGAAAAATCGTCAAAACCAAGATTTCGGGTACCG  
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AGTCATTATTTCATGCGTCAGCAAATGCTGCACTTGGCACTGCAAAATCCAACTTTATTCGCATGCGCGCAACGCGCGCTGGATTTTGGGCTATATGATTGACGGCACGCGAGGCGGAA  
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GTCGGTATCCCTGCAACTTGGAAATATGTGCCAAGACATCGTGAAACCCGCGGTCATATCGCGTCGTCGCGCGTACGCGTCAATCCGTTGATTTCAAACTGGAAAAACTCTGGGATTTAAA  
ATCTTGCCATCAGTACCGGTTTGTGTCATGCAATCGGCAACACCCCGAAAATCTGATGAAGGCAATTTTCAGCAGTACGTGGATTACACCAAAATGTTGACCCACCGTTTCAAATTCAGCCAAATP  
GGAAAGGCTACGACGCTGTTCAAAACACGCGCGCGAAAACCAAGCGA



## SEQ ID 4642

MKAMVHGANDIRFEKPRQI IDPTDAVVKIVKTTICGDLGIWGNFVADGRILGHEGIGIVEEVGAIVKNIKVGDKVII SCVSKCCTCDNCKIQLYSHCRNGGWLGYMIDGTQAE  
YVTFPYADNSLVPFHDNVNEELALLSDALPTAHEIGVQYGDVKGPDVFIAGAGPVGMSALLTAQLYSPAAIIVCDMDENRLKPAKELGATHHTISPAAGDVSKQVFAIVGEDGVDAIEA  
VGLPATWNCQDQIVKPGGHIAVVGHVQSVDFKLEKLIKINLAITTLVNAVNTTEILMKAFSSSVDYTKML/THRFPKSQLEKPTTCSNTPPKTKR

## SEQ ID 4643

TTCGAAAAATTCCTTTCTTCAACACGCCGACATCCAACACAGGTTTTTCGGCTGTTCCTGTTCAAATAACCGCCGTTCCACCAAAAATATCCCATTAATCCCCCTTAAATATAGTGGAT  
TAAATTTAAACAGTACGCGCTTACCTCGCCTTCCCTACTATTTACTGTCGCGCTTCCTGCTGCTGATTTAAATTTAATCCACTATATC

## SEQ ID 4644

LQNSPSSNRHPTGFSAVFVSNRRSHQNIPLIPLKYSGLNLNQYGVTSPCRITILLSAASLPCPDNLNLIHYT

## SEQ ID 4645

ATGGGATATTTTGTGGGAACGGCGTTATTTGAAACGAAACACGCCGAAACCTGTGGTGGATGTCCGCTGTTTGAAGAAAAGGAATTTGCAAGGTCTCTGAGCGTTATTTTAA  
CGACGGTTAATCTGTAGTTTACGCCGCTCATCAGGCATTTACCGATAGGGCGATTTTAA

## SEQ ID 4646

MGYFGNGGYLKRQPKNLWLDVGLKKRNFKVSERYFLTIVNLLVSAHHGILPIGRFL

## SEQ ID 4647

TTGCCGCTTGGCGACTCAGTCGGCATACACAGCAGCACGCCCTTAAATGCCCATCCATCTCCAGAACAATGCGAATGACGCCGATATGCGGAGACCTATGACGAAAAATAATTATAA  
TATATTTATCAATAGTCATAAAATCGCCCTATCGGTAAATGCGG

## SEQ ID 4648

LPLGDSVGIHSTAPKMPIHLQNNANDARYAETVDEKIIITLSISHKNRPIGKMP

## SEQ ID 4649

CCGCTTCAACGCCAACGTCACACGCCCGCGTAACAGCCCCAAGCCTATCCATTCCTGCGTGTCCGGCGTTCGTCGAAGAAAACCCGCCAT

## SEQ ID 4650

PLQRQRQHARRNQPAYPFLRVAFVQENHRI

## SEQ ID 4651

GTGCTGTGATGGCGATTGACGACTTAAGCACCGCGCTGATTTGTCCCGCGCCTTGTGGAAGGGGCAATCCCCACCTCGAAATTAACCTTGGCGACCCCGCTGGACTCGAGGCAATCC  
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ATCCCTCGCAGAGCCGCGCGCAACAGCGGCATTCCTGATTTCCCGCGTTCGCCATCCGGGCGAAGTCCAACCTGGCTTTGGAACACGGCATCGACACTCAAACTCTTCCCTGCCGAA  
GTGCTTGGCGGCAAGCGATGCTCAAAGCCCTTACGGACCTTACGCCGACGTACGCTTTCGCCGACCGCGCGCATCAGCCTCGCCACTGCGCCCGATTACTTGGCATTGCCCAACGTCT  
TATGCTGCGCGGCTCTTGGCTGACACCGAAGAGCGTGAAGAACAAAGACTGGACACCATCACCCGCTCGCCAAAGAGCGCGCATTTGAACCCAAAGCC

## SEQ ID 4652

VFVMAIDDLSTAVDLSRALVEGGIPTLEITLRTFVGLAIRLIAKEMPNAIIGAGTVTNPEQLKAVEDAGAVFAISPLHESLARAGNRSGIPLIPGVATPGEVQLALEHGDITLKLFPAB  
VVGKAMLKALYGPYADVRCPTGGISLATAPDYLALPNVLCVGGSWLTPKEAVKNKMDITTLAKBAALKPKA

## SEQ ID 4653

TTGTCTGAAACTTAAACCCCCCATCCCGTTTGACCTCAACAAAAACGACACCCCCCACTTGAGAACCGAATGTCCAACTGACCCCCCGGAAATCTGACCGCGCGCAGTTGTG  
CCTGTGATGGCGAT

## SEQ ID 4654

LSENLTPPIPFDLNKNDFPLENRNVQTDPPRNPDRRRSCACDGD

## SEQ ID 4655

ATGAACACACACTCCATCCACCCAACTCGCGGAAATCACCGGGCGCATTTATCGAACCGAGCGCTCCGACGCTGAAAAATATCTGGCGAAAAATCCGAGTGCCAAACAGATGGGACGCT  
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CGCGTCCATCCACATGACCGCGGAGCCCTGATGGGCGGCAACATCGCAAAATCCGTACCGCGGACCTGATTCGCTTCGACTCCGTTACCGCGGAACTCAACGCTCTGATTAACGAGGC  
CGAATGGAACGTCGAGAGTGCAGCGCATCGATTTGGGCGGAAACCAAGGCTGCGCGCGGAACTCTTCGCGGCTTCGCGAGTATGACGACAGTGCAGGAAACCGGTGCGATGAGC  
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## SEQ ID 4656

MNHTPIHPKLAETIGRIIERSRPTREKYLAIRSAKQMRRLERNQGCNSLAHGYAAMPKSIKIEMLQETVPLNGIITAYNDMVAHQPFKDFDQIKDEAQKNGATAQVAGGTPAMCDGI  
TQGYAGMELSLFSRDVIAMSTAVGLSHQMPDGLFMGVCDKIIVPLMIGALSFGHIPGIFVPAQPMSSGIGNKEKARTQLFAEGKVRDELLKSEMSYHSPGCTCFYGTANSQMMHEH  
MGVHLPAFAAFVPHYDRLREALTRYAAGHLARGIKNGTIKPLGEMLEKSFINALIGLMTGGSTNHTMHLVAMARAAGVILWDDFDEISSIIPLLIRVYPNGKADVNHTAAGGLPFVIR  
ELLDAGLHDDVDVTVVGHGMRHYTKEPFLIDGKLEWREAPETSGNDDILRKADNPFSPDGLRLMKNIGRGGVVKVSAVREGCRIIEAPAIIVNDQREVLAAPFERGELERDFICVVRYPGP  
RANGMPELHKLTPPLGILQDRGFKVALLTGRMSGASGKVPASIHNTPEALMGNIARIKRTGDLIRFDSVTGELNVLINEAEWNVREVERIDIGANQCGGRELPAFGRSMTSSAETGAS  
PGGEFA

## SEQ ID 4657

GTGGATAGGAGTGTGTTTCTGCTCTCTGCGGAAACGGGTGGTATTTGGGATTTGTTTGTGCTTTCTGATTTTGTATCGGGTATGTTAGACGGTGAGTATAGTGGATTAAT  
TAAACCGGTCCGCGCTTGCCTCGCTTCCGCTACTATTTGTGCTGTCTCGGCTCGCGGCTTGTCTGATTTAAATTTAATCACTATATTTAAAGGTACGCGCTCTGAAAGTGGAA  
CGGGTGTCTATTA

## SEQ ID 4658

VDRSVVHVRSPGCTGWYGFVCAFLIFVSGMLDGEYSGLNLARSVASPCRTICAVCGSPPCPDNLNLIHYILKGTPESESGKRVLL

## SEQ ID 4659

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GAAGGCGCTTCCCTTCTACCTGCGTACCGCAACCGCATGCGCGGCAAGTGGCGGCAATCGTTTGAACCTTCGCGCGTGCAGAAACCATATTTGCAACACGCGCAACCGCGCGAAC  
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AACTGGGCAATAACACCGCGCGGACGCTTACGCGCGACATCTTGGGCTCTGGAAGCGCGCGCAACTGTGCGCGCGGACGCAACAGTGGCAGGAAGAACG

## SEQ ID 4660

MSTQTNFDLVLFATGDLAMRLLPCLYQAHVAGLLHPEERILGVSRSELDTEGFLAKVETSSKIHVKNFSGEAWASFVERLAYLVKVDVTPDDPAALGLVLRKARKETDNVVTYLSAPK  
FFAQACENLAATGIANADNRVVRVLEKPLGTDLASSQINTDVARYFKEGQIYRIHLYLKGESLQNLILALRANVMFEPILWNNKYIESVQLTIAQLGVEERGFYDITGALRIMVONHLMQ  
LCMTAMEAPAGLDADAVRDEKVKVLSLKLPLTIESVNVENVRGQYTAAGMNGYLEEINVPQDSFTETTYVAIKAEIENERWKGVPFYLRTGKRMAGKVAEILVNFRLPNHIFDINSQTAPN  
RLVIELQPNESVRLYTQVKTGAGNKVEVTPGLVDLGAKEGRRAEYERLLDVLINGKIALFNRRDELEAAWEYVMPILNMANNTTPHGYGABSWGPEARELLARDGNKWHSEQ

## SEQ ID 4661

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CGGTCTGGTGGCGCAATACCTGTTTAAAGAACAAAGCGCTGCGCGAGTGTGGATTTCCTATGTTGGAAGACGGAAGAACTGAACCGAATTACATCCGATCGTGTGTCGATTATGCGCTG  
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CCAAGCGGCAAGCGGAAAAACCGGAATATCCGATCAGCGCTCGTTTGAACCATCAAGGAGTGAAGTGCATGCTCTTCTACGCGGAA

## SEQ ID 4662

MFVWEYENAEAAQSLADAVADALQALDEKGAVALVSGRSPIAFFNALSQKDLWKNVITLADERIVPTNHADSNTGLVREYLLKNKAAAAVWIPWVEDGKTETELHPDAVVDYAL  
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## SEQ ID 4663

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TTTGAAGGCAAGGATTCAGACGCGCATCGGCACTACACCAACCGTCTCCTTATCCGACGCTGCACCTCATCCGCAAGACAGCATTCGCAAGCGCGCAACGCTTTCGCGACGCTTCG  
CAATATTCGAAGCAATATCGCGCTGCTGGAAAAAATGGAACATGAAGGCTGGGCAAACTCGGTATCATCTCCGCTTATCCGCAATAGAAAAATATTTCAAAA

## SEQ ID 4664

MNIDTSENKDAVAEHTGQWLEKAVIGLNLCPFAKAPHVKNLVRIASEAKHLDGFLDELDEELQRLGNTPATETELTLLVHPTLFPDFVDFNDMLDIADAADVENGLEGIVQIAPFHPYFQ  
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## SEQ ID 4665

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## SEQ ID 4666

MSSTPNKHADYPRLVADIGGTNARFALETAPCVIEKVAIVLPCKEYDTVTDAVRAYLNQSGATGVRHAFAALANPILGDWQVTFNHWFASIEETTRQALGLDILLINDFTAQALAVQTSS  
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## SEQ ID 4667

TTGCAGAGGCGCGCATATTCGAAGGGCATATCATTTATGTTAAGCAAAATCAGCGAATCACTGCGCGGACCTGTCGCGTGGCGGAACGAAAGTGGCGGAATGCGGCTTGGCGAAGCCCAAGT  
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CGCGACATTCGCGGACGAGGATGCTTATGTTCCAGGAAGCACTCAATCGCGACGAGATATGCGGAATGTTGGTTGAAAAAGTGTGGGCAACCGCGCGGACGCTTGTGGGGGAGAG  
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GAACCTACACGCGCATGTTTCCCGCTTTCGAGCTTGCCTGATCGATATCTTCGCGCATCGGACTTGCCTGCGCTTGGCGGATGCTGCCAGCTGCAATTCGAGAAAGCAAAAAA  
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## SEQ ID 4668

LQGGRIIEGHIIMLSKISSESLADLSGAERKVAECALAEKPNVHAAVAETADRASVSQPTVIRPCLSLGYKLPKLSLSASIGHEGMPVVEELNADDNANVVEKVLGNAALIGER  
RPLKESELENGIATLMHARRVEFYGVNGSIVAQDAQHKFFRFGHSTFVAYVDHTQLMAASVLSDDVLVALISNTGSSIELLDVSLAKENGASVIALTRINDSPLAQLADCVLSVATQENA  
ELYTFMVSRLQLAVDILAILGLRLGDAASLQLQSKRSIHNKHIDYDKD

## SEQ ID 4669

ATGGCGGAAACCCCGCTTTAAGCGCGCAGGGTTTCGGGTTTCCGCAACCCCTTCCAAATCGGGCGGTACGAGGTTTCGCGCTTATGTCGCGATCGATGTCGGAACCGCGCGCGCT  
ACGGAAACCTCAATCGGAGCATACAGA

**SEQ ID 4670**

MAETPPFKAAGFGPAATPSKSGRYAGLRMLCASHCGNAPRHGKPOSGAYR

**SEQ ID 4671**

ATGAACACACCTTCACGACTTACCGGCTTGGTCAAAATTGTGGAACCACTTTGACGACAGCAAAACATTTGCATATGCGCGAAATTTTCAGCAAGAAGCCGACGCGGGCGGAACGCTACTGGC  
TGCAGTTCGGCGGACTGACGCTGGAGCTACTTCAAAACCGCATCAACGACGAAACCAATGTCCTTACTGTTGCAGTTTGGCGCGTGAAGCAGGCGTGC CGGAGCGGATGCGGCAGATGTTCCA  
CGGCGAAAAATCAATACCACGAAAAACCGCGCGCTCTCGATGTGCGCCCTTCGCAACCCGCAAACTTTCGCGGATTTATGGTTGACGTTGAAGATGTGATGCCAAAAGTCAACCCGCGTTTTC  
CAACGTTATGGGCGAATTTGCACAGAAGTCGCGACGGAAGCTGCTGGGCTATACCAACCAAGTCATTACCGACGTTGTCAACATCGGCATCGGCGGATCGGATTTGGGCGCGGTGACGC  
TGTGTACCGCGTCAAACTTTTCGCTTTCGCTTCAFCGCGCGCTCAATATGCATCTCGCTTCCAACGTGAAGCGGCTCGACRATGCGAGCGATTTGTCCAAAGTTCACCGGAAACACGCTGTTCAT  
CATCGCTCTCAAAACATTTTACACGACGGAAGACGTGACCAACGCGCTGACCCGCGCGCAATGGTTTTTGAATCATGCGGGTGACGAAGAAGCGGTTCGCAAAACACTTCGCCGCGGTTTTCC  
ACCAATCGAAGAACCGCTCGCGCAATTCGCGCATCGCATGCCAATATGTTTGAATTTTGGGATTTGGGTCGCGCGGTGCGTACAGCTTGTGTTCCGCCATCGGATTCGCGATTAATGCTGTATC  
TCGGCGGAAGAAAGTTTCATCGAAATGCTCAACGCGCGCGCATGATGACCAACCACTTCATCAACCCCGCTCGAGCGCAACTTCGCCCTTCGCTGCCCTCATCGGCATCTGTGATATF  
CAACTACTATCGGTTGGGCGGACGCGCATCGCTTCGCGCTTACGACCAACATTTGCAACCGCTTGCACAAATTCGAGCGCTGATATGGAAAGCAACGCGCAACACGATTTACGTGTGACGCGC  
AAAGCAGTCGGACACGAAACCTTCGCGGATTTATTCGGGGAGAAACGGGCATTAAACGGTCAGCACGCTTCTTCCAACTGCTGCATCAAGCACGACATCATCCCCATCGACCTGATTGCCT  
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GCAAGGTATGGATGAGGCGCGCATCGAAGAGCTGTTTCGCGCAAAACCTTCTCGGCAACCGCGGCAACCTCATCTGTATGATAGGTCAACCCCCGCAATATGGGACGCTGATT  
GCCATGTACGAACCAAAACCTTCGCTCAAGCGCAATTTGGGGCATCAACAGCTTCGACCACTGCGGCGGCGGAACTCGGCAACCACTGGCTAAAACCACTTTTGGGCGAACTGCACGCGC  
AAACCGACGCTCAAAACACGACGACGCTGACGCAAGCGCTGATTAACTCTACTCTCGACAGCAACCGCAAA

**SEQ ID 4672**

MKHLHDLPAWSKLNHNFDDSKTLEMRMFEQDPQRAERYWLQVGGILTLDYSKNRINDETMSLLELAREAGVPERMRQMFEGEKINTTENRAVLHVALNRNTNSPINVDGEÓVMPKVNRVL  
QRGGEFAHEVRSGSWLGYTNQVITDVVNTIGIGSDGLP/LMCTALRPFHPRLNMHFSVNVDSQSLRDVLXSVHPETTLFI/IASKTFTTQET/LNAL/AREWFLNHAGDEEAAVAKHFAAVS  
TNRKAAEAFEGIDIANMFEPWDVWGGRYLSWSAIGP/IMLYLGEENFIEMLNGAHLMDHP/INTPELRLNPVILALIGITWYINNYGGGSHVIAPYDQHLHRLPKFIQQLDMESNGKVTLDG  
KAVGHETSPIIWNFTGNCQHPQQLHQLQHTIPI/DILIASKEENSPLGHEILILANVFAQAEAFMCGKTP/DEBRAELKAQGMDEARI/ELVPHKFTSGNRPTNLILMDKVNPRNAGSLI  
AMYEHTFVQGIWIGINQAFWGLGKQALIKLGLTGETEPQRHDSXTERLINLYLQ/TKR

**SEQ ID 4673**

ATGAAAAAAAATTTTACCCGCACTGGCAATTGGCAAGTATGCTGATTTTGTGCGGCTGCGACCGTTTGGGAATAGGCAACCCGTTTTCGGAAGAGAAATTTCTGGGAGCGAAGAGACTA  
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GGTCTGAAGCTTTGGGCATTAACCGTCGATGAAGTCCGAACTACCGAGAACCCGACACGTCGACGACAACTCAATAGTGGAAGCCGCGTTAAATCTGGACGATGTGTGTCGATTA  
GCGTCGCGCGCAACAACATCTATTAGGACACGCGATCAAGAAAAGCCGCGACTTTTGTGAACCTCATCCGCCAAGGAAGGCGGTATTATGTCAAACTATTCTTACAGCGTCGCGCGCA  
CAGACGACAAAAGCAAAATCTTTGCCGAACCTAGTCAGGCACACGATATCATCCATCGCTCAGCGAGCTGGTGTCTATGGCACTAGTTAAAGAGCCGTTGGACAAAGCGAAACAAAGGAA  
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TACAAGCTGTGCGCGACGCGAGTTCGAGCAGTTTGTGAAAGGATTGCCCTCAAACGTGACAGAATAAGCTGCAGAGCCTCGCAGAAAACATGGAAAGCGGTATGGACACAGATCTGTGGCAACA  
ATGCGAAAAGCGAAGGTGAAACCGCCAAACGGCATAAAAGTCACTGAGTGTGGCTGTAAAACCGCAGAAAACCGAAGCACGCTTGGGAAGAGCTGCACACCGCTAAAAAAGCCCTTATCGACGA  
AATGGTCAGGGAAGGAGGACGAAAGAAAGTTCGCAAAAGCGCGCT

SEQ ID 4674

MKKNLPALALASMLISGCDRLGIGNPFSKEISCGSEETKEILVLRDNRVEGETVTKT/DDDAFKDQAFADIGISHRRMVERLGITVDEVRTTEKTDSSKLKCBRAALKLDVPDDVVDY  
 AVAANQSIGNSHKPTPDFEPYRKEGAYVTKTISYSVQPTDDSKIFAEALSQAHDIHPLSELVSMALIKEPLDKAKORNEKLEAAEATAQEAAREAEAAAQALGREQEAARVSEHBER  
 YKLSRSEFQFNGLPOTVONKLAOSKRTWKGSGMDKICANNAKABGETPNGIKVSELACKTAETEARLEENRKKALIDEMVREEDKKELPKRL

**SEQ ID 4675**

ATGCCCCAGTACCCGCAACTGGCAAAACGGTTTGGGTGCCAAATGCGCGACGGCGACGAATACGGGGTGGCACAATCTGACTGCCGTACCAGAGAAATCAATGCGAAAACCAAGAAATCC  
AAGGTATCTGATTGAC

SEQ ID 4676

MPQYRNWQNLGAKCADGDEYGVAQSDCRTREINAKTKEIQGYLID

SEQ ID 4677

TTGACGGTTTTTTGGAAAGACTTTGGACGAAGAAGCTGCAGCGCATGGGCAATACACCCGCCACCGAACTGGAAACCAACCTGCTGGTTTCAACCCGACCCCTATCCCGGATTTGACAGTATTTCAA  
CGATATGCTCGACATATGCCGATGCCCGCGTTGTGCGAAACCGGCTTGGAAAGGCATCTGTCCAAATCGCCCGCTTTCATCCCTATTTCGAAATTTGAAGGCACGGATTGACAGCGCATCGGCAAC  
TACACCAACCGCTTCTCCCTATCCGACGCTGCACCTCATCCGCGAAGACAGCATTTGCCAAAGCCGCAACAGCCTTTCCCGACCGCTTCGGCAATATTGCGAAGCGCAATATCGCCCTGCTGGAAA  
AAATGGGACATGAAGGCTGGGCAAAACTCGGTATCACAATCTGCCCTTATCCGCACAATAAGAAAAATATTTCAAAATGATCCGTTATCTTTTAATTGCCTGCGCGGCGCATCTCCCTGCTG  
TTGGGATAATCGGCATTTTTTTTGGCGCTGTTCGGCACCACGCCGTTGTACTATCTCCCGCGGCTGCTGGGCAAGGCATCCCGCGCTTTCACCGCTGGCTGACCGGCACCGCTATT  
TCGCGCCCTGCTGCTCA

SEQ ID 4678

LVVFWKTTTKNCSDWAIHPPPNWKPKWCFTRPYSPISITYSTICSTLMPPLSKTAWKASSKSPRFIPISNLKARIQTASATPTTVLPIRECTSSAKTALPKHPKFPFTRLQYSNAISPCNK  
KWDKAGONSVSHPALIRTIKRI FONDPLSPNCLRRHLPAVGDNRRHFFAAVAADHAVRTTLRRLLLGKGIPALSPLAAPAPLIRPDGS

SEQ ID 4679

ATGCCGCTCGTGAACCGGAGGACACAATGGATATATCACCGCGCTTAAGGCTGCGGCATTTGGCGGGGTTACGCTGCTCTTTGGGGCTTCGCGTATTTATGGAGGTTTATAGATACGACCATCGCCA  
ACGTTCGCGCTCCCGCTCATTTGCCCGGCACCTCGTTCGGGCAACCAACGACGGGACGCTGGCTCATCTCTCTTTTCGCTGGCAAAACGCCGTTTCGCTGCGCGCTGACGGGGCTTTTGGCAAA  
ACGTATCGCGCGAGGTCAAAATTTGTTTACCGCGCGCGCGCGTTCCTCATCGCATCGCATCGTTCGCGGCATCGCGCCAACTCTTCAGTCGCTGTGTGTTTTCGCGATTTTTCGCGATGGCGGCTTT  
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CGATATCGGGCGTTGGATTTCGGGAACTGGCATTTGGGGTTGGATTTCCTTCATTAATATCCCATCTGGGATCATATCGGCATGGATTACATGGAACACTTTGAAACACCGCGAAACCGG  
AACCGTCAGAACCGCCAGCCACTATGTTCGGCTGACGCTGATGATGTTCGTATCGGCGGTTACAGATGATGCTGGAACAGGGGTAGGAAACTTGACTGTGTCGCTCTGGAGAAATCATTT  
ACCTTGGGCATAACCCGCTGTGTGCTGTTCGTATTTTATGTTTGGGAAATGGGAGAAAATAATCCGATTCGTCATTTATTCGCTGTTTAAAGATCGGAATTTACCGCTCGCGCTTAATGT  
CCACTCTCTGGGTTTCATGTGTATATGTTGGCGCGACCGCTGTCGGTATGTGTCAGAGCAACTATGGCTATACCTCCGCTGGCGAGGCTTTCGTCGCGCGCCGCTCGGCTACCTCT  
CCCGCTCTCTCATATCTCGTAAATCGCAGGTTTCGGCAATAAAATCGATATGTCGCGCTCTGCTGAACCGCGACGCTTACCTGACCTTTTGCTCATCTTTTATGGCGCACTGATTTTATGCG  
GACATGGATATCGGCAACGTCATCTGCGCGCAGTTTTCGCAAGGGGTAGGCGTTGCCATGTTCTTCTGCGCGCTGACCAACCATCACACTGTGCGCATGAAGGGCGGACAGATTTCGCGCG  
CCGGACGCTCTGCAATTTCTGCGCGCTGTGATGGCGGTGTGCGCGCTATCCGTCGTACGACACCCCTGTGGGAACCGCGCGAAGCGTTGCACCAACGCGCTTTTGGCCGAACACATACAGCC  
CTAATTCGCGCAACTTCGCGCAACCGCGCGCATTTGTGCCAAAGGCATTTCCGACGGTCAAACTCTAGGACCATCATCAACATACCATACGCAACAGGGCTTCATATCGGATCGAAC  
GAAATATCTCCGCTGCGAGCAATTTGTGTTATCGTCTGATTTCCCATTCGCTGCGCTGCGCGGCAACCGCGCTTCCACAGCGCGCGCGGTGGACAT

## SEQ ID 4680

MPSETEDTHDYPPLKGAALAWVTLGLAVFNEVLDTTIANVAVFVIAGNLGAATTQGTWVITSFSVANAVSVPLTGFIAKRIGEVKLFATAAAGFVIASWLCIAPNLQSLVVFRILOGF  
IAGFLIPLSQSLIMASYPAPAKRMLALALWMTVVAVPLGPILOGWISGNHMGWIFFINIPIGIIISAWITWHLKHRETATVTRPTDYVGLTLMVIGIALQMLDRGKELDFASGEII  
TLGITALVCLSYFIVWELGEKYPIDVLSLFDKRNFTVGVIALTSIGPMVYMGTLTLLPLVLQTNLGYTSAWAGLAAAPVGLFVFLSPLIGRFGNKIDMLLVTSPLTFAPTFTWRTDFYA  
DMDIGNVINPQFQWGVGVAMPFLPLTTITLSHMKGGQIAAAGSLNFLRLVLMGGVGVSVVSTLWERREALHHTFAEHITPYSATLHETAHLSDQGISDQGTLCIINNTITQDGFIIIGSN  
EFLAGSILFIVLPIGWLAKEPPHSGGGGH

## SEQ ID 4681

TTGCGCGCGCTTTGCCATCGGCAAGCGCTCGGCAACCGTATCGCGGACAGGATGCGAGCCCGGAGATCGGGAATAATCACGCCCCAGTTGCTTTGATCGGGGTTTTGGAAACGACGCGG  
GGATAGTAATCATTCCTTCCTTCCTCGGATATCGGTATCGGCAAGTCCAAACGCAACGAAGGGGATTTAAACACGCAAAACGCAAAAGCGCGGACATTCGCCATCCAAGTTCA  
GTCATCAGA

## SEQ ID 4682

LRRLWHRQARRQFYRRQDAARQIGNHAPVALIGVLEQHGIVNHCFLSRICGIGKVQTRRGFKNDKNAADIPASKFQSR

## SEQ ID 4683

ATGTTCCATCTCGAAGGCGCTTTTTCAGGAAAACCTGCGGATTCGCGAGGCGCAAGCATAGAGGTTAATCGGGAACAATCCCGATTATGCGGATGCGGTGTTGAGACATGTTGAAGCGG  
ACGATGCGCATTAACCGGACAGGTGCGGTTTAACTGTCATGCGCGCAACATATCTCAACCGTGTGATGCTGCACTGCGCGCGGTATGAAACCCGAGCGGTTTTTTCGCGAAGCC  
GCT

## SEQ ID 4684

MFLEGLQENLPIPEAQSEIENRNDPYADAVLWIMVEADDAALTGQVRFNVSNPQHILNRVDACTAARHETRAVFWRKPF

## SEQ ID 4685

ATGCCCCGCCAATCTCGCACTCTTCGCCATTCCCGGCAAGCGGGAATCCGGAACCCAAACGCGGAGGAATCTATCGGAAAGAAATACCCGACCGCGGTATTCGCGCGAGGCTGGAA  
TCCAGACCCACAACGTTTAAAGCGGTTTATCAGAAAAACCGAAACCGAACGCTTAGATTTCGCGCTGCGGGGAATGACGAAGAGTTGGGAGTGACGAAGGCGGGAACAACCGCGCAA  
AAAGCGCGGACTCTTCAGACGGCATCGGCAATAAAAGCGCGAAATAATCGCGCTGAAAT

## SEQ ID 4686

MPRQCHSSPPFRKRESGTQTRQESIGKNPTAVIPAQAGIQTHNVKAVYQKKPKPNALDFRLRGNDRELGSDEERREQPRKKPTPSDGIGNKARKNRAES

## SEQ ID 4687

TTGCGCGTTCGGAACGAAGCAGGAAGCAAAATCAACGGCACGTCACAAAGTATTTTACACTGGGCAACACCCAGACGCGCGCGCTCGGTACGAAGACCGCAATGAAAGCGAAA  
GAAGCGCGCTCGTATCGACTTGGACGGACGGCGACTTAAACGACAACGCGCTTTTAAACCCCGGATTGGACAGCAAAATGGCAACGGCGCGCGGAGCAAAACCGCCCAAGCCCTGTTT  
AAAACCTGTGCATCAAAGCGCGCGACACCTTGGCGAAGCGGTGTTCCGGATAAAGTCCACCGGGAACCGCAACGCGCGCGCTGACGCGCTCAAGGCTGGCGCAAGGTTTTCAGGAA  
AAAGCGCACCGGACCAACCCACACACCGCCCAATCCAAGGGCTGACGAAAAAATCAGCGCGCGCTTGGCGCGCAATTCACACGCAACCATCGCGCGCTGGATATTGTCAGAT  
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CGAACGCAATTCGCGGACGCGTCAACGGCGAAAGGCAACCAACTGGCTGTTATCCGCGCAAAAAACACGCGCGCGCATATTATACCACTGGTACGAAGAGCAGTTGCGATGCGCC  
ATCGGCAATTCGCGCTCGGGAAGCGCGGACGCGGACGCGGATGTCGCGGAAATACCTGAAATCGATGAAGAACCGCAAGAGAGAGTGGAGATCATCAACCGGACTCCGAAACCGC  
GCGGCAACGAGGCTCGACTTCCCGTGGGGTCG

## SEQ ID 4688

LAVGTKQJEDIKRHVHKVPFSWANHPDAAVGYEDRNERQRSALVSTWTDGLDNLNGFLTPLRLSKMATGGAENRPAKLVLCIKTAAADTLGEAVFRIKSHGETANAGALDASRLAQLOE  
KADRDHTHTAQIGLDEKISAAVAQFTRQITGGVDIVRFPDGTMTGTSYRPARGGSPFIGNEVVPLAFADGNVVKFVSERHSRGRVNGERQHNWLFIRAKNHAAAIITNWYESSCWMWA  
IGKSASGNAASPTPIVPEIPEIDREPPRESGRSSTGLRNRPRHGLDFPVGS

## SEQ ID 4689

TTGAACAGCTCAAAACCGACGGCTCTATTCCTGCGGACGGCGGTGCGGAGCTCGAACCTGCGCGTTGAAACACCGCTGCCATATCCAAGTCATCGCGGACGCAACCGCGCTGGT  
GCAGCGAGTTGGGTATCCCGCTACACGTCCGACGTGTACGAACGCTACACAGACGACGCGCAACGACGACTGGAGCGGTGGAAGAACTCAATTTCGGAAGGATCCCGCGCGGCGC  
GATCGTGCTTTCCCAAAGCGCTCGAAACCGCGAGGCTATCTCAAGCGCGACGCGACGATCTTTGCACAAAACACCTTCGAGCTTTACCGCGCGCTGGCGCAACAAACAACTGC  
CGGAC

## SEQ ID 4690

LNSLKTGVYSLPTAVGSSNLPEVTACHIQVIAGTQFGWCRQLGYPAYTSDVYERYQTSSANDWSAWKKLNSEGI PAGAIVSFPAVRNPAGYLKADGTIFAQNTFTSTFTAPWATQTN  
PT

## SEQ ID 4691

ATGGCAACGCAACCGAACAAAACCAATTGCAACAGCGCTCCGCTCATCGAACCGGGCAGACGCTGCTGCGGCCAGGCGCGCGCTCAACCAACCATGCAAGCCCTCGGCAAC  
GCACCTTTTGTCTAAAAACCAACCGAAGCCCTTCAGACGGCATCCGACCAAAAGCGCGCAAGCACCGCGTCAACGCGGCGACGAGCTGACGGCGCGCGGACGCTTCGCCAAAG  
CCGACCATTCGCACTGGGCGCGCGCGGCAATCAGCGCAACAGCCAAACACCGTCCCAAAAAACGGCCACACCCACGCGCATGACACCGCACGACCGGACCGCGCGGATCGTCGGA  
TTAGACAATGCCATTAGCGAAGCGGAGACACCGCGCGCACCCCAAGCGCTCAAAACCGCGCTCGACCAAGCGCGCGCGCGCGCGGACCGCGGACCTCAAGTCTCCCTCTCGGACA  
ACCAACCGTTACCGGCAAAAAACCTTTACCGCGCAACCAATTCAAAGCGGATCCGCGTGTCCGCCAACCGGACGCA

## SEQ ID 4692

MANATEQNQFDQAVRLIEPGDSVVVGPAPVNPQLQALANRTLLLNQTEALQASDTKAAAATAVNAGDGLTGGGSLAQSRITLALGAPGQITATSDNTVPKNGHTHAIDTARTDRAGIVR  
LDNAISEAEDTAAATPKAVKLTALDQARAAATADLKVSLSDNQTVTGKTPFAETQFPQSGIRLSANPTH

## SEQ ID 4693

ATGATCGGTATCTTTTAAATGCTGCGGCGGCATCTCCCTGCTGTTGGGGATAATCGGCATTTTTTTCGCGCTGTTGCGGACCAAGCGCTTCGTACTCTCCGCGCGCTGCTGGGCA  
AGGCATCCCGCGCTTTACCGCTGCTGACCGGACCGCTTATTCGCGCGGATGGTTCATACTGGGAACAAACGCGCGAGTCCCGCGCAAGCGCAAGATTTTCGCTATGATGAT  
GACCGCATCTGCTGATGATGTTTGGCAGTTTCCCAACGCTGCTGGTGGGCGGGCTTCATCGGTTTTTTGTTTCCCTTGTGCGCATATGATGTTGGCGAGACCGCAATCT

## SEQ ID 4694

MIRYLLIACGGISLLIGIFLPLPTTFFVLLSAACWAKASPRFHWLHRHRYFGPMVHNBQNAVPRKAKIFAIISMNTASCLMMFQFFQRMVWGAUVSSVFCSLVAIMMWRPES

## SEQ ID 4695

GAGAATCGTCTCTTTGAGCTAAGGCGAGGCAACGCGGTACCGGTTTTTGTAACTCACTATAAAGGCTTTTCTAAAATATGAGATATCGAATGTCGAATTTGCTTATGATTACGG  
TTTTCTGTCTATCCGCTTAAATGCCGATTCGCTTTGAACCAATATATTTGCGGAACACTCAAAATCTCCCTTACCTGCGGACAGACATCAAGACTTCGTTGTTGTAAGTGA  
GAAAAATATATGAAGTCCGATCCCTAATCAAGCCTCAATACCGGAACCA

## SEQ ID 4696

ENRSL\*AKARQRTGFC\*STIKGLF\*NMQIFECRICIMTVFCLIRLMPVFRNLQIIFAETLKNLPYLPDRHQDFVVVTEKNILKVRIPNQSLKYRNE

## SEQ ID 4697

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GGTTTTCACACGATACGATGCCGTGAAAAAGGCGACGTGCTGGCGGTGTTGATGACGATATGATGTCGCTTACGAGCGGGCAAAACGAGTTGGTTACGCGGTGCGCAA  
AACCGCGCGCAAAATGCCGCACTTCGAGCGGGGGCGCAGGTTCCTTGGCGCGTGGGATTTGGCGCGCGCAGGATGATTACCGCGCGGTCCGCTTGGCGGAATCGGGTGGG  
TGTCCGCGAAGAGCTGGCACACGCCGTCAGCGAGTGTCTCAGGCGCAGGCGCGGTTAAGCGCGCTTTGGCGGAAGAATCTTGGCACGCGCGCTTTGGCGGAGATGTTCTTTGCG  
CGAACAGCGGAGGTTTACAGCGGCAATCGGAGGTTGAAAGATGCGTGGCTGAACCTTCGGCGGACGCAAGTCCGCGCGCGCGGACGGTACGTTGGCGAAGCGTTCCGTCAGGTCGG  
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GGTCAGCGCGTCCCGTCCGTATCGTCTGAACCGCGAAGATGTGGACAGGATCCGTTGCGTATCGGTTTGTGATGACGCTTAAAGTGGATACTTCCCGCGAGGCGCGCTGTTTCA  
AAAACCGCGGTGGCGCATTCGCGGAATGAAAGTACCGACTGGTCGGAAGTCGATCGGACGGTTCGTAATTCCTCGGCAATCCGCGGCC

## SEQ ID 4698

MKSGNSEPHMETHTDETKLQNTQVKKRRLTALTLFALSAAAGSAFFLWQHEEBTADYVAGRVVQVTPQGGTVRKVLHDDTDAVKKGDVLAFLDDNDVLAAYERAKNELVQAVRQ  
NRGNAAATQAGAGQVALLRRADLARAQDDLRRSALAESEGAIVSAEELAHARTAVSQAAVKAALAESSARAALGDDVSLREQPEVQTALGRLKDAWLNLRRTQVRAPADGQVAKRSVQVQ  
QVVAAGAPLMAVPLSDVWVANDANFKETQLRHKIGQPAELVSDLYGKQIVTRGRVAGFSAGTGSAPSLIPAQNAATGNWIKVQVRVPRIVLNRKEDVDRHPLRIGLSMTVVKVDTSAAGAPVS  
KTPGAALPEHSTWSEVDRTVDELLGQSAF

## SEQ ID 4699

TTGCGGCTGGGCGAAATCCAAATTAATCGAACGCGACGCGAGTTCAAGTGGGACGCGTCTGTTTCGACGCGACGCGCACATTCGGCAGGCGCGAGGGTGACTGGGCGGAATACCGCA  
TTGCTTAAACGCGCGCGTCCGATCCGCAAAACGCGCGCATCCGCGCATGTTGGCGGAATCGCCCCCTTGGCGTGCAGACTTACCGCGCTGACTACCGCAACCATCCCAACCGCTG  
GAACGCGAAATTCGCTTTAACGCGGAATACGCTTTCGCGACGACA

## SEQ ID 4700

LRLGEIQTIERDGFKWDGSLVFDGSRTPGRREGDMAEYRIVLTFVPSIRQTARIRAMLAELIAPLCELALDYRNHPRHNGKIRPNGEYFGFT

## SEQ ID 4701

GTGAAAAAATCAGACTGCACAGCCCGCTGCCGACATCGAATGCGGCAACGCGGAATACATCCGAATCAGTCCAGCTCGAGCGGAA

## SEQ ID 4702

VKILTLHSPAADIECGNGEYIRITSTLRE

## SEQ ID 4703

TTGACGGGGCTGTGTTTCGCGGGACGGTGTCTTCATTTATTCGCGCTGAGCGTGGAGCTGATTTCGGATGTATTTCGCGGTTCGCGCATTCGATGTGCGGACGCGGGCTGTGCGAGTGT  
ATTTTTTTCACCGCGGGGTGTCTAACGCGCGGATGATTTTAGACAGGCGGAGGATGCGCGGATGTGGCGCTTTTTCGCGCATAGGTTATCCAAAGCTTCGCGGCGGTCTGCGGTTCGCG  
T

## SEQ ID 4704

LQGAUVRGDGAHLFALERGRSDVFAVAADFVSGAVQCDFFHAGVSNAPMILDRATDAPMFAFCHRLSKASQAVCRSA

## SEQ ID 4705

TTGACCGCGCGCGGCAATACCTGCGCGCGGAAACACGCGCGCCCCCTTTGTGACAACGTGCAAGTAACCGCGCGGCAACCCAAAGACACGCGAGTAGAGTATTCGCGGAATACCAACCGCG  
CCGCAATATTAAGCGCAACGCGGAGCGCTGCCGAGCGCTTGGATAACCTATGCGGCGCAAAACGCCACATCGCGCATCCGTGCGCTGTCTAAATATACGCGCGGTAGACACCC  
GGCG

## SEQ ID 4706

LTAAREYLPAETRRPLCDNVQVTAAPKDTAVEYSAEYHPAANIQAERTACEALDNLWRQNAHIGASVALSKITIGALDTPA

## SEQ ID 4707

ATGGGAAACAGCGGATTAAGCCAACTCCCGCGCGCGCGCCATCGAAGAAACCGACTTTAGGGGATCTTCGCGCGCAAAAGCGCGCTCACCGCGCTATGTCCGAAAGCATCCGCG  
AAACCGTCCGCAAACTCTCGAATTAGAATCAGAACCCCTAACCATCGACTTCAACAGCAGCAAGCTATCAAGAGCTGCTCGTCCGCAACCGCATCAACGAGCGGTCAAGGCCAACTCTT  
GGCATACGCAACAGGCAAGGCACTCGACACATCGCGCGCCCAATACGGACTTTCACGCAAAACCATCCGCGCGCGGACCGCGGCAACCGCGGTTCGCGCGGAATACGAAACCGAC  
GACGATTCGCGCGCGCGTCCAGCCATCCGCAAAATACGCGCGCGCGCGGCGGACCGCATACGAGGCCACGCCATCGACGCGCGCGCGCAATACACACGCGCGCGGTGCGCG  
CGCGCGCGCGCGGTGGAGTTTACATCAAAACCCAAAGCGGCGCGCGGACGCAACCAATTT

## SEQ ID 4708

MGNRLSGLPAPAAIETDFEGIPARKKAALTALCPESIRETVAQTLLESEPLTIDLQQAYQELLVRNRINBAVKANLLAYAQGSDLDHIAAQYGLSRKTIRAADPDANPPVAEYETD  
DAFRARVQAHPEKYAAGPRTAYEAHAIDAPKSHTPAPCAAPPARWRFTSKPAARPTKFP

## SEQ ID 4709

ATGGAATTAAGCGGTTCAGGCTGACCATCGACACCCCCAAACCACTAACCGGACACTGACCGTCAACCAACCAACCGCGCAAGGGCTGCTGACCTACCAAAACGCGCATGA  
ACGCGCAAGCGCGGCGCTGTCGAGCACACCCACCGGACGACTCGCGCGGTACAACGAAAAACCCAA

## SEQ ID 4710

MELKAVTSITIDTPTQTTITGHLTVNQTTTAQGLITYQNGMNGQGSLSSEHTPDDSGGTTEKQP

## SEQ ID 4711

TTGGAAGCCTCGCGAAACGCGAAAGCCCGCGCTTCGCCATTAACGGGCGGTTCGCCATCAAGACGAGACAGAAATGACCGACCGGCAATAGACAACTCATCAAAACCGCGCAC  
ATCGCGGACACCGACCCCGCTCCGCGCAACACGCGCGGATTAACCGGACTGGCTGCCCTATATGTCCTTTCGAGCGCGGTGTGAGTATGGCGCATCCCAAGTGTGCGGGAAGC  
CTGACCACTCTTATCCCTGCGCGGCAACCGGAGACGCGGTAGTTTATGCTGCCAAGCTTCGCGGATACACCGCGCGCGCGCGCGGCAACCGGTCTGCGGATTCATCCG  
CTACACCAACAGCGCGGCGGATGGAATTAAGCGGTTCAGAGCTGACCATCGACACCCCAACCACTAACCGGACACTGACCGTCAACCAACCAACCGCGCAAGGGCTG  
CTGACCTACCAAAACGCGCATGAACGCGCAAGCGCGGACGCTGTCGAGCACACCCACCGGACGACTCGCGCGGTACAACGAAAAACCCCAATGACCGACGCGAGAAACGCGCGGCGCA  
AGACACCTTCGCGCACATCGCCCAATCCATCGCAACATCTGTTTCAAGAATAGGAACGCGGCTGATGCGCGGAAGAATACGCGAGTTTATTCGCGACTTGATCGATATGCGCGCGGT  
CAGCGCGCATCGCGCTCATCCACCAAGCGCGGTTCACCGCTCGCAAGATGGAACCCGCAATACCGTCCCGCGCATACAGGACAGACCGCGGACTCGCGCGCGGCAAAATCAAAAT  
TAACCTAGAGCTAACCTTTCGCGACGCGCGGAGCAACCTACCGCATCAAA

## SEQ ID 4712

LEACRKRQKPPRSATIGRFPTRRRDRNDPNNRQPHQTRHRRHRPRVRAHQGGITTDNLPTIVPPAGGVSVMRIPSVGEACTILSPAGEPENGVLCCQASDRYPAPSADPAETVVRPH  
LQPPQRDRGIKSRYPKPHRRPNNHNRTPDRQPNHRRPRAADLPKRHRPRQPVRAHPRRLRYNGKTPMTDAENGRQD/LAHIAQSIINILFTIRI/RLMREYGSFIPDLIDMPAG  
HAAIALIHQAQVATLARWKPRTVVRRIQADTADLAAGKIKLTLDTLADGGERTYRIK

## SEQ ID 4713

TTGATCAAGTCCGCGTAAACACATCGTACAGCGCAAAACCGGATGGGAATGGCAAAATCCGGAACAAACATTTTCAAGCGTACAAACAAAAATACCAACCGGAGGTGGTATTTCT  
TTAATTTTTCGCGCGCGGAGCGGCTCGAACCCGCGACCGCGG



SEQ ID 4714

LIKSALKHIVQRKFGHEWQNPETNIFQSVQTKNINRRLVFLNFWRGGRGSGNPRPPA

**SEQ ID 4715**

SEQ ID 4715  
TTGGCCCTTATCCCTTTTCAGACGGCATCTCAAGATTCGGGTCTGCGCCACATCCATATGGCGACAAGGGAACAAAAACCGATGAAACCGCCCCGACCCACAGCGTTGGGGAAACTGCCAA  
ACATCATCAGGCAGGATCGGGTCATCATGCTGATGGCGAAAAATCTTGGCTTTGGCGGGCACTGCGCGCTTTTGTGCCAGTTA

**SEQ ID 4716**

SEQ ID 4716  
LPLSLSDGIQDGLRHHMATREOKTDETPATHORWGNQNIIRQDAVIMLAKILALRGTAFFCSQL

**SEQ ID 4717**

SEQ ID 4717  
ATGACCGACCGCCAANTAGACAACCTCATCAAACCGCCACCATCGCCGACACCGACCCCGGTCGGGCACAACACGGCGGCATTACCACCGACTGGCTGCCCTATATCGTCCCTTTGC  
AGGCGCGGTGTCAGTATGCGGCATCCCAAGTGTCTGGGGAAGCCTGCACCATCTTATCCCTCGCGGGAACCCGAGAACCGCG

**SEQ ID 4718**

SEQ ID 4718  
MTDROIDNLIKPATIADTDPA SAHNFAALPPTGCP ISSPLQ AACQYGASQVS AKPAPSYPLPANPRTA

SEQ ID 4719

SEQ ID 4719  
TTGGATAGAAAAAACAACGCCGCTGTGAACCTTCAGACGGCATTTTATCCACCCCCAAACCTAAAAACCACAACCAAGCCCTACACCGCTTGCCCCACCTGCGCGCGCCCCAAA

**SEQ ID 4720**

LDRKNKRRLKPSDGIFYPPPNLKTTHKPYTACPHLAAAPK

SEQ ID 4721

SEQ ID 4721  
ATGCGAAACAAAATAAACGCCAACACATGGAACCTCGGCTACACGCCCTTACAACCTTCGCACCCTTGGCGCAACCGCTGCAAACTGACACAGGCCGAGTTGGCGCAAAATCGTCGGGGTGAAGC  
ACTACATACAGGTAGGCCGCTGGGAAGCCGAACCCGATACCGAAACGCGCGGGCCGATATGCCCTGGAAAAATGGCGGCAGTTCCTCGATTGGATAGAAAAACAACACGCGCTC

SEQ ID 4722

SEQ ID 4722  
MRNKNINRNDMELGYTFYNLRTLNRNCKLTQAEALQIVGVKHYIQVGRWEAEFDTETRRADMPLEKWRQFLDWIEKTNV

SEQ ID 4723

SEQ ID 4723  
TTGCCGTTTCGCGGAGGCTTCCAACAGAGTGAGGTTATTTTGGGGCGCGCGGAGGTGGGGCAAGCGGTGTAGGGCTTGGTTGTGGTTTTTAGGTTTGGGGGTGGGTAATAAATGCCGTC  
TGAAGGTTTCAGACGCGGTTTGTTTTTCTATCCAAATCAGAGAACTGCGGCCATTTTCCAGCGCATATCGGCCCGCCGCGTTTCGGTATCGGGTTCGGCTTCCAGCGGCCCTACCTGTA  
TGTAGTGCCTTCAACCCGACAGATTTCGCGCCAACCTCGGCCGTGTGTCAAGTTTGCAGCTTGCAGCGGTTGCCGAGGTCGAAGGTTGTAGCGCGGTGTAGCCGAGTTCATGTCGTTCGCGGTTATTTTGT  
TCGCATATTTTGTGGCTGTACTAGATTATCCCTAAATTCACACCGATCCCGAGGATTTT

**SEQ ID 4724**

SEQ ID 4724  
LPPFAGFQQSEVTLGRRRGGGKRCRAWLWFLGLGVGKKCRLLKVS DGVCFYPYIEELPPFFQRHIGPPRFGIGFGFPAAYLYVVLHPDDLRLGLCQFAAVAQGAQVVRKVAEFHVVAVYF  
SHIPCGGTRLSLNSPTPIQDF

SEQ ID 4725

SEQ ID 4725  
ATGAAGATAACACACTGCAAAATTAAAGAAAGAAGTACAAAAGAACCCTCCGTCCTTTGTACCGGAAGTTACCGCCCGTCTGCCCGCATATTTTGGGTATTCATCCCGATTTCGGCGG  
CACTGTTTTCACGTAATAATCCGACAGGTTACCAATCATCGTTTGGCCTTGGCTGCCAGTGAGGTTTTCGAGTGCCTCCGCCCGCGGGCCGGGCGGAAGCTATTTCGGCGGACGGCGTAAAGCGG  
ACGCGGTGCCGCGCGCGGAGGAAAAGCGGTTCGTCTCGGCATTTCGAAACGCAACGGCGCGGCCCTATACCGTTGCCGCGGACGATGCCGAGCCTGAAACGTTGCTCCCTGCCGTTAAAAAG  
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ACATTACCGCATTTGGGAACCTTTTGAATCAGGCAAAACGCGCTTCGGAAATACAACGGAATCGATCGTAAACCTTTCCCGCCCTGTTTGAGGGAATGCGAATTTTCGACTTAACCTCGG  
CACACCGTCCCGGACGTAAAAATCTGCGGGATCGGTGTGGAATT

**SEQ ID 4726**

SEQ ID 4726  
MKITHCKLIKKEVQKEPLRSFVPEVTARSAADILGIHPDAAALFYRKIRTVTNHRLAALAEDEVFECAPAGPGGSYFGGRKKGGRGGAAGKAVVFGIPKRNGRAYTVAADDAEPETLLPAVKK  
KTMPPGIVYADSPGSRGKLDAAGFTCRINRSKEFADRRNHINGIGNFWNQAKRALRKYNGIDRKPFPPLRECEFRFAGTSPRQLKLADRCGI

SEQ ID 4727

SEQ ID 4727  
GTGTGTTATCTTCATATTTTCAGGGTAACATATCTGCTAACTCGGTACAGACCTATTTTTTTGACTGCCCGGGCAGGTTTCGGTAAGGACGGCGCAAAATCGGGCTCTGCTCGCGGT  
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AATGGGTAAATGAAACGGCTTGGCGCGTCTTCCCGATAATCCATTCCGGGTAGCGGTGAA

SEQ ID 4728

SEQ ID 4728  
VCYLHISRVTYLLIWRPYFDDCPAAGFGKGGKSGFVCRFAAEKNRIVKGDVFGMAVMPARAFVCLPVDFGNQAGLAAMGNETACAVLPDNPFGVAVE

SEQ ID 4729

SEQ ID 4729  
ATGAACACAGCCGCACTATTCAACCGCTACCCCGAATGGATTATCGGGCAAGACGGCGCAAGCCGTTTCATTACCCATTGCGCGTATCCCGCGCTGATTGCCAAATCCACAGGCAGACAG  
ACGGCGAATGCCCGGGCGGGCACTACCGCCATTCCGAAAACGGCATCACCCCTTTACGATTTTATTATTTTCGCGGGCAAAACGGCAGACAGAACCCGATTTCGCGCGCTCTTACCGAAAC  
CTGCGCGCGGGCAGTCAAAAAATAGGGTCTGTACCAGAT

**SEQ ID 4730**

SEQ ID 4730  
MNRRAALFNRYPEWIIIGDQASRFITHCRYPRLLIAKIHRTDGECPGGHYRHSNGITLYDFFFGGKPADEARFAAVLTETCRRAVKKIGSVPD

**SEQ ID 4731**

SEQ ID 4731  
ATGGCAGACATCCTGCCATCCGACAAGCGGCGGCAACCGCCAAAAACGAAAGGAAATCCAATAAACATAATCGAACAGAAACAAAACGCACCGAGTTAAGAAAAATAGATGCCGAAATCG  
CCAAAATCATTGGCGAGCGGCACAAAATCAACGCCGAATCCGTAAAAATAGCCCAAGAGTCCCGCTGGTATCCCATGATGGCGGCCACCGGTCTGGTTACCGCCATCGCCGCCGTGTGGC  
ACTGATATTCAAATTGGCC

SEQ ID 4732

SEQ ID 4732  
MADILPSDKRRPPKTKGNPINIIEQETKRTTELKIDAEIAKILADAHKINAEVSKIAQESRWYPMHAATGLVTAIAAVLALIFKFA

MADILPSDKRRQ

[illegible]

TTCTTGTTTCGAT  
GTCID 1704

SEQ ID 4734

SEQ ID 4734  
INFORMATION

SEQ ID 4734  
 LNSAALFILLRDKAPRGACQGNLISANTAAMVTRPVAALNGYQRDSWAIPTDSALILCASAMILAISASTFLNSVRFVSCSIFIGPPVPVGGCRRLSDGRM  
 SEQ ID 4735  
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SEQ ID 4735

SEQ ID 4735  
ATGGTGCGGGCGGCGGTGTTTGCCATGTCATATAT  
SEQ ID 4736

**SEQ ID 4738**

SEQ ID 4739

**SEQ ID 4740**

SEQ ID 4741

**SEQ ID 4742**

**SEQ ID 4743**

**SEQ ID 4744**

**SEQ ID 4745**

**SEQ ID 4746**

SEQ ID 4747

SEQ ID 4748

SEQ ID 4749

SEQ ID 4750

SEQ ID 4751

SEQ ID 4752

SEQ ID 4753

SEQ ID 4753  
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 GCACAAACAGCTGCTCCAGCGCGGCATAAGCGTTTGGTGGCGGATATTTTGGCATCTGCTGTAGACGTCGCGGTACGACGCGCGTTACCCAAACATCGCATAGCTTGCCAGCACGAGTCCGGT  
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GAAAATTCGTTTCATGACCGTCCGACAGGAAATACAGAAATATGCCGTCTGAAACGGCATACGCGCGGTATTATAACAAACACCGCGCACCATCCGAAACGGGCGCGCATACAAAT  
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## SEQ ID 4754

KEIISFFPACDHQVTAFCQKRGIRVFNPAAGAADEQEFDAVSRRHRADCFADGVCPSQRKGVADGFAIFAESCLIIITDKQSLQRGITAVADIChRLIDVPVRAVTVQRIACQHESG  
FFGVHRHFPFRTHIGKRFHIIIVGGARTYGHIMGHQHI\*NVLRVFIIVERNHHFSPQTGGFYYPAPRIAERHRLACTSGYLHACDVQVVEREIRNILLGEDASDRLEPAPAEADNQHMI  
RLAHRPHQHAVQIERLHVPA\*LDQAPDQRLIAAQEBERDNHRQQRNRRRLFPQWRNHILKLPNGQHHEARLAALREIQSRFEAVADRMILHFEFCNGKHNCQLQHQQHQQHQLPAAADQC  
LNVQLHADRDKEBAQNIARANVVDLETVFRFRKHAGNECAQRHRQTFQLSISHTQGYQHIHDKHEFRPAFCHPEPSRHNFAADEKQDQQRQHQFCKRQTVQRPNISVPSASQRG  
NQNHQRHDGDLVHQHARHLTVRLPQLRFRQNPANRRGRHRQARYGKRIPIERHARQHOYAHYQRHNADLTAQTEHQPHRPQLQ\*KLQDAEHQBNHPDQAIIRRMARFNQJAE  
HTGPRQAHQVQVAGHGNVELAAQDHRNDRHQNNHNRKRFVHGPSEQENTKCKLRKHTPPYNYKTPRTIRNGRIQF\*\*NTFF\*PAPPEH

## SEQ ID 4755

TTGTCCGATGCCCGCAGTAAATATCCCTTTTATCTCCGCGAGAGCCGATGCTTTTACGCAAAATCATCCACATGCACATGGACGCGTTCACGCATCGGTAGAACATCCGCGAGCAGCGCG  
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GCTGTGTCCGCAAGCGGTGTATGTGCTCCGCAITTCGATTTGTATCCGTCAGGTTTCGCGCAGATTCACGCGGTATTCAGGCGTTATACCGATTTAATCGAACCCCTTGTGCTGGAACGAA  
GCTATCTTGCAGTTACCGTAAATTTCAAAATATCCCTTACGCGCGCAAGTTCGCAAGAAATCCGTCGCCCATTTTTCGCGAAACGGGTTCGCGCATCCGACAGGCATCGCGCGA  
ACAAATTTCTGCGCAAAATTTGCTCCGACTGCGCGCAAGCGCAAGCGGCGAGTTGTGTGTCGCGCGCAAGTATGCAATTTTGGAAACCTTGCTTTGGGCAAAATCCCGGAGCGGG  
CAAGGTAACTGCTGAAATAATGCACTGCTGGGTATCGGACGCGCGGCGGATTTGCGCGGTTTCGAGCGCGCGAGCTCTTAAATCATTTCCGACGCTACGCGCTACCGCTCTATGATTTC  
GCGCGGTCACGACAAACCCCGTCAAGCGCAAGCGCAAGCGCTCAAATTTCCACAGAAATCACCTTCGCCGAAGACCTGCCGCTCGCGCGAGCTGCGGCAACCTGCGCCATCTTCG  
CCGAAGACCTGTGCGCGCAAAATCACGCGCAAAACGTCGAAGCGCAAGCGTAACTGCTCAAGCTGAAGACCTACGATTTCCGCATCATCAGCGCAGCGTACTTATCTCCGCTATTCG  
CGACTGCGCAGCTCTGCTGCGAGCTGCGCAAAATGTTGATGGCGCGCTCCGCGCGCAGACGGAAGACGCGTTCGCCCTCATCGGTATCGGTGTCGCGAGGCTTGTACCGCAAAATCAGCAG  
CAGGATTTGTGGCG

## SEQ ID 4756

LSDARSKISLLSAPMSLRKI IHIDMAFYASVELREQPHLGRPVVVAEGARSVICAASEYARQFGLHSAMSVATVKRLCPQAVVYVPHFDLYRQVSAQIHAVFRYITDLIEPLSLDE  
AYLDVTRNFKNIPYAGEVAKEIRAAIPAEITGLTASAGIAPNKFLAKIASDWRKFNQGFVLPFHKVMAFLETLPGLKIPGAGKVTLLKMKQSLGMRTAGDLRRFERGELLNHFGRYGRYLDL  
ARGTDEHPVKAERERLQISTEITLPEDLPLGQAAGHLPHLAEDLWRQITRKNVEAQSVTLKLTDFRIITRTITYSVLPDCAALLQAAQMLMARVPQTEDAFRLIGIGVRLVPRNQ  
QDLMA

## SEQ ID 4757

GTGCGGCACTCGACTGCCTCGAAAGCGCGCGAGCTGATTTTCAGACGGCATCAAAACATGATGAAACTCAATGCCAACAGCTCGAAGCGTCCGCTACCTCGCGCGCGCCCTGTTCGTC  
TTGCCGCGCAGGCGAGCGGCAAAACCGCGCTGATTACGCAAAATCAAGCATTTGATTTGCAATGTCGGCTATCTGCCCATACCGTCCGCGGATTAACCTTTACCAACAAAGCCGCTGC  
GGAAATCGAGAGCGCGTCCGCAAAATGCTGCCAAACCGCAACCGCGCGGCTGACGATTTGCACTGCTCCATCTTTGGGCATGAAGATTTCGCGCAAGAGCGCAACCATATCGGTAC  
AAAAAAATCTTCTCATTTCTGACTCTACCGACAGCGCAAAATCATCGCGCAACTCTTAGCGCGCACGGGAAAGAGCGGTATTCAGGCGCAGCAGCAGATTTCCTTTTGGAAAAACG  
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CTTAATTCGCTGCTGCGCTGCTGTTTCAGCAAAACAGTGAAGTGGCAACAAATGGCAGCGCGGCTGCGTTATCTGTTGGTTGACGAATGCCAAGATACGAATACCTGCCAATTTGCG  
CTGATGAACTCTTGACAGCGCGCGAAGGATGTTTACCGCGCTGCGCGCAGCAGCAGTCCATCTACGATGCGCGCGCGCAACATGGAACCTGCGCAAAATGCGCAAAATGCGAAGAACTATC  
CGCAGATGAAGGTATCAAACTGGAGCAAACTACCGCTCCACCGCGCGGATTTCTCAAAATTTGCAACAAAGTTCATCGAAACAAACCCCAAGCTGTTTACCAAAATCTTGGTGCCTAAT  
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GCACGAGCAGAAATGCAAGCTGATGAAGCCGCAACAAACGAGAGCCCTTGCCACATGAAACATCAACCGCCCAACCTGCAAGCTTTATGGAATATGTCGCAACTTACCGCGC  
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GAACGCGCGCTGATGATGTCGCGCATCCCGTGCACAAACGCAACTCAGCTGACCCATCTGTCGCAACGCAAAACGAGCATATGCGCAATTTCCCGCAACCGCGGATTCATAGAG  
AAATGCGCGAGGAAGATTGAAATCTCGGGCGCAAGCGCGCAACCGATTGTCAGCAAGAAAGAGGACAGCTAACCTTCCGATATATTCGGAAGGATCGCAACCTTAAAAAAG  
CGGCCGCGCGAT

## SEQ ID 4758

VRHSTASKAAQZDFRRHQNMMKLNAAQOLEAVRYLGGPLFVLGAGSGKTGVTQKIKHLIVNVGYLPHVVAITPTNKAABEHQERVAKMLPKPQTRGLTICTPHSLGMKILREANHIGY  
KKNFSILDSTDSAKIIGELLGGTGKEAVPKAQHQISLWKNLKTPEDEVVQTASNVREQQTARVYASYQETLSYQAVDFDDLRLPAVLLQNSEVRNWKQRRLRYLLVDECDTNTQFPA  
LMLKLTGAEGMPTAVGDDQSIYAWRANMENLRKQENYPMKVILEQNYRSTARILKLANVIENNPKLPTKLLWSQLGEGEPVKVACQNEQHEADVVSQIVKQKLIIGDKTRYAD  
FAVLYRGKHQARIPEERLARGARI PYRLSGGQSFQDKAEIKDVLISYVRLANPNDDPAFLRAVPTPKRGIDVTLGLKLNAYHEHECSLYEAAQNEBALATLNNWRLHQAQFMDMFGNYRA  
KAEIDAGEFINSLBEIDYENHLMQNEEGKAGEIKWRNVGELVSWFARKGERDKNVIELAQTVAMTLLEKDEESTDAVSLTSHAARKLEYFVTVLWCGEBGLPHENDSIEENGVSE  
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## SEQ ID 4759

ATGCACACAGCCTGACCGTCAAAATACCGTTATCGGAAGCGGCGCACCAAAATCCCGCTGCCGCTTGTGCGCCGAGATCGCGCGGATTTATCTCCGCTGCTGCCAAATCAAAAC  
TGCCCTTCGATATCGTCGAGTTCGCGCGGACTTTTGGAAATCGCGGCGAGCATCGCGCAAGTATTCGCGCACACGCGAGCGCTCCGCGACGCGCTGCCGCAAAACCGCTGCTGTTTAC  
GTTTCAGACGCGATTGCGAAGCGCGCTCGTTCCGCTGTTCCGAGATTTATTTTGAATGCTGCGACGCGCTGATCGAAGCGCGCTGCCGCAATTCGATATCGAGCTGTTTTCGCG  
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## SEQ ID 4760

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ETAVRRVANAKNGIALALCNHEFHRTTPQEEIVCRKQMEDCGADICKIIVMPQSEEDVLLSATLEAKRLVAKPVI THSGQTGAVSRLAGQVFGSSTTFGSGTQNSAPQIGVSAL  
RAALDCLESAD

## SEQ ID 4761

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CTGCAACCGCTGCATCGCGCTCTGCTGCGGATGCCATTATGGGCGCGGCAAACTTATGCACACCGTCATACCGAGAAATGCACCGCTGCGGACTGCGCTGCGCCCTGCGCGG  
GACTGCATCCATATGCAGCGCTTGCAGACACCGCTCTGCGCGCGCGCGCGCTTTCAGCCTGTGCGGACGACAGCGCTTTGCGCGCGCGCAACCGCGCTGCGGCTACCTCAAACGCA  
ACGAACGCAAAACAGCGCGAAGCGGACGAAACGCAAGGCCATGCTTGCAGAACGCGAAGCGCGCTGCGCAACGCGCTGCGCAAAACCGCGGACACACCGGAAACCGCGCTTCAACCGCG  
CGACCTCATCGCAAGGCAATGGCAAAAGCGCAAAACCAAGGATCGCTCGCGCGCGCGCAACCGCCAAAGGCTATCAGGCAAAACAGATAGCGAAGCGCGGAAACGCGCGGAAATG  
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## SEQ ID 4762

MTATAADLRLLPQTQRCBEGYEGCLPYARAMLGEAHNLCPAGGATVVRDLAALLGKFLVAPAKTQAKALARIDETACIGCTACIRACPADAMGAKLMHPTVTECTGCLVAPCPV  
DCIHMQPVADTVLPRARRFSILSDSRFAAAEHARARYLKRNERKQREADERKAMLAEREA VRNARPTPTPEKPAFNPADILAKAMAKAQTDRLAADDNRQGYQAKQIAERERAE  
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## SEQ ID 4763

ATGTCGCCCAACCAAGAGCTGCAAGGCATCTCTCTTTGGGTAAACAAAAACCAATATCGGACCGGCTACCGGCTGAAATTCGCAAGCAATCGACAAACCAACATCCGACAAACG  
ACTATTTGCTCAATTTGCTCTGCGCGGAAATTCACAGCCTCTGCGCGATGACCGCGGACCGCGACTTCGCCACCATCGTCATCCGCTATATCCCGCACATCAAAATGGTGAAGCAAAATC  
CCTGAAACTCTACCTCTTCAGCTTCCGCAACACCGCGGATTTTCATGAAGACTGCTCAACATCATGAAAGACCTCATCGCCCTGATGGATCCGAAATACATGAAGTGTTCGCGGAG  
TTCACACCGCGCGCGGATCGCGCTTCATCGCTTGCACACTACGCGCAAGCAGGACAGAGTTGAAGCATTTGGCAGCAACACCGCTGTTGCGAGCAGCAGCACA

## SEQ ID 4764

MSRNNELQGISLGNQKTQYPTGYAPEILEAFDNKHPDNDYFVKVFCPEPTSLCPMTGQPDFATIVIRYIPIHKMVESKSLKLYLFSFRNHGDFHEDCVMIIMKDLIALMDPKYIEVFG  
FTPRGLIAPHFPANYGKAGTEPEALARKRLFEDAQ

## SEQ ID 4765

ATGACGACCGATTTCATATTCGCGCGCGAGCGCGTGTGCGCGCGAGCCACATACCGCATTTGTTCCGGAGTAACCCCATGTGACAGCAGCAAAAGCAAGCCCTTCCCGCGCGACTGG  
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CGCGAACACGCGCTTCGATCCCGTTTACGCCCGCAAACTCGCGGTAAAGTGAAGAGCTTTACCTGTCCAGCGCGATACCGCGCAACAGCGCTTTGAAATCTGCGACACGCTCGTCCGTT  
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GTCAGGCGAGATTGACATCTCTACGAGAGAGGATCAGTTGGGAAGCGCAATGATGACATCGCGCGTGAAGAAACGACATCATCAACAAATCCGCGCGCTGGTACAGCTACAAACGCGC  
GAAATCGGTCAGGCAAGACACGCTCCGCGCTGGCTGAAGAAACCCGCAATTTCCGACGAAATCGACGCAAAATCCGCGCGCTCAACGCGCTAGAAATGCACATACCGAAGG  
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## SEQ ID 4766

MTDRFIFRAARVAPQPTYRICSGVTPMSDDKSKALAAALAIKESFGKGAIMKMDGSOQENLEVI STGSLGLDLALGVGGLPRGRIVRIFGPRESSGKTLICLEAVAQCKNGVCAFD  
AEHAPDPVYARKLVKVEEYLSQPDTEQALEICDTLVRSGLDNDVVSVAALVPKAEI EGDMDGSHVGLQARLMSQALRLKLTGHIKRTNTLVVFINQIRMKIGVMPGSPETTTGGNAL  
KPYSSVRLDIRRTGSIKKEEVLGNHETRVKVIKNAVPPRQAEFDILYEGEISWEGELIDIGVKNDIINKSGAWSYNGAKIGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITG  
TQDETDERPER

## SEQ ID 4767

TTCCTCGCTCTGCGCTACTATTGTTACTGTCTGCGGCTCTCCGCTTGTCTGATTGTTTGTAAATCCGCTATACCAAACTCAAATCAAGCGCTCCGGAGCGCGCTCAAAAAACGGTA  
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TCGTTGCCCAATACCTCTCTGCTTTTGTGATGATCGGTCGCGCGGATGTGAGCGCGGACGGAAGATAGAAATTCAGCGCGTTTCGCGCGCTGCTGCTCGCGGCTGCGCAACATTA  
CGCGGATCTTCATTCGATTTGTTGATGAACACACAGCGTATGTTGTTTTGATGTTGCGGTCAGTTTCGCGCAAGCGCTGACTCATCAGCGCGCGCTGCACTCGGATGCTGCTGTC  
CCCCATATCGCTTCGATTTGCGCTTTGGGACGAGTGGCGCTACGGAATCGAGACTACCATATCTATCGCGCGGAAACGAGCGGCTGCGCAGATTTCCAAAGCCTGTTTCGCGGTA  
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CGCTTCGAGGCGAGGTGTTGTTTTGCGGAGGATTCGGGCGCAAGATTTTCAGCATGCGCGCGCGCGGACGCGCGGACTTCGAGGGCGAGGTC

## SEQ ID 4768

LPRLAVFLVLSAALRLVLI FVNPLYQNSNQAVRRRLKKNKTSQQKYRLSGFQVLFPGSAVGFVLRPGDVHYPYAVEGADFCVDFVGNFGVFPDADVVFLATDFRAVVAVPRAGVDDV  
VFHADVDQFAPPTDAFSVEDVLCLETERGGDFVDFDAGFVAQYFFAFDFDGSAAADVEADGRIEFQVAAAGRLGAAEHYADLHSDLVDEHNQRIQFDFWSGQFQSLTHQARLQSDVAV  
PHIAPDFGFGDECGYIDYHYIAARTDERVADFQSLPAGILGQVKLPDFYAEFAGVNGIEGVFGIDKGAHA VFLALDGFPEACGFAGGFGAEDFDAPARQAADSEGEV

## SEQ ID 4769

TTGTTAACTCACTATATTTTACCCGACGGGGTGAAAAATACAGTGTCTACAGCCCGACCTACGCGCGCTTTGCTCTATCTCTGCGCGGACTTTACGGA

## SEQ ID 4770

LLIHYIFTRRGEKYSCTPTARPASTILRLLYG

## SEQ ID 4771

GTGCAAGTATTGCACATAAAGGGCGCAGGCTTATCCGTAAGTCGCGCGAGGATAGAGGCAAGCGGGCTAGGTGCGGCTGTAGCAACTGTATTTTACCCCGCTCGGGTAAAAATA  
TAGTGGAT

## SEQ ID 4772

VQSLAHKRAQASSVESAQDRGKAGVGRAVATVFTPSGKNIVD

## SEQ ID 4773

GTGCAATACCTTTGCACTTGCTGAACAAAAATCAAACGACCCCTTATATCAAAATGCAAAAAATATGCCGTCATTCGCGGAGAGCGGGAATCCGACCTGTGCGGACGCAAAATTTATCGAG

## SEQ ID 4774

VQYFALAEQNSNDPLYQMQKICRHSREGGNPDLSAREKPIE



SEQ ID 4775

SEQ ID 4775  
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TTCAGATTCTACGTTCTAGATTCCCGCCTGCGCGGGAA

**SEQ ID 4776**

SEQ ID 4776  
LHLINKIOTTLYIKCKKYAVIPAKAGIQTCRHGNLSSKTVFQILSRFPFPARE

SEQ ID 4777

SEQ ID 4777

ATGCGACGCCGAATCACTGGAATTTGGCGGCAAAACCGGCCATAAACAGATATAATGCCGCCGAACCCCTCGGACGGCATTGCCGCTTCCTCTATTTCATTAACAACAACAGGAGTATTCAGTATGTTTCGGAAAGCCGGGATTAGCGGGCTGTAGTACCAAGCCGACGACAAATGACAGAAACATGAAAGAGCCACAAGCCAAACTTCCGGAACCGGAATCGAAGGCGAAGCAGCGCAACGGCTTGTCGTCAAAATACAAATGACCTCGCGCGCACGAGTAGCGCAAATCGACATCAGCCCCGATTGTGATTCAAGAGCCCGCGATGACAAAGAAATGCTCGAAGACCTCATCTCTCGCGCCCTCAAAATCCGCGCGGGGCAAGGCCGAAGAACCGCAACAAACAATGGCGCGATTACCCAGATCTGCCCCCGCGCGTGGGCGACTTCTTCGGC

SEQ ID 4778

SEQ ID 4778  
MAARITGGGGKPAINRYNAARTLTALPLPSFIQTQGVFSMFGKAGLGGMLKQAOQMENKKAQAKLAETRIEGEAGNLVKITMTCAHEVRRIDISPDLIQEAAADKEMLEDLILAA  
KSARGKAETANKTNGAFTQDLPPCGVDFR

**SEQ ID 4779**

SEQ ID 4779

ATGCTAGAAATACGCCGCCGGAAGCCGCCGTTTCAGACGGCATTCGACGACACCGACAGAAACATCACGACCGAAACCAAGAGAAAACATGGCCATCAAGTTCTCGCCCGAAAATGGCGCG  
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CACCATCGCCCGCATCTCTGCCAAAAGCCCTCAACTGCAATGATATGCGCAACACGCGGAACCTTGC CGCGCTGTGCCAAGCTGCACCCAAATTCGATGCGCGACGCTATGTGCACTGCTCGAA  
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CGTCTTACGCAATATGACGCGCGCAACAGGTGCGCGACCACTTGCACCGTCTTCGACGCGGAAAACATCGCTACGACACCCCGCTGCACTTTTGGGACGTGCCGCGCGCGGATCG  
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CCGAAGCGCGCGCACCGCGGACAAAACCGGCTCGACAAATTCGCGGACACCTCGCCCAAGCTTCGCGGCTGACCTTACCTCTGCAAAACCGAAGACTGCGCGACGAAGCGCGCGCGGA  
AACCCCGCGGATGCAGGACAAGCTGTGTCGAAGCGGAAGACGCGCAAAAGCAACGATCTGCTCGAAGCGGACCGCGCGCACAAAAATCTCCAAAGCATTCGCGCGCGCAATGCGCAGCCC  
GAATCACTGGAATTTGGCGCGCAACCGGCA

**SEQ ID 4780**

SEQ ID 4780  
 MLEYAARSRRSDGIPTHRQKHHDNRQEKNAAYQVLARKWRKPTFSDLVGQEHVVKALQNALDEGRHLHAYLLTGTGRGVKTTIARTLAKSLNCENAOHQHEPCGVCQSQCTQIDAGRYVDLLE  
 IDAASNTGIDNIREVLENAQYAPTAGKYKVYIIDEVHMLSKSAFNAMKLTLEEPPEHVKFILATDPHKVPVTVLSRCLQPVLENMTAQQVADHLAHLVDSEKLYADPPALQLIGRAAAGS  
 MRDALSLLDQAAILGSGSKVAENDVRQMGIVADVQYLYELLTGIVNQDGEALLAKAQENACAYGFNDALGELAILLQQAALIQAVPSALAHDDPDSDILHRLAQTISGEQIQLYYQIYAVHG  
 KRDLGLAPDEYAGFMNTLLRMLAFAPLAAASCDANAVIENTELQSPSAQTAETKETAARKKPPRPEADAAQTFVQTASAAAMPSBGKTAGFVSHQENNVPPWEDADPKTETAAGTARTSAK  
 SIQTASEAETPPENQVSKNKAADNETEASLSEVPSENIQATPNDEAVETETFAHEAPAEFFYGFINDCPPEDEGVLEIIPPMANVLADPTAGGNDDEBARAGGIGGNNTPSAPPKFSYE  
 NWAATVRHFARKIQAQMPAQHSAMTEYRSDTGLMVLMTAEARATADKRLKLDLTLAQYGLQLTLQTEDWRDEAGRETPAMQDKRVQAEQRKAQALLADPADPAQKILQAFGAQWQF  
 ESKLEAANRP

SEQ ID 4781

SEQ ID 4781

ATGCCACGCATTTGCCGCCCTTGCCTGCCACCACTCGTCAACCAAAATTCGCCGCCGCCGAAGTGGTGCAGACGCCCTGCCAACGCCCTGAAAGAAATCGTTGAAACACGATAGACGCCGGCGCAAT  
CGCGGGTGTGATGTGGAACATGGAAGGCGGGCGGCATCCGCCCTCATCCCGCTCGCGGACCAACGCCGGCGGCAFTCAACCCCGACGACATCGAACTCGCGCTCCACCGCCACGCCACCAGCAAAAT  
CAAAACCCCTGAACGATTTTGAACACCTTTGCCAGCATTTGGGCTTTTCGCGCGGAAGGCTTGGCCAGTATCGCTTCGGTCAGCGCCCTGACCTTGACACGGCCGCCAAGAAGACAGTTTCGCATCG  
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AAGCTTGCATGAACGTATCGCGGCCATTTGTCGGGCATGATTTTCAGACGGCATCTTTGGAATTTGACAGCGGCAATAGCGCGCTCGCGCTCTATGGCGGATTTGCCAAGCCGACTTTGCGC  
AAAGGCAAAACCGATPAACAATATTCGCTTCGTCAACCATCGTTTGTTCGCCGCAAAAGTCACTGCTCCATCGGCTCAAGCAGGATACCGCGAGCTATTGCACAACCGCACTGACACCTGCTT  
TCGTCCTTTTCTCGAGCTCGCCGCCGAAGCCGCTGGATGTCAACGTCCACCGCAACAAACCGAAATCCGCTTCGCCGACAGCCGGCAAGTACACCAACTCGTGTTCACACGCTCAACAA  
AGCCCTTGC CGCAGCACCGGCCCAACTCGGAGAGTGTCAACGTCCACCGCAACAAACCGGAGGCAAGTGTGTGATGACATTACCGCGCTTACGCTTCGCCCAATGCGGCTTGAAAACGACGGCGAAATCTG  
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GTTGGGCAAAATCCGATGCTGCTCTCCCTCGCACCGAGCTATTTGGGCGAACTCGCGCCAACTCGGCAGCAGCCAAACCATTCGATCATCACGAAAACCGCATCTCGCCCAATGCTCGGCCAC  
GGCTCAATTCGCGCGCGCGCGCAGGCTCACCTTGCGCCGAAATGAACGCGCTGCTCGCGCATATGGAATAATACGCGCGCGCAGCAACAGTGTCAACACCGCAGGCGCAGTGGGTCAAACTGA  
CTTTGAAAGAAATGGACACACTGTTCTTGC GCGGACAG

SEQ ID 4782

SEQ ID 4782  
MPRIALPDHLVNQIAAGEVVERPANALKETIVENSIDAGATAVDVLEGGGIRLIRVGDNGGGIHPDDIELALHRHATSKITKTLNDLHVSMGFRGEGIASIASVSRILTLTSRQEDSSHA  
TQVKAEDGKLSPTAAAHFVPGTTIEAAELFFNTPARRKFKLSENTFYAHCAHTLERLALAHPIAFSLKRDGQVFKLPAQSLHERIAAIVGDDFQTASLEITDGSNSALRYGAIKPTFA  
KGKTDQKQCFVNHFRVDRKVMILHAVKQAYRDVLHVALTPAFVLFLLEPPEAVOVNVHTPTKTEIRFDRSRQVHQLVPHTLNKLALADTRANLTESVSNAGEVLHDTITGVTPAMPSPENDGENL  
FDSASNHTPGNKPDTRNAPGSSGKTAPEMPYQAAARPOQHSLSLRESRAAMDITYAELYKKTDDIDLELSQFEQARFGNMPSETPAHKTTDTPISDGIQPSQSELPPIGLFALQQLIGITYLAQAE  
DSLILLIDMHAAAEIRVNYEKMQRQRENGNLISQSHLLIPVTPAASHEECAALADHAETLAGFGLSDMGGNTLAVRAAPVMLGKSDVVSILARDVLGELAQVGSQSTIASHENRILATMSCH  
GSIRAGRRLLTPENALLRDMENTPRSNQCNGHRPTWVKLTLEKLDITFLRQ



## SEQ ID 4783

TTGAATCGAGGAACACGATGCGCCACCTACCCCTGTTTCTACTAATGCTTTTCCCGGCATCGGTTTACGCCGAGATTCGGAGCGCGCAAACTAAACCTGCTGTGGGGCTTGCCCTTTG  
CCCTGATTTTGTCTGTCTATCGCATTTGGGTCCCTTGTTTTTTTCGCATACCTGGCATCACCATTACCGGCAAAATCACCCTTTTGGACATTTGCTCTTCTCATCCCGTTCAAGTTTGGTTT  
TGGCGCGTCCCGCGGTATACATACCGTCGCACACGCACTCGTTGAAGAATATATCCCTTTCATCTGCTGCTGCTTGGCTGTACACCATTTACAGCGCGCATTTTGGTTTGGGGCGACTTG  
AACGGCACACCAAGCTCAACACCGCCCTGCTTGGCGTGGTACGGCACTTGCTCTATCATGGGAACGAGCGCGCGGCAATGCTGATGATTGCTGCGCTGTGAAGGCCAACCAAGACC  
GTACCGCGCGCTGCACATGCTCATCTTCTTCTATTTTCCGTGTCGAAACATCGCGCGCGCTGACCCCTTTGGCGGACCCCCACTCTTCTCGGCTTCTCAAAGGCGTAGATTTTCAT  
GTGACCGTCAAAATATGTTGCGCCCGTCTGATTAGCAACCGCTGCTGTTGACCGCTTCTATTTTCATCGACAACCGTTTCTTCAAACAGGAAAGCATTTGCACAGATACCGCGGCA  
CAACAGGAAACCCGAAATATCGCATCTTCCGCAATGGAATCTCTCTGCTTTTGGCGGTGGTGGCGCGTCTTAATGTCGGCGCTTTGGAAACCCGAAACACCCGGGATTTGAAA  
TCTTCCGAGCGCTTACCGCTTCAAAACCTTGTCCGCGATGTCATCTGATTACATTGACCGCGCTATCTATGGCAATCAGCGCCAAACAGTCCGCGAGGCAACGAATTCACCTTTGA  
ACCCATCGCGCAAGTGGGCAAACTCTTCTCGGCATCTTCTCATCACCATCTTCCCGCTCTGAGCATTTCTGAAAGCAGGCGAGGCGCGCTGGCGGGTGGTATCGCTGCTTCAAGAT  
ACGGCAGGTCATCCGATTAATACGATGTAATTTCTGGATGAGCGCATATTTGTCGCATTCTTGGATAACCGCGCCACTTATCTGCTGTTTTCATATGCGCGCGCGATGCCCAAGCT  
TAATGACGGTCCCTGTTTCTGCTGCTGCTGCGGTCTTCTATGGGTTCGCTATTCATGGCGCACTGACCTACATCGGCAACCGCGCAACTTCATGTTCAAGGCCATTGCCGAACGCG  
CGCGTACCGATGCGCATTTCTTCCGCTATATGATGTTGGTTCGCTGCTTCTGACACCGCTTCTCATGTCATACCTCGCTTTTTCGTTTCAAACACTG

## SEQ ID 4784

LNRGNTMRHLPLFSIMLPASVYAADSDGANLNLWGLPFPALILLSIALGLPLFSHTWHHYKITAFTLLFLIPLSLVFGASAGIHTVAHALVEEYIPIFLLLLALYTIISGILVWGL  
NQTPRIALTALLAVGTALASIMGTGAAMLMTRPLKANQDRTTRRHVHIVPIPLVANIIGGLTFLGDPPLFLGLKGVDFMFTVKHMFAPVVLSTAVLLPAPYFIDNRPFQKQESIAQDTPA  
QKQKPEKIAIFGKWNFLLLSGVGVAVLMSGLMKPEHPGFEILGSRYALQNLVRDVLITLFAVSMATTPKQVRAGNEFNFPELAEVGLFLGIPITIFPVLSTLKAGEAGALGGVSVLVD  
TAGHPIINTMYFMSGILSAFLDNAPYLVFPMAGGDAQALMTGPLFSLLAWSMGSVMGALTYIGNAPNFMKALAEQRGVPMPTFFGYMMMSVAFPLPVFIVHTLVFVFKLL

## SEQ ID 4785

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TCGATGTAATTTCCGATCCATCAGGCGGATGAGGCTTTTCATGATGATGTTGACGCGAGTCTTCATGAAATTCGCGGTGGTTCGGAAGCTGAAGAGGTAGAGTTTACGAGATTGCTTTTCCA  
CCTTTTGAATGTCGCGGATATAGCGGATGAGGATGCGGCAAGTCCGCGTCCCGGTTCATCGGCGAGGCTGTTGAATTCGCGGCGAGCAATTTACGAAATAGCTGTTGTCGGGATG  
TTTGTGCGAATGCTTCGAGAATTTACGGCGCTAGCGCGTGGATATTTGGTTTTTTGTATTACCCAAAGAGAGATGCTTGCAGCTCTTCTGTTGTCGGGACATAGGGTTTCTCTAG  
TTTTT

## SEQ ID 4786

LCVLEQAFACQCFKLCACFVAVGKRMNGDAAARCELAENHDFVRIHQGDEVFDDVDVAFMKIAVVAEAEKVEFQGFAPFHFVDVRDIADDDGGEVGLPGHRAEAGEFGADEFDEIVVGH  
FVVECFENFRVRILGLITQKRDALQLFVAGHRVSLVF

## SEQ ID 4787

ATGTACCACTACCAATCCGAAGCCACACAATCTCAACCGCTGATCGAAGAAAACTGAATTTGGCGCAAGAACGTTTGAAAAATCAAGGGCTTTTGGGATGTGCAACTCAATCCCG  
AAGAGCAAAAACTTTGAATCGCAAAAGTGGGAAAAACCTTATACCTATTAACCAAGAC

## SEQ ID 4788

MYHYQSEATQFLNRLIEEPKELAQRERLKNQGLNDVLENPBEQKNFESAKVAKFPYTYQD

## SEQ ID 4789

TTGGACAGATGGGTCTGCTATTTCGGCGGGTTCAGTCTTGGTAATAGGTATAAGGTTTTTTCGCCACTTTTGGCGATTCAAAGTTTTTGTCTCTTCGGGATGAGTTTCGACATCCCAAAA  
AGCCCTTGATTTTTTCAAACGTTCTTCCCAATTCAGGTTTTTCTTCGATCAGCGGTTGAGGAATGTGTGCGCTTCGATTGGTAGTGGTACATCTTTCGCCCTCAAATTTTACGGGATAC  
GGC

## SEQ ID 4790

LDRWVVISAGSVLIGIRFRHFCRPFVLLPGIEFDIPQKPLIFQTFLRQFRFFDQAVEELCGFLVVVHLCAPILRDTA

## SEQ ID 4791

ATGACGACCATCTGTCCAATGTGCGACCGGACCTGCAAACTATTTGAATGCCATCGCGCAACCCGAACATCCCGTTTTGACCGCGCTGCGTGAGAAGCGCGGCATCACCCTATGGGCA  
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AAGCGCGCATCATCGCCATGCAAAATTTTGTGAACGGAAGGTGATGCGCGAAGCGGCTTTGATGCGCGCCCACTGTCAAAATCTCAAAAGATTCAATCAAACTGCGGCAACGA  
TACCGCGATTGTCGCCATCACCTGCGCGCGGCTTGACCTGCTCTGAAAAA

## SEQ ID 4792

MYTHLSNVAPDLQNYLNAIGEPHPVLRLREKAGHHRMGKMAIAREQAAVLVWLAKLIRAEKYLEIGVPTGYSSALALALPEHGRITACDINVTPTDARQVWNEAGVAHKISLHLQPA  
LLTLDDLIAQGEAGSYDLALIDADRPPTPOYFERCLKLVRRQGGIADINLLNGRVMREAFDAPPSVKILKDFNQLPNDTRIVPITLPGVGLTLLKK

## SEQ ID 4793

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GCATTCCTCTATCCCGTTCCTCACTGCAAGACCGTTTGGACTATCTGGAAGCAAAATCGTCCGCTGTGCAACGAAGTGAATGTTAAACGGGAAAGTCAAAGCATTTGGAGCATACGAA  
AATACACCTTCCCGCAGGACATACGTCAAAACTCGACGACCGCAAAATGAAAGAGCATTTACCTCAATACCGAAGCGGCGAGCGCATCCGACATACCGTGAACCGCACAAAACTC  
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AAAGCAGGGCGCGTATGGGGAATGTGAATCTGTATCGAAATCGGAGGCGGTACGCAACCGTTTCAAAGACAGCCCAACCGCGCGGAGTCAATTCAAATCGGCAATGCCAATA  
CAGGCTTCAGCAAAAGACATTGCAAGGGCGCATTTGGCGCAGCTGATACAGACCTATCCCGCAGCGCGCGGCAAAACCGCGCGCGCGCATACGCAAAAGCA

## SEQ ID 4794

MKTKLPLFIWLSVSASCAVLPVPEGRSTEMPTQENASDGIYPVPTLQDRLDYLEGKIVRLSNEVEMNGKVKALEHTKIHPSGRITYVQLDDRKLKEHYLNTGGSASAHVETAQNL  
YNAQKHYQNGRFSAAAALLKAGDGGGSIQSRMYLLQSRARMGNCESVIEIGRTYANRPKDSPTAPEVIFKIGECQYRLQKDLARATWRSLLIQTPYPSFAAKRAAAVREKR

## SEQ ID 4795

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CTCCGGATTGATGTTTGAATACCGCGAAACCGCAGCGCGCGCGCATCAAGCCATCATCGCGGGTGGCGGGCGCGCGCATTTACCCCGCATGTTGCGCGCAAGACACCGTCCC  
CGTTTGGCGCTACCGCTCCCAAGCAATFACCTGCGCGCGAAGATTGCTTTTATCGATTGTACAAATGCCAAAGCGGTACCCGTGCGGCATTCGCCATCGCGCGAGGCGCGCGCA  
AATGCCGATGTTGCGCATCTCATGCTCGCCAACGAAACCCGAACTGGCGCAAAACTGGCAGACTTCCGAGCCAAACAGGAACAAACCGTTTAAACATGGAATTGACAGATT

## SEQ ID 4796

MIQIGIMGSNSDWPMRQAQFLEEFVGEYEAHVSAHRTFDLMFEYAEARARIGIKAILIAGAGGAHLPGMVAAKTTVFLGVFVPSKYLREGDSLISIVQMPKGVVATTAIGEAGAA  
NAALFAISMLANENPBLAQKLADFRKQEQTVLAMELEQI

## SEQ ID 4797

TTGACTATATTTTGTACTGTCTGCGGCTTCGTGCGCTTGTCTGATTAAATTTAATCCATATATTTTCAAAATTTGAAACCCGCACAGATTGTTAAACCCCAAAACAGGGGCGGCGAA  
ATTCTCCGGCAATGGGTTTCATGCAAAACAAATGCCATCTGAACCCCGAAACAGGGCTTCAGACGGCATTGTTGATTTCGCGGACGGCGGGTTT

## SEQ ID 4798

LTIPLVLSAASSPCPDNLHLYIFQKLPQIVKPNRGRNSSNGNFMQTKCHLPENRASDGICVFDGGF

## SEQ ID 4799

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## SEQ ID 4800

LYGSRRLPCAQTDADGAQKTKAAYKGQDPKVTHTLTPAGPSCQVRVCDETGFDRRLFRPYARSLKGMARISGKRYRRLSLVSAQVGNRPAPMVCQNTVAGVFFEARFQCLLPA  
LAQKSVIISDNARFRMGALRGTEKLGHKVLPPAPCSPENPIEKVWAMIKRYLRTVLSYARFDDALLSYFDNF

## SEQ ID 4801

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ACGCGGTCCGCGCGCGCGCAGGAAAGCGGTTGTCTTCGGCATTCGCAAAACGCAACCGCGCGGACCTATACCGTTGCCCGGCAATGCCGAGCCTGAAACGTTACCCCTGCGCTCAAAAG  
AAAATCATGCGCGGAGGTTATGTTATGCGGATAGCCCGCGCAGCGCGCGCAAGTCGGACGCGCGCGGTTTACCCGTTGCCGCATCAACCGTTTCCAGGAATTTGCAGACCGTCCGAACC  
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## SEQ ID 4802

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## SEQ ID 4803

TTGAACAACAATACAAACACATCCGAAAAACCGGAACCCCGCTCAGATTGTCAACATTTTAAACCAAAATACCAAGCAATACAGCCCCGTTGCCGATA

## SEQ ID 4804

LNKQYKHKIRKTGTPRQIVNLNQMIQAIQPLRI

## SEQ ID 4805

GTCCGCCGTATGGAATACTCGTCAGGGGTAGCCGCCCGGATGCCGAGCGCGTGAATCATGCCGCTGAAAAATAAATCTTTAGCAGCGATTGACCGTTTCTGACGGTTTCAGACGGCTT  
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## SEQ ID 4806

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## SEQ ID 4807

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## SEQ ID 4808

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LSREPIDVADYGLIYAGAKNIGPAGVTVVIVREDLLERCNDIPDVFNYSRLNRDGMVNTPTSTYAIYMSGLVFRWLQAQGGVKIEAVNRLKAQTLYETIDSGGFTYINDIHPDARSKN  
VVFKTASEDLRRFVLEAELQGLCLLKGYSVGGMRASIYNAMPLEGVRLADFMDFQRRYG

## SEQ ID 4809

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TCAAGAAACACGCTTACCTGCGGATTCGCTTAAAAAACAAACAGGCGAGC

## SEQ ID 4810

MAYSADLRNKAHLNHSGLTKIRTRRAADGTNGTEPIRALHHLRESFPLSRGGATPYRFLIRYITDNAKTPAKPQQLTQETRFCTGPFALKNQAA

## SEQ ID 4811

TTGTTTTTAAACAAAAACAGATGCGCTCTGAACCTGGTTAAGGTTACGGCGGCATTTTCATATGGCTGCGCTTTTTTACAGTATATTCAAT

## SEQ ID 4812

LFFNKKQMPSELVKKQVAAFSYGAFYSIFN

## SEQ ID 4813

TTGTTTGAATTTGTTATAGTTTATTTGTTTTTAAACAAAAACAGATGCGCTCTGAACCTGGTTAAGGTTACGGCGGCATTTTCATATGGCTGCGCTTTTTTACAGTATATTCAATAAAAACA  
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## SEQ ID 4814

LPEIIVYCYFLTKNRCLNWLFRRHFMMAALFTVYSIKNKIVQHSYLRV

## SEQ ID 4815

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## SEQ ID 4816

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## SEQ ID 4817

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## SEQ ID 4818

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QGGNSQDLLEITGDASGRTTVISVGDKENIIDSGISGLSDRYKRAAVVKVLGGDKGAETGKLNIEDAKHTYTMRTDTSCTAKTTGAGELQVSHKDEAGATEYFWTLTTPNQDKTLI  
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## SEQ ID 4819

TTGGGGGACGTTGTGCGCGATGGCGTAAACGGCGGCTGCACCGGCTGCTGAGGTTGAGTTTGGGAGCAGGTTTTGAACGTGGACTTTGACGGTGGATTGGCAAGATCAGGTTGGCGG  
CGGATGATTTGTGCTGTCTGCTCGCGGAGATAGCCCAAGATTTCAGTTTCAAGAGGGTAAG

## SEQ ID 4820

LGDUVVDGVNGLHPAAEVEFAEQVLNVDFDGGFGKIEVAGDDFVAVSCGELAQDFQFTRGX

## SEQ ID 4821

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## SEQ ID 4822

MTYKILIDHDTLFRSGIKALLSRQHGFEVIGEAADGLSGIKMISRLQPDVLLDLDMPGMNGREALSQIISINPQAVIMLVSESDDLTECMRIGARGYLKKNINADFLLESIRKAAE  
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## SEQ ID 4823

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CAACCTCGCGCACTGCGGTGGAAGAACTCGGTGCTGATTTGGTCAATGAAATGACCGCGCGCTTACCAGCAAGAAAGGCCAAATCCACTCGAAGCGCGCGCAAAAGTCTCTC  
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CGGTTGCCAAAGTGTGACGCAAAAGCGTGGCATCTGCAAAAGCGCAATGACCACTCCACGCACTGACCAACGCAAAACCGTTTACCGAGCTGCGCCCAAAAGACTGCGCGCGCGCG  
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## SEQ ID 4824

MGIKVAINGYGRIGRQVLRIYDQIQDLQIVAVNAGSLETAHLTKPDTVHGRFADVDHGGNLIIVNGDKIPFFSTRNPAELPWKELGVDLVMECTGAPTSEKAKIHLESAGAKVL  
ISAPGGDDVDATVYGVNDSVLTADMTVVSNACTINCLSPVAKVLSVSVGIVKAMTTHALINDQVTTDVRHKLRRARSGVENNIPKTKGAARKVGLVPELKGRLDGLAIRVPTVNV  
SLVDSLQARDDTTFVEINALMKAVSEAGALKGVLYNTLPLVSMDFNHTTEASHFDATLTKVVDGNMVKVFAWYDNEHGFSCQMLATARRMFLGLEVRPLK

## SEQ ID 4825

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## SEQ ID 4826

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QVABQTHNLEKQNRNLTLLYRTTRDLHQSTTPRQAAEFNLHLPAVGAQSGNICLENGSDTDLVHTAEHGKPPLEKYHDETFPIEYQNEKLGMSLGFSDGTSITGDDRTLLQTLIRQ

LGVS LAGAKQEEBKRL L AVLQERNLIAQGLHDSIAQALTF LNLQVQMLTAF AENKREAAENIGFIKTGVQECYEDVRELLLNFR TKI SNKEFP EAVADL FARPTQQTGTITVETVWENG S  
FLPTQDEQLQ MIF LQESLSNIRKHARATHVKFTLSEYGG RFTMTIQDNGQGFDP EKI GEPTGSHVGLHIMQERAKRIRAVLEIRSQAQQGTTVSLTGAPKESLP

**SEQ ID 4827**

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**SEQ ID 4828**

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**SEQ ID 4829**

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**SEQ ID 4830**

MKTSNFPKSPALKTYPALILAGGLADRMGGEDKGLALLEGRPLIDRVIGKIRPQVSHIVISANRNLEYYARRSPHVFPDARQWQHFGLSALCTAANDLQLAADWLLIVPCDMPYLPDDL  
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**SEQ ID 4831**

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**SEQ ID 4832**

VQDRRPARKGKVAYRAVFARTGGTTPSEGVSDGIFRGEMLQFAPFLPTQGNRIMFTGIVQGLKLTAIHRPSEAFQTYVVELPQEAENLQHGASVANNCCLTITEIEGNRVSPDLMAE  
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**SEQ ID 4833**

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**SEQ ID 4834**

HQSEVHELNELDKAYAVLRLRLDAVLPPPEGHDTWNAALFRWQSAKKGFLEHLPDPHFVPLSLAGVGRQTELLVRNTEQFIAGRPNANNVLMSCARGTGKSSLVKALIHEDKGLRLI  
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**SEQ ID 4835**

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**SEQ ID 4836**

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LIQSGILWTLARTRPFSKIPAVDAEPFALFVNAMDTPVILKEAAEDFKRLGLVLSRLTERKLIHVCKAAGADVPSENAANIEHFEFGPHAGLSGTHIHFIIEPVGANKTVWNTY  
QDVIAIGRLFVTLRNLTRVVALGGLQVNRPLRLTVLAKVSQLTAGELVDADRNVISGSLVNGALQAQAHYDLGRYHNQISVIEEGRSKELFGWVAPQPKYSITRTTLGHFLNKLFP  
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**SEQ ID 4837**

ATGTACGCATTGACCGCGCAGACAAAGAGGCACTCTTCCGGCTGGTGCTTTTCCATATCTTCATCATCGCCGCCAGCAACTATCTGGTGCAGTTCCTCTCCGATTTCGGCATCC  
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GGACAAATCTTGATATTTTCGATTTCGACAAATACCGCGCTGAAAGCGTGGTGGATTGCCCGGCGCATCAACCGTATCGGCAATGCACTGGACACGTTAGTATTTTTCGCGTTG  
CTTTTACGCAAGCAGCGATGAATTTATGGCGGCAAACTGGCAGGGCATCGCTTTTGTGCAATTACCTGTTTCAAACTTACCGTCTGCACCTCTTCTCTGCGCGCTACGCGGTGACT  
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## SEQ ID 4838

MYATAAQQKALFRLVLFILILIAASNYLVQFPFRIPGIDTWTGAFSPFIFLATDLTVIRIPGSHLARRIIFWVMPALLSYVSVLFHNGSWTGLGALSQPNFTVGRILALASFAAYAL  
GQILDIFVFDKLRRLKAWNLAPAASTVIGNALDITLFFAVAFYASSDEFMAANWQGIAPVDYLFKLTVCTLFFLPAYGVILNLLTKRLTALQTKAQDRPVPSLQNP

## SEQ ID 4839

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## SEQ ID 4840

TKETMGIKVAINGYGRIGRQVLRAIYDIQDQLIVAVNASGSLETHAHLTKFDTVHGRFEADVSHDGNLIVNGDKIPFFSTRNPAELFWKELGVDLWMECTGAFSTKEKAKIHLESG  
AKKVLISAPGDDVDATVYVGVNDSVLTADMTVVSNACTTNCLSPVAKVLSSEVGIKVGAMTTIHALTNDQVTVDVRHKLRRARSQVEMNIPYKGAAGAAGVLVPELKGRLDGLAIRV  
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## SEQ ID 4841

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CGCGCGCTGTGTTGGAATGCAATAACCTTCAACGCGCGCTGTGCGCGCGCAATTTGAAGGCGCGCGGATTTTACGCACTCATTTGCTGCTGACCGCTGTGTCAGCGCGCGCGCTATGT  
CGCAGTTCGGTTGAATTCGTTGCGGGGATATAAGCGTGGCGCGTGGGAAAGTGGCAGGAAGCAAGCCATACT

## SEQ ID 4842

VLDPQFVHRKIHAGVVAADFIIARLVPIKNIRNDFDRAAAAVFGMHNLTQRPVARIHFEAGDFTQLIVLTLCPPEPAYVAVRLKIVRGDISRGVGGKLAGQSHF

## SEQ ID 4843

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## SEQ ID 4844

VAANESWQESKAILKKEAAGLAKRQAGSGTAFPLIRIFRTIYLIIV

## SEQ ID 4845

ATGCGCGCGCAGGCGCGCTTTGAAGGTTATGCATTCGGAACACAGCGCGCGCGCTCTGTCGCGAAATCATTTCTTCGGATGTTTTAATCGGAACGAGCGCGCGATTTATGCGAA  
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## SEQ ID 4846

MAGDRARLKVHSEHSRRRSVVEIISDVFNREARDYVESRYHSSMDFAVDELEIQHRFFHILTPQQQMMNLSSCLK

## SEQ ID 4847

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## SEQ ID 4848

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## SEQ ID 4849

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## SEQ ID 4850

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## SEQ ID 4851

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## SEQ ID 4852

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## SEQ ID 4853

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## SEQ ID 4854

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## SEQ ID 4855

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## SEQ ID 4856

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## SEQ ID 4857

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## SEQ ID 4858

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## SEQ ID 4859

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## SEQ ID 4860

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## SEQ ID 4861

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## SEQ ID 4862

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## SEQ ID 4863

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## SEQ ID 4864

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## SEQ ID 4865

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## SEQ ID 4877

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## SEQ ID 4878

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## SEQ ID 4879

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## SEQ ID 4880

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## SEQ ID 4881

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## SEQ ID 4882

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## SEQ ID 4883

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## SEQ ID 4884

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## SEQ ID 4885

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## SEQ ID.4886

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## SEQ ID 4887

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## SEQ ID 4888

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## SEQ ID 4889

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-375-

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## SEQ ID 4890

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## SEQ ID 4891

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## SEQ ID 4892

RRPARRTGPKHRQDRERHNCQQAAYAWQFSKNTDGIQNH

## SEQ ID 4893

GTCCGCTTTGAAAAAGGCATAAGGGCGGTGGCGTCTCCGACGCTAGGCATCGGAACGCCCGCGCGCGGACGCGCATCTCGGGCGGATTATTCTTG

## SEQ ID 4894

VPFEGIRGGVLPFTVIGTPAPPARHSGGLFL

## SEQ ID 4895

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## SEQ ID 4896

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## SEQ ID 4897

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## SEQ ID 4898

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## SEQ ID 4899

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## SEQ ID 4900

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## SEQ ID 4901

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## SEQ ID 4902

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## SEQ ID 4903

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## SEQ ID 4904

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## SEQ ID 4905

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## SEQ ID 4906

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## SEQ ID 4907

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GCAGGTATCCCATGTCTCTTTTATTTTCCCGA

## SEQ ID 4908

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## SEQ ID 4909

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## SEQ ID 4910

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KELGEEDENGELDALEAGIKAGMTKEAEKCLSELKLMPPMSAESTVVRNYIDTLGLPLWKKSRVSKDIAGAGLVLDADHYGLEKVKERILEYLAQVKRMOKLKGPIILCVGPPGV  
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LDRMEIIRLSGYTDEKINIAMQYLVPRQMKRNGVKEGELVVEESAURDIIRYITREAGVRLDRBIARKCRKVMQITLINEDKKRLSETKTSKAKPRAVKVNEKNLHDYLVGRRFDYGV  
AENSENRIGQVTLGAWTEVGGELLVTEAALPGKGMICQTLGDUVKESVSAAWSVVRSAESVGLAPDFYEKKDIHVHVPBGATPKDGPAGIAMTAMVSAFTKIPVRADVAMTGEITL  
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## SEQ ID 4911

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AGGTAAAGCATTTGAAGACGCACTG

## SEQ ID 4912

VNKSELTEALQADISKAQAQKALDATTNAVTNALKQGDVTLVVGFTTFVGERABRQGRNPRTGEPLTIAAAKTLKFRAGKALKDAL

## SEQ ID 4913

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## SEQ ID 4914

MAFFPHGLTSPSSSDGQTPILIRRGKQKADSSRLRLKLSLQVCPQCTFTEPKRFGGNGQRLAGGVAALAFRTFADVESTETDQSNQVALPQGVYCVSGIQLCGGPGNIGF  
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## SEQ ID 4915

ATGACTGAGCGAAACAGAAACCGGACGGAAGAGCAGGTTCGCCGCGCAAAAAAGCAAAAGCCAAATCCGACCATTCGCGATTGGGGGTGGGTCATTTTGGCGTTGCTCGCTTCAA  
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GACCTGCTCGCGCGCAACCGCTTTGAAACTCGAGACAAACATGTGTGCGCGGATTGAAAGCCGAT

## SEQ ID 4916

MTEPKHETPTESQVAARKKAKAKIRTIIRIWAIVLALLASTALLSQCAMSKPQAKKIVESCMEINPFAEKWQNDLKARGLDADNTRLAVDYCKCMWEQPLDGLSEKQISSPGKLAGDQBL  
DLLGGANAFETRDQVCADLKAD

## SEQ ID 4917

TTGATTCAAAGTGGCGCACAAATATACCGGACGGGATATTTGCTTTTCAATATTTACATTTTCAGTGGGCTTACAAGGAGACACAATGAAGCCAGTAACATCGGCTTTTGAAGCTTAG  
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## SEQ ID 4918

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## SEQ ID 4919

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CAACCG

## SEQ ID 4920

MLFENPIDGQFAEYECGAGGIRLAGQSFHKPVLVHKDSVCLPQCRITSLDTPENILSDIKPVDYPEILLIIGTGAQDEFIHPKIMADFSRIGISVECMNTDSAFRTLVFLHSEGRRAHANL  
QP

## SEQ ID 4921

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CGGACGGGCACTCGGACACAGACAGGTAATAACCGCTTAAGCGTA

## SEQ ID 4922

VIDDAVAVFLGDFVLQGFDFGIVEFRYLAALHADDMMVVVALVQLINLARFKMVALQNAIRLLELRQHAVNRRHTDFHALFQONAVHIFRTQMLFRVLLLEQIQNLQTRAGNLQTAVFQLRW  
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## SEQ ID 4923

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## SEQ ID 4924

MADMKRLKHLMFSPFIDNPALQVLGICSAIAVTKLQTAIVMGISVALVTGFSFFISLVNRYIPNSIRIIVQMAIIASLVTLVDQLLQAFAYELSKQLSVFVGLIITNCIVMGRAEF  
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## SEQ ID 4925

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## SEQ ID 4926

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SDKEGGGGNYIEDGRVLQEKGGFNIPLVYTRI SSPFGYRHPHLLHTWRLHTIDYAAPQGTVPVRASADGVIITFKGRGGYGNVIMIRHANGVETLYAHLISAFSAQGNVRGGEVIGFV  
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## SEQ ID 4927

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## SEQ ID 4928

MHEYRFGIQDIGFALGRAQGLGLASTVNFPPQTASALTFR

## SEQ ID 4929

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**SEQ ID 4930**

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**SEQ ID 4931**

TTGAAACTGAAATCGAGAAACAGTTTGCAGGCGGATAAAGAAGCGCGGGCAGGTGCTTATCTTTGCCTGCCAATAACGGTATAAATTCGGACGTTACCAACCGCCTTTTACTTTTACCGGTA  
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SEQ ID 4932

LKLSRNSLSPLSDKEARAGCCLSLPANNGIITRLPPPPYFTGINRLFAALGLLSLGGAAQAQSTYHCNSNGKSVYTSDFSGSCADADLPKISSHOGGGYRLKIKKLSQEAQIHTGNKKKKK  
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**SEQ ID 4933**

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CACTGCAAGAGAAATTTGGGAGCTGTAT

**SEQ ID 4934**

MKSKLPILILNLSSPLGANAARIYTCITNGETVYTTKPKSCHSTDLPPIGNYSERYILPQTEPAPSPSNGGQAVKYKAPVKTVSKPAKSNTPPQAPVNMRSRSLAEALSNERK  
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**SEQ ID 4935**

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GGCTGCCTGTATCTATTGAAGGTCAACGTATTCGCCAATACCGGCTACAGTACAACGTGTTTCCGA

**SEQ ID 4936**

LTEEMMKQENFWDKLGDLLFAPVDIMFWIKKVAAYPVCRLPVTVLKVNVPNTGYTYNCFR

SEQ ID 4937

ATGCTCGCTGTTCCGCGCCAGGCATTGCGCGCAAAATCGGCAATGGCGGAGGAATTCACGGCACGCTGGCAATTTTCATTGCTGTTTTTGTCGCTGGGACATAATGGAATGGTTGCCACCA  
CCACATCAAAGGCGAAATCCGTTCTGCCCTGTTCTTGCTTATCTAGGTTATTGCAAAATATGAGTTTGAAAGATGGATATTTTTGTTGCTTTTTTATTGTTTC

**SEQ ID 4938**

MLAVPPOALPVKSAMAEFTARWHFHCCFCRWDILEWLP'TTTSKANPFCPCSCLSRLLONMSLKDGYPCLLFYLF

**SEQ ID 4939**

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**SEQ ID 4940**

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SEQ ID 4941

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**SEQ ID 4942**

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SEQ ID 4943

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SEQ ID 4944

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SEQ ID 4945

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## SEQ ID 4946

MYAADTRITETASARSAYFRCPAESGKTALLFLDGVCAESSIIARSFVVRHQMKLTLALPSLNLDEDEIRIPLCLPAPNKILQYGSFHRQSTASAFYARYLWGRILAQRPAQSLNHP  
SETVALATPVWQKHLHQANVLTAEYLDVGTDEAERLCRDLISAFYGDIPHRFPVPLPELWVSLPRAYRWGAKPVLDLGGLLGADDQPDGEDALEWLRVQTEIQHNLNAHPVNHNRKRGL  
PELNLNLWDSLHGSAGGGTLFADTVNSRFHFNRRALPDSFRAYETAHLDPDTHHLLFMDLRLTALTGDRERYAAILQWEEWRFAPLYEAVRTGKIRLRLDIATDGHGGTLFFKPTDR  
RKFWRCTKTFFDGIW

## SEQ ID 4947

TTGTGCAAAAGAACCAATCATGAAATCAAGCAATTTATCTTGGCACTGTTTGGGGCGGACAGCCTTTTCCGCTTGGGGCGGACGATTATACCAACATATCCGTGCAGTCAGAAATCC  
TGCTGCTGATATTGTCTGTTTGGTGGTAGG

## SEQ ID 4948

LCKRSNIMKFKQFILATVLGATAPSAWADDSYQHTRAVRILLILLISWVCVG

## SEQ ID 4949

ATGCCCAATTTGGTGACGGCGGTGTTGGCGGGCGGTTTTTACGTGGCGGATTCCTTACCTTACGACCAAAACAGACAATATCAGCAGCAGGATTCTGACTGCACGGATATGTTGGTATG  
AATCGTCCGCCCAAGCGGAAAAGCGTGTGCCGCCCAAAACAGTGGCAAGAAATAATTCCTTGAATTTTCATGATGTTGCTTCTTTTGCACAAAGCGTTCCGAATAGTGAAGCCCGCAGCCTA  
TGGCTTGGCGGACGTGCGAGCTTTACAAGCGGTATTGCAGGAAACCTTAAACACCATCATTCATCAAGAGCTGTTTGAATTCGCCCAA

## SEQ ID 4950

MFNLVTAVLAGFLRWRIPTYTHQFINISSRLITARIWYESSAQAEKAVAPKTVARINCLNFMHLLHKAFGIVKPAAYGFAAVALQAVLQETLKHDCIKSCSNSAK

## SEQ ID 4951

TTGCTTGAATTTTCATGATGTTGCTTCTTTTGCACAAAGCGTTCCGAATAGTGAAGCCCGCAGCCTATGCTTTTGGCGCAGTCGAGCTTTACAAGCGGTATTCAGGAAACCTTAAACAC  
GATCATTTGATCAAGAGCTGTTTGAATTCGCCCAAATGAACCTGACACGCAAACTT

## SEQ ID 4952

LLFPHDVASFAQSVNRSEARSLLHCGSRSTSGIAGNLKTRSLHQLPEFRQMLTRKL

## SEQ ID 4953

TTGGCAGATGTCATCGCGCGGAAAAACAGCAGCGGTATTTTCAGGAAATTTTAAATGCGGTACAGGAGGAACTTTTGTGCGGGCAAATTTATCTATCCGCGGAGGCGGATGTTTCAAC  
GCATTCGGCTGACAGCGTTTCGACCGGGTCAAAGTCGTATCTCGGACAAGATCCGTATCACGGGTAGGGCAGGCGCACGTTTGGCATTTTCCGTCCGCGAGGTTGTCGCATACCGC  
GCTCTTTACTCAATTTTACAAAGAAATTTGAAACCGACATCGAAGGCTTTTCCATTTCCCGCGCAGCGCTGCTGACAGCGTGGCGGAGCAGGCGATATGCTTCTGAACAACGTTTGGAC  
GGTGGTGCAGGACAGGCGCATTCGACCGCCCTTTAGGCTGGGAACGCTTTACGATACCGTCATCAGGACGCTTGGACACACCGCAAGCACTTGTCTTCATGTTGTGGGGTGGGTAT  
GCACACAAAAGGAGGCTGATAGACAGTCAAAATCATTTGATCTGACCGCGCTCATCCGTCTCTCTGTGCGCATATCGCGTTTTTTGGCTGCCGCAATTTTTCACAGGCAAAACA  
GCTATTTGAGTCAACACGCTATCGAACCGATAAATCGAAGCTATGAATCCGCTATTCAGCGTCAAAGTTTGGCTGTCAGGTTTATTTGGCGGAATTCGAACAGCTCT

## SEQ ID 4954

LARCTRRRKTAAPVFSGNFKCGAGTFVGNLYLSAGRCVQRIPADSVRPGQSRHSRTRSVSRGRAGARFGIFRPAAGCPHTAVFTQYLQIRGNRHRLPHSRARLPDSVGGAGHIASEHGPD  
GACTGTAFARPFRLGTLYRYRQAACDTPQAPCLHVVGWVCTTKREADRQSKSFDTRASSVSVGISRFPWLPPTFTGKQLFESTRYRTDKLEAMNAVFRQSLRVRFIWRNSNS

## SEQ ID 4955

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TGTTCACACGCAATTCGGCTGACAGCGTTTCGACCGGGTCAAAGTCGTATCTCGGACAAGATCCGTATCACGGGTAGGGCAGGCGCACGTTTGGCATTTTCCGTCCGCGAGGTTGTCG  
CATACCGCGCTTTACTCAATTTTACAAAGAAATTTGAAACCGACATCGAAGGCTTTTCCATTTCCCGCGCAGCGCTGCTGACAGCGTGGCGGAGCAGGCGATATGCTTCTGAACAG  
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GGCAACACGATTTTGAAGTCAACACGCTATCGAACCGATAAATCGAAGCTA

## SEQ ID 4956

MDTWHDALGGERQPPYQRIILNAVQRERLSQIITYPEADVFNAPRLTAFDRVKVVLGQDPYHGVQARGLAFSVRQGVRIPPSLNIYKELETDIEGFSIPAHGCLTANABQJILLWNT  
VLTVRAGQAHSHLGMWERTDTVIRQLATHRKHLVFLMGYAAQQKRLIDSONHLILTAPHPSLSAYRGFPGRHFSQANSYLSQHGISPIINHL

## SEQ ID 4957

GTGCATCGTCCAAAGTGCCATATCTGCCCTATCTTTCAAATTCGGCTATACCTGCTGATATTGCGTTATTTTGTCAAACGACCGGCTTTTGGGGGAAATGATGACTGTATGGTTTGTG  
CGCTGTTGCCGTCTTAATCATCGAATTTATGACGGGAACGGTTTATCTTTGGTGTGACCGCGGCTTTGGCGGTTTCGGCATTTGCCATCGGGCTGACTGCGCAGCAGCGCTGCCCGCT  
CTTGACCGCGCACTGCTTTCCGCGCTGGGCATTTGGTTCGTACATGCCAAAACCGCGTGGGAAAAGTTGAAACCGGATTCATATCAGGATTTGGATACCGGAAAATATGCCGAAATCTC  
CGATACACAGGCGGCAACCGTTACGAAGTTTATTCGCGGTACGACTGCGAGGCGCAAAATACGGGGCAGGAAGTGTTTGAACCGGGAACCGCGCGCTCATGTGCCGAAAGAGGTA  
ACCTTCTTATCATGCAAAACCTT

## SEQ ID 4958

VHRAKCPYLPYFPKFGYTDIALFCQTRFVGRKMTVFWVAAVAVLITELLTGTVYLLVVSALAGSGIAYGLTGSTPAAVLTAALLSALGIWFWHARTAVGKVEDSYQDLDTGKYAEIL  
RYTGNRYEVFTRGTHWQAQNTGQEVFEPGTRALIVRKBNLLITANP

## SEQ ID 4959

ATGGAATTTTTCATATCTTGTGGCAGCGCTGCGCGTTTTTCGGCTTCAAATCTTTGTGCTCATCCCCAGCAGGAAGTCCACGTTGTGGAAGGCTCGGGCGTTTCCATCGCGCCCTGA  
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## SEQ ID 4960

MEFFIILAAVAVFGKFSVWIPQGEVHVVERLGRFHRALTAGLNILIPPIDRVAYRHSLEKIPLDVPSQVCI TRDNTQLTVDGIITYQVTDPKLASVGSNNYIHATQLAQTTLSVIGR  
MELDKTFEERDEINSTVVSALDEAGAWGVKLYEIKDLVPPQELRAMQAQITAREKRARIASEGRKIEQINLASQREARIEQSEGRQAQAVNASNAEKIARINRAKGAESLILV  
AEANAIRIQIAALQTOGGADAVNLKIAEQVVAFFNNLAKESNFIIMPANVDIGSLISAGMKIIDSSTAK

**SEQ ID 4961**

GTGAACAAAACCTCACTCGCCCTTTTCGCGCTGTTGACCGTGACCGCGTGACCGTGAACGCGTCTCGCTGTTTCCCTCTCAAACTCAAANTCATCCAAGGCAACGAACTCGAAC  
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CCGCAACGGCATCATCAAGAAGCGAGCAACCTGACCGTCTATTTGAAAAACGGCGTACTCGTCCGCAACGAAGGCGAGCGCCTCCAAAATGCCCGGAAGCCCTCGCGCGCAACAAAAC  
GCAGACAAACAA

**SEQ ID 4962**

VNKTLLILALSALFSLTACSVVERVSLFPSSYKLKIQQGNELEPRAVAALRPGMTKDQVILLILGSPILRDAPHTDRWDYTFNTSRNGI IKERSNLTVYFENGVLVRTEGDALQNAABALRAKQ  
ADRO

**SEQ ID 4963**

ATGGAGATTATTTTAGGTATCGTAGTGTTTACCGTCATCGTCTTAGCTTTGGCACTGATGATTCGTGTTGCCAAATCCAAGTTGGTCAGCGAAGGCGACATCAACATCAAAGTCAATGATG  
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AAGCGCGCGCGCGCATCTTCGCCGACCGAGCTGTCCCACTCAGCAAAACGCGAAGCAGCGAAGGCTGCCGTTGTCTGCCAAGTCAATGTCAAAACCGCATGGACATCGAAGTACCC  
GAAGAAGTGTTCGGCGGTGAAAAATGGGAATGCACCGTGCATTTCCAAAGCACAAAGCAACGTTTCAATAAGAACAATCAAGCTTGTCCATTCCTCCGAAGGCGAAGAAGTTCCTTTCCGCGCGCG  
CGGGTACATGTACAAATGCGAGCGCCCGCGACACCGTGTCTCCAAAGACTTCGACATCTCCCAAGTGAATACAGAAAGACTGGGACATAACATATCTGTGGCAATFACGTTTTCCTTAAGTGA  
CGAGCCGATTTTGCSCGCTACTCTATGGCTTCGTATCTGAAAGAAAAGGCATCATTTATGCTGAACGTGCGTATCGCCACGCCCTCCCCCGCGGTACCCAAATGCACCTCCGGGACAAATG  
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CGCGGAGAAATTCGGAATTCCTTGGCAGCTCGCCCTGTCCGACCCATTGCTTGAAGACAACCTGGGACGCGTACACGGGCTTCATCCACAACGTGGTTCACGAAAACCACTGAAAAAC  
CAGGAGACACCGGAAGACTGCGAATTTTATATGTGCGGCGCGCGGATTATGAACCACTCCGTATCAAAATGCTCAAAGACTTGGCGGTGGAAGACGAAAACATCTCTTGGACGATTCG  
CGGT

**SEQ ID 4964**

MEIILGIVMFVIVLALALMTLPAKSKLVSGEDITIKVNDKEKELTMPAGGKLLGALASQIGFVPSACGGGGSCGQCRVVVKSGGGDILPTFLSHISKREAREGCRLSQCVNVKTMIDIEVP  
EEVFGVKWKECTVISNDNKATFIKELKLAIPGEEGVFFRAGGYIQIEAPHTVAYKDFDIPKEYHEDWKYLNQWYVSKVNEPILRAYSMASYPEEKGITLMLNVRIATPPRPVHPAPPGQ  
SSYIWSLPGDKVTISGPFGEFFAKDTDAEMFVIGGGAGMAPMRSHIFDQLKRLHSKRKITFWYGARSKREMFVYVEDFDQLAAREPNNFTWEVALSDPLPEDNDWGYTGFTHNVVYENHLK  
HEAPEDCREYMGCPPTMNOVSIKMLKDLGVEDENILDDPGG

**SEQ ID 4965**

ATGTATTCGGAGAAAAGGACGGGGCATCAAGCCGTGGATGGGTGCCGCGCGCGGTGTTCGCCCTTTGGTCTGGCGTGTTTACGCGCTCGCGCATACTTTGACTCCGTTTTCGGGTTGCGGCGG  
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TATTGTCCCTATGCTGGTGGCGGAGTTCAATAATTTGGCATCTGCCCTGCCCAATTAATCTGGTTTATTATGAGAACACGCTGCTGCCGTGGTTGAAAATAACAATCGGCAGATATGTGGAA  
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TTGCGCGTGGTCAAGTTTCTCGAAAGTTTTCATATCGCGCAAAATTTGATAGGACAGCTTACGCGCTTCGCGCGTTTTCGGGTTATCTTTCGCGGTATGGCGGTTTCGAGAGCTGATGGGCTT  
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**SEQ ID 4966**

MYRRKGRGKIPWNGAGAAPALVNLVYALGDLTPFFAFAVLAAYVLDPLVEWLQKKGLNRASASMSVWVSLILLALLLIITVPLVGPNNLASRLPQLIGFMONTLLPWLKNTIGGYVE  
IDQASTIAWFOAHTGELSNAKAWFVFLMKQGGNTVSSIGNILLPPLLLYYFLLDQWRSCGIKLVPRRFAGAYTRITGNLNEVLGEFLRGQLLVMLTGLVYVYGLNLVGLDSCGFAIG  
VAGILVEVPYLGATPGLLATVAALLQFGSWNGILAVWAVFVNGOZLESPFTTKIVGDRIGLSPFWVFLMAGFELMGFVGMAGLPLAAVTLVLREGAOKYTAGSYRGR

SEQ ID 4967

ATGCCCGTCCTTTTCTCCGATACATAAAATCCACCTTCCGAAAAATAATATTGCGCGCCAGTATAGCAGAACCOCGCGCCGTCAAAAAGCCCTCCGCCTCCCGATAGCCTGTTATCGT  
GGTTTAGGTAAATACTGCACATCCGATGCCGTC

**SEQ ID 4968**

MPRPFLRYIKSTLPKIILRASIAEPPRRQKSLRLPDSLSSWFLKYCTSDAV

SEQ ID 4969

MTGAGGGATGTTTFFGTGTTCTGTGTTGGTCAATGATGTGCTGGCTTATCGTGTAACGGTATGCCGTCTGAAAGCGGGTTTGCCTTTCAGACGGCATCGGATGTGCAGTATTTTAGCCATAAACC  
ACGATAACAGGCTATCGGGAAGCGGGAGGCTTTT

SEQ ID 4970

MRDVLFCSSVMCLIVYGMPSESGFAFQTASDVQYFSLNHDNRLSGRRRLF

SEQ ID 4971

ATGGGGGCGGTTTCATCCCGAGTTCGAGCAAGCGGTTTTAGAAAAACCGTCCGCTTCACGCCCCGACGACGAGGCTTACCACATCACCACGGTCCGAGCAGCAAAAGGCAACTATACCGGTG  
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SEQ ID 4972

MGAVHPEFEOAVLETVRLHAPDTHAHHITRPSKGNYYTGATVOVKVENOBOLDNTYRALTSHELVKVWL

SEQ ID 4973

ATGAAATCATACACAAAGGTTTGGTCGAATATCTGCCGACTTTTGGAGCAATGAAACCTTTAATGCCGGACGGAAATGCAGACACCGAAGACGAACTGTGGTCTGTGCAACACCCGCCGCTCTTTACGCAAGGACTGGCGGGAAAAACCGAGCACCTGCTGATTTAGGAGACGACATCCCGTCTGTCCTAAATCGACCGGGCGGGCAGATTACCTATCACGGGCCCGGGCAATTTGGTCTTTATACGATGATTGATTTCAAACGGCGCAAAACCGAGGTCCGCAACATCGCTTTCGCGCTTGAAACAGCATCATCGCCACATTTGGCGGAATACGGCATTCGAAGCGGGCGGCAGATCCCAAACGCCCGGGCATTACGTCGGCGAACGCAAAATCGCCTCACTGGGGCTCGTATCAAAAAACG6TTCGCTTATACGGACTCGCACTCAACGTCGAATATGGAATTTAAGCCCGTTTACCAAATCAACCCCTGCGGCTACGCGGTATGAAATGACGCAAAATCGCGGATTTTGTCCAAACCTGCCCGCGCGACGAAGTCGCTCCAAACTACCGCACACCTTGAAACACAACCTCACACCGAAAGCCGACCAATGAG

SEQ ID 4974

MKIIHKGLVEYLPTEAMKTPNAGRNADTEDELLWVZHPVPVTOGLAGKPEHLIIRDIDPVVQIDRGQITYHGPGLVYVTHIDFKRRKTSVRNIVSALENSIIATLBYGYIEAADPKR  
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SEQ ID 4975

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CAACTTGGAAACCACTCGGAGCTGTACAGAAAGCCCGTCCCGTGCCTTATCAACATCTTTAGACTTTATTAACAGCTTATAAGAAATGATGCGCGATATCCCGACCAAAATCCGCG  
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CTGCTTTCGCTACGTTACACCCGAACATTCAAAATATTTGAAAAAGAACATACGAACCTGGCTTTACCAATGCCCGCATCGGCGGATGGTACGTTCAAGTTACCATGCGGACGAACA  
GGCGGCGGAGCTTACCGGAAAGCCAGCGGCTTGGCGGATCAT

## SEQ ID 4976

LKHNSHRKQYTMSEIKTDDPKRGIKLRGADKTARIPIKVVPLQEKLLKPEWIRAKLPSRKFFIKDILRBQMHTVCEEASCPNIGECFSKGTATPAMGDICTRRCPDVDGHRPNMLD  
PDEPKNLAEISVKAMNLRVYVITSVDRLDRDGAQHFDACIKATRETSPTNKILILVDFRGLDIALKILAEPTPDVNMHNLETHPSLYRKARPGANYQHSLLDLKRYKEMPHIPTKSG  
DMVLGETDEVDREIMRDMRAHNEMITTIQVQLPDSGHLVPLRVYVTPQFKIFKEKAYELGFTNAIGAMVRSYHADEQAARALRSHGGCGHH

## SEQ ID 4977

ATGCGTGCATTGTATGCAAAAGCTGTGCGCATGACAAATTTCTATTATAAATACAAACATTTATCAAAATAAATAGCGGATATTCGCCGATGCTTCCAAATCAGTATGCTGTTCTTAT  
CGGTTTTTTTTCGCTGCTAAACCTAAGAATCCATCTCATCA

## SEQ ID 4978

NRALYAKAVGNTNLFKIQTIIKINRAYSPMPKSVCCFLSVFFAAKTKNPSHQ

## SEQ ID 4979

CACTAGACATCCCGATTTCACAGAAAGTTCTCCCGTGAACAAACCTCATCTCGCCCTTTCGCGCTGTTACGCTGACCGGTGCGAGCGTGAACGCGTCTCGCTGTTCCCTCTCT  
ACAACTCAAATCATCAAGCAACGAACCTGAACCGCGCGCGTTCGCCCTGCGCCCGGCTGACCAAGACCAAGTCTGCTCTGCTGCGGACGCCCATCTAGCGCGACGCTTT  
CCATACCGACCGCTGGGACTATACCTTCAACACCTCCCGCAACGCGCATCATCAAGAACGCGAGCAACCTGACCGCTTATTTGAAACCGGCGTACTGCTCCGACCGAAGCGGACGCGCTT  
CAAAATGCGCGCGAAGCCCTCCGCGCGAAACAAACGAGACAAACAAATGAAGAACACAC

## SEQ ID 4980

H\*TSRPAQKGSFVNKTLILALSFLTACSVKSVLFPYSYKLKI IQGNELEPRVAALRPGMTKDQVLLLLGSPILRDAFHTDRWDYFTNTSRNGLIKERSNLTVFVENGVLVBTGDAL  
QNAEALRAKQNAKQ\*GTH

## SEQ ID 4981

GTGTTTGAAGCCGAATATTTAAGCCCGGAAATCGTCCAAGAGGATGPTTTCGCTTCCACGCCCAAGTCTTTGAGCATTTGATGACGGACTGGTTTATAATCGCGGGCCGCACATATAA  
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GCGGCGGCGCATAGTCACTTCTTTTCATCATTTGACTTTGATGGTATGTCGCTTCGCTGACCACTTGGATTGGCAACAGAAATCATAGTCCCAAGC

## SEQ ID 4982

VFEAEVLTAEIVQEDVVFHAQVFEHFDGLVHNRAAHKIPAVPRCFVVFQVFNHVVDARVAVPVVFRQWVGQDVPSEVREFCRELVEVFDIEHFAFGACAVPEGDPFPGVQTFQL  
VENVGTHRGHTRTAADKYHFYIGVFGKFAERAGNRFVAGFERPDVGRHLSSRRICGYARRGRDTHVQHNDAPFRIIRSHRVGAQNLRVHFGNVLQIVFVFPVFIPLNGNEVFVNGVR  
RGFDLNVAGAERNFPAFNGKLEFFNERCFVVGNDGAFPPFHAHEFFGYPDVHVGFDIDLAGQTAAPACAFADVQGLGRQNVAAAAPHNALSARTAAATAGGDKDALAGKRAQEPFA  
AGHSQFFFIIDFGDVAFDQGLFGKQNHQCS

## SEQ ID 4983

TTGTCAACATATTCACGATTTCCTCATCAAACTCCCGTACACCCGCTTTTTCCTCCCAAAAAACACAAAAATAATCAACACTTTCAATTTCTCCGCAAAAGCGGTTATAATCACGCCG  
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ATTCAAATTC

## SEQ ID 4984

LSTFTTISHYKPPVHPLFVSPKTNKSTLSFLRSGYNHADFSTPDEKWRPHFFIMYIGSSMDIQTILEKTLPLGLGYELVDFRLAAQGLRVFIDKEGGITVEDCATVSNHLSRVFHVED  
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## SEQ ID 4985

TTGGAAGGCATCGGGAATACGCCCTATTTATTTTGATAATTGTTGTATTTTAAATAGAAAAATTTGTATGCGGACAGCTTTTGATACAAATGCAGCATCCCGAACAGCGTTACAGAAC  
GCCGTTTAAACCGCACGAAACCAAT

## SEQ ID 4986

LEGIGYALFILIIVCILNRKFMPTAFAYNARIPNSVTERRILPARNFN

## SEQ ID 4987

ATGCAAGGCAATCAAGCTGTTGTTGATACATGAACGAATGCTTCGCGGAGCTGCGCGGACGCGAACCAATCTTCACTCCACTCCCGCTCTACTCCGAATGGGGCTACACCAAACTTT  
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CGTGGTTTCTGCTCAAGCCGACCTGCAACCGAATCAAGTGGCGGACGCTTTGAAAAAGGCACTAACTGTGCGAAGAGGCTCAAGACTATGTTACGCGGACCTGATGTTGCG  
CAACTGAAGACACCGAAGAACACGACACTGGTTGAACAGCACTGCGCTGATGAGCTGATTTGGCGAAGGCAACTACTACCAAGCCAACTG

## SEQ ID 4988

MOGNQAVVDYNNELSGELAARDQYFIHSRLYSEWYTKLFERLNHEMERETTHAEDFIRRLMLGGTPKMARSELNIGTDVVSCIADLQTEYBVRDALKKGIKLCREAOQDVVTRDLMAV  
QLKDTEDHAHNLBQQLRLIELIGBNYQSQL

## SEQ ID 4989

TTGGCTTTGGTAGTAGTTGCTTCGCAATCAGCTCGATCAGGCGCAGCTGCTGTTCCAACAGTGTGCGTGGTCTTCTTCGCTGCTTTTCAGTTGGGCAACCATCAGGTCCGCGTAACA  
TAGCTTTGAGCTCTTCGACAGTTTGTATGCTTTTTCAAAGCGTCCGCACTTCTGATTCGCTTTCGAGTGGCTTTGAGGACAGAAACCACTCCGCTGCGGATATTCAGTTCGAGC  
GTGCCATTTTCGCGTACCGCCGACATCAGGATGCGTGGATGAAGTCTTCGCGCTGTGTGGTTTCTTCTTCATCTCGTATGAGACGTTCAAAAGTTTGGTGTAGCCCCATTCGGA  
GTAGAGCGGAGTGGATGAAGTATTTGGTTCGCTGCCCGCAGCTCGCGGACAGCAATTCGTTATGTAATCAACAACAGCTTGAATTCCTTCGATATATCTCTCTTTCTTAATTTGGG  
TTTCGTCGGT



**SEQ ID 4990**

EQ ID 4990  
LALVVVAFANQLDQAQLLPQPVCVVFFGVFQLGNHVQARNIVLSLFAQFDAPFQSVAHFVFLQVGFEGAGNEHVRADIQGACHFRRTAQHQDASDEVFGVCGFFFLHLVLETFKKFGVAPFG  
VEAGVDEVLVACRQLAQGOQFVHVINNLSIALHNLSLFLWVSCG

**SEQ ID 4991**

SEQ ID 4991  
ATGAAAGCGCACCCTTTGGTTATCCGCGAGCTGAACAAAACTTAGGCTTCTCTGCTGTAACCATTAACCAATATTTCCTTCACGCCGCTATTTCGAAAACTGGGGCTTTGAAGAACTCG  
CGCAACATTTCCTCAAAACATCAATCGTAGAATGAAAGCTGCCGACGATTGTATGAACCCATCTCTCTCCTTGAGGGATTGCCCAATTTCGAAGAGCTGGGCAAGCTTCTGATCGGTGA  
ATTCTACCGAAGAAATCATCGCTGCGATTTCGACCAAGAACAGGAAAAACGAGGCCCTGCTTGCCGCCATTGCCACAGCAGAGAAGCGCAACAGGATTATGTCAGCCGTGATTTCGTTGGAA  
AATCAAAAAGATACTCAACGAAGAACACATTCGACTGGCTCGAAACCCAGCAGGAAGCTGATCGGCAAAATCGGTTTGCCGAATACCTGCAAAACAGCGCGCCAGAGGAC

**SEQ ID 4992**

SEQ ID 4992

MKGDRIVIRELNKNLGLLLVTINQYFLHARILKNWGFEEGHEFFKQSIIVEMKAADDLIERILFLBGLPNLQELGKLLIGESTEEIIACDLTKBQEKHEALLAAIATAEAQQDYVSRDLLE  
RQKDTNNEEHIDWLEGTQOELIGKILGLPNYLQTAQRD

**SEQ ID 4993**

SEQ ID 4993  
TTGATTCAAATCAATTTAGATTTTATTTCGTAAACCGGCAAAGAAAACGGCATACCGGTTTATACGGGATATGCCGTCGTATGATCCAGGGGACTGCTGTATTGGCAGTGGTTTGTGTTT

**SEQ ID 4994**

LIQINLDFIRKPAKKNIGIPVYTDMPSSDAGDCCIWQWVFV

**SEQ ID 4995**

SEQ ID 4995  
ATGATGGGCAACAATTGACTCTGCTGCCGGAATTGCCTGACGAACAGGATTTCGGGCGGTATTGGCATACAATATGCGGCTTTTCCGCGTGAACAAGGGTTGGTCGCAAGAGGAATTGG  
CGCGGCAATCGGTTTGGACAGACATTATGTGTCGGCAGTCGAGCGCAAAACGCTGGAACATTGCCCTGTGCAATATCGAAAAATGGCGCGCGCTTTGGGCGTGGCGCGCTATCAGTTGCT  
TCCGCGCGCGCAGGAACGGTTGAACCTGATGACCAATTCCGCCGATACCCGACAAGTGGCGCTCGAAAGCGGTATT

**SEQ ID 4996**

SEQ ID 4996

MMGNKLTLPAPLPPDEQDLRAVLAYNMLFRVNWGSQEELARQCGLDRTYVSAVERKRWNIALSNIKMAAALGVAAYQLLLPPQERLNILMTNSADTRQVPSGSI

**SEQ ID 4997**

SEQ ID 4997

ATGGCTCGGCGGTCAAAATACCGCTTTCAGACGGCACTTGTCTGGGTATTCGGCGGAATTTGGTCATCAGGTTCAACCGTCTCTCGGCGGCAGCAGCAACTGATACGCGCCACAGCCCAAAGCC  
CGCGCATTTTTCGATATTCGACAGGGCAATGTTCCAGCGTTTTCGCTCGACTCCGACACATAGTCTCTGTCCAAACCGCATTTGCGCGGCCAATTCCTCTTGCAGCCAAACCCCTTGTTTCA  
CGCGAAAGCCGCGATATTGTATGCCAATACCGCCCGCAAAATCTCTGTCGTCAGCAATTTCCGACGACAGAGTCATTTTGTTCGCGCATTAATGTTGTTTCGCGATTAAGTGTAAAGGTTTAAAG  
TATTTGCTGTTACGGATTTTTCATTCACATAAAGCCAAAAAAGGGGTGGCGGCAGCCACCAACACACACACATCATCCAGGAGAAAGGTAAAAATCGGATCGGATTTTGGAAACAG  
CAAAACAACAAATCATAGATTTTCATATCGGTTGATTTCACAAACAAAACCGGTATTCGAGTATTGATTCAAATCAATTTAGATTTTATTCG

**SEQ ID 4998**

SEQ ID 4998  
MVRRSNTAFRRHLSGIGGIGHQVQPFLRRQQQLRRHAQSRRHFFDIROGNVPAFALDCRHISPVOTALPROFLLRPTLVHAEKPHIVCQYRPOILFVRQFGRQSQFVAHHLFPDKMLKVK  
YLLRLILHIKAKKKGWROPHPNTHWQERGGIKTDWTSTANKQSRFHIGI IKQPLSSIDSNQRFYS

**SEQ ID 4999**

SEQ ID 4999  
ATGATACCGCTCAAAATCGCCATCGCGCGCAAAACGGCCGATGGGACGCGTCTCTGTCGAAGCCGCTCAACAACATCCCGACACCGTCTTTCGCGCGCGCTCGAACACTCAGGCTCAG  
AAGCCCTCGGGCTGGACGCGGGCTAGCGCGTCGGACTCAAAACGGCATCGCCATTTTCAGACGACGTTGACGCCGTTCTCGCCCAAAGCGACGTTACTCATCGACTTCACCCGCCCCGAGCC  
GACCCCTAAGCACCTTGCAAAAATGCGTTGAAAAACAAGTCAACATCATCATCGGCACAACAGGCTTTCAGCATGCGGGCAAGCCGCCATCTCGCGCGCGCGCCGCAAAAAACAGGCATCGTT  
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ATGCCCCCAGCGGCACAGCAATTACAGATGGGCGAAGTCATCGCGCGCGCGCTCGGCGCGGACCTCAAAACAATTCGCGCTTTACGCGCGCGGACGGCCACATGGTTCGCGCGCATCTTCCAC  
CATCGGCTTTGCCACCGCTTCGCGGACGACATAGTCGCGGACCAACCGGCCCTCTTCGCGCACGACCGCGGAACGCGTGGAAATCACCCACAAAGCGCGCAGCCGATGACCTTTGCGCGC  
GGTGCCTCCCGCGCGAGTTTGGGTAACCGGCAAAACGGGTTTGTACGATATGCAGGACGTACTCGGGCTGAACAACCGT

**SEQ ID 5000**

SEQ ID 5000  
 MIPIKIALAGANGRMGRVLVEAVNNHPDVTVLSGALEHSGSEALGLDAGYAVGLKGTGIAISDDVDVLAQSDVLIDFTREPTLKLHKQCKVEKQVNIIGTGTGDDAGKAATRAAAEKTGIV  
 FAANFSVGVNLTFFHLLDTPARVLNEGVDIEIIEGHHRRHKVDAPSGTALRMGEVIALAGLRDLKQCAVYGREGTGPRDPSTIGFATVRAGDIVGDHTALFATDGERVEITHKAGSRMTFAA  
 GAVRAAVVWNGKKTGLYMDQVGLGNRR

**SEQ ID 5001**

SEQ ID 5001

TTGATAATGGTTATTTTATTTTATTTTGTGGGAAGACATTTATGCGCTGCACGAAACAGATGGATGCTGCTGCGCTTTATTGGCAAGCGCGGCATACGCCGAAGAAACACCGTGCGAAC  
CGGATTTGAGAAACCGTCCCGAGTTTCAGCGCTTCATGAAGCGGAGGTCAAACCGATTCGACAGGGAGAAGGTACCGGGGCGAGTTCGGGAAAAAGGAAAAGTTTTCAGGTTGACCGCGAAAC  
CTCTGCTGAAAATCCCGAATTGTTGTCTGCGTGCATGTATTCGCGAGTGGTCTCAAACAATATTGCCGGTATCCGCGTGATTTTGGCGATTACTTACACAGGCGCGGCAGGATAAGATG  
TTGGCACTTTATGCACAAGGGATTTTGGCGCAGGCAGAGGGCAGGGTGAAGAGAGCGGTTTCCCATTTACCGGGAATTGATTGCGCCGCCAACCCGACGCGCCCGCGTCCGTATCGGTTTG  
CGGCGGCATTGTTTGAAGACAGGCAGAGAGGCGAGGCGCGGCAGACCGATTTCGACCGCTGAAAAACAGAAGATCTGCCGCCCGAGCTTATGGAGCAGGTGCGAGCTGTACCGCAAGGCATTGG  
CGAACCGCGATGCGTGAAGGTAAACCGCGGTTTCAGCGCTTACCGCGCAACACATTCATCAACCAAGCCCGGAAACAGCAGCAGTACGGCAATTGGACTTTCGGAACAGGTGGACGGCACG  
CGAGTCAATTACCGGTTTCGGCGCGGCAAAAAATGTTGCTCGTGAABAAACCGCGTGTACACAGCGCGGCGCGCAGCTGTCCGCGAGGTTTATCCGGGGAATAAGAAATTCACGATATGA  
CGGCAAGTGTGTTTCGGCGCGCATCGGTTTTCGCCACCGCGCTAAAGATGTCCGGCTGGCAGTGTTCACGAACCGCCGACCTACGGCAACGACCGCTTATTTCTACCGCAACCGGCGCACGCT  
TTATTTCAACCGTTGGCAAAACCCGAGATGGCAAAACGCTGTCTTCGGCGGAGTGGGGCGCTTTGAAGAAATACCGCGCGGCGCGTTTCGACAATAACCAATTCGAAATTTCCAAATTCCTG  
GTGTTTTCACCGGAATGCGGCGCAATATTTGAGCGGGCGGTTTGGATTTCACCGCGAGCGCAACCCCGGACCGCTGGCGACAAATTCACCGGTTACGGCTGCGCTTGGCTGGGGCGAG  
AATGGGCGGCGAGCGGCTGTCTCGCTGTTCGCGCTCGGCGTGGCGAAACGGCATTTATGAAACCCCGGCTTCTTCACGAGTTTAAAGCGGAAAGGCGCAGGGATAAAGAAATCGGACAC  
ATCTTTCAGGCTTTGGCACCGGCATTGCATTTCAAAGGCATCAGCGCGGCTGACGCTGTGCGCACCGGAAACGTGGAGCAACGATGTGTTTAAAGAAATACGAGAAAAACGGCGGTT  
GTCAGTTTAAACAAACGTTTC

SEQ ID 5002

SEQ ID 5002  
LIMVIFYFYFCCKTTFMPARNRWMLPLLIASAAAYAZETPCFPLRSRPEFRLHEAEVKPIDREKVPQVREKGVQLQVDGETLLKNPELLSRAMYSAVVSNLIGILVILPTYLQOARQDKM  
LALYAQGILAQABGRVKEAVSHYRELIAAQDPAPAVNRMLAAALPEDRQNEAADQFRLKLTEDLPQLMEQVELYRKALRERDAMKVNNGFSVTREENINQAPKQOOYGNWTFPKQVDGT  
AVNRYFGAEKKWSLKNQWYTTAGGDVSCRVPYGNKKFNDMTAGVSGGIGFADRRKKDWGLAVFHERRTYGNDAYSYANGARLYPNRWQTPRWQTLSSAENGLKXNTRRARSNDTHLQISNLS  
VFYRNARQYWTGGLDFYRERNPADRGDNFNRYGLRPAWQGEWGGSLSSLFRLGVAKRHYEKGPGFSSFGKGERRRDKESDTLSLHRAHLHPKGITPRILTSHRETSWSDVFNVEYKKNRAP  
VEFNKTF

**SEQ ID 5003**

SEQ ID 5003  
ATGCTCTGAAGAACCTGCTTCAGCACTGTGAACCTTCAACAGCAGCGCAATGCCGCCGAAGCGCATATTTTGAAAGCCAAACCGGTGTCGGTATTTTTTCAGAGAAATACACGGCGGCAGTGG  
AAACCTTGCTGGCGGCATTGTGGGCAGAACATTTTCAAAACAGCGCGTTATGCCCTGATGGCGTAGGCGGCTTCGGGCGCGCGGAACCGTATCCCTGTTCCGATGTGGATTGTGGCGGTGT  
CTCCCTGCCCCGCTTTTCAGACGGCATTCAGGAACAGATTGCCCGGATTTATGCCAACTCTGTGGGATTGCAAACTAATGCCCTCTGTAAAAGCGGCAGCGTTGACGAACTGTGCGGAAAGC  
TGGCGACGACGATTAACGGGGGACACACGCGTTTATAGAGCTAGGTTTGTGTTGGCAACCGCAACAGCAGACGAATTTGGCGGAAAAATGAACGTGTCAACGCAATGTAGCGGCATTTA  
TCGAAGCAAAAATTGGTGAGATGGAACACCGCCACGCCAAATCGCAAGGTTTCGGGCGCGGTGTGGAGCCGAATATCAAAAGCTGTCCGGGCGGTCTGCGGACATCCACACCTGCTTTG

GATAGCGAAGGCGCAAGGCTTGGCGGCCAACCTGCCGACCTGCTCAACAGCGGATTTTGACACGTGCCGAAGCGGTATGCTTTGCGACGGCTACCGCGCGCTCGCCACATCCGCAATC  
CGGTCGCAITTTAAACGCCAAGCGCGCCGAAGACCGCTGCTTTTCGATTTGACGCCGCAAGTTGCCGAAGATGCGTTATCAAGATGAAAACCGCGCGCTCAAGCGAAGAACTGATGC  
GCGTGTGTTTACCGTGGCTCAAAACCGTCAAAACCTGGCGGCATCTCAGCCCAATGCTGGAAGCGCGGTTCCTCCACGCGCGTGGCGTTACCTTGGGATTGACGACGACTACAT  
CCAAGTCAACAACCAATTCGCGCGCGGCACACCGATATTGTTTTCAGACGCGCCGGAACACATTTTCAAAATCGTGAATATGTCAGCAGCGCAACGACATTTACGCGCTCGAAGCGCAA  
ACCTTGGCGCATGTTGGGGGGCGACGCGCAAAATCAACCGCAGCTTCTACCAAAATCTGAAACCGTTCGCGCTTTCGCGGTGTTTTCGCGAGCGCAACGAGTACGCCAAACCTGTC  
GCTTCTCAACCTCTACGCGGTGTTGGCGCTATCTGCCGCGTGGGAAAAATCGTGGCGTCTTCAACACGACTTGTTCACATCTATCCGTTGACGACGACATCTTTCGCGTGT  
CCGCAACGTCGCGCGCTTGCCTAGATATGACACGCAATGAGCTGCTTACGCTTCGCGCTGATGAGTCTTGAAGAACAGACATCTTACCTTGGCGCTTCTTCCACGACATC  
GCCAAGGACGCGCGCGGACCATGCGGTACAAGGATCGCAGACGCGCGCAATTTGCCGCGACCACTTCTGACCGAAGAAGAACGACCTGCTGCGCTGGCTGTTGAAACCCACC  
TCTTATGCTGCGCTGCCCAAAAAGACATCCAAGACCGCGGCTACTCGATGCTTCTGCAACGCGTCCAAACCCACGAACGCTCAGCGCGCTTACCTCTGACCATTTTCGA  
CATACGCGGCACCAATCCCAAGCTGTGGAACGCTGGCGCGCCAGCGCTGTGGAAGCGCTTCCACGCGCGGACGCTGCTCGCAGCGCAACGACGCAACCGCGACCGCTCTTCGCG  
CGCGCGCGCAGGAAGCGCGGACTTACCTTACCGCGCGCGCTGCCGAAAAACAGCAGAAAAAATCTGGAACGCGCTGCTTCCGCTATTTTCGCGCGCATGCTCCGCGAAATTC  
TGTGGCAGCGCGCAACCTCTGACAGACTTTGAACCCCATCGTCCGACGCGCATCTTACCCCAAGCGCAGCTTTCAAGTGATGCTTCTTATGCCAAACGCGCGCGCTGTTTCG  
CGCGCTCTCGCGCATCTTACGCGCGCAGCTTCGATATCTCGCGCGCGCGCTTATCAGCGAACGACATACATCTCGACACCTTACGCTGCAATTCGCTCGCAGCAGCGCCCC  
GAAGACTACCCGACATCCAAGCGCGCTCGAAGCGCACTCAACAGCTTTATCCACGACACACCGTTCGCGAAACCAAGCTGCAACCGCGCGCATGCGCGCGCGCATATATG  
CTATTGCGCAAGCATCACCATCACCCCGAAGAAGACTATCCGACGCGGTATTCGTCGAAATCAGCGCGCTCAACCGCGCTTCTGCTCGCGCATGCGCGAAGTCTTCTTCGCGCA  
CAACGTCAGCGCTGCGCTGCGCAAAATCTCCAGCTTGACGCAACGCGTGAAGACAGCTTTACGCTTTCAGCGCGCATTTGAAAAACCAAAATCCAGTCTCATTTGAAACAGGCTTTG  
CTGGAACAGTTGGCA

## SEQ ID 5004

MPENLSSALETFKQORNAEAHYLKANRVSVFPRYTTAAVETLLAALWAHFNQNSALCLMAVGFGFGRGEPYPCSDVDLAVVSPAPLSDGIQEBQIARFIQTLWDCKLMPVSKSGSVDELCE  
VRDDITGDTAFLEARFLFNGRQTADELAERKMNVRNVAFTIAKLVEHEHRHAKSGGSAVLEPNKISCPGGLRDITLLMLTAKAQLAANLFDLLKQRLITRAAGMLSHGYRRIAHTRI  
RLHIAKRAEDRLFLDLQPVASMGYQDENRRQSEELMRVYFAVKTVKQGLLITPLMRSVSSTFVRVTLRIDDIYIQVNNQIARHTDIFRRPZHIFKIVEMQORNDITALEPQ  
TLRAWGATRKINRSFYQNSENRFRFAGFRSNGLTQTLRLNLYGVLGRYLPANEKIVGLLQHDLPFIYPVDHLLAVVRNVRRLALDMHSHLPHYAALMQSFERQDILYLAAPFHD  
AKRGGGDHAVQGIADARQFAADHPLTEESDLALWLVENHLLMSAVAKEDIQDPGLDAPKRVQTHERLSALYLLTISDIRGNPKLWNAWRASLLESLPHAAAGCLAGNDGNFHALFG  
RRQEAADLLTRAAPVPEKQKLLNALGSAYFARHQSREILWHAANLVHDFBPPIVRSRLPQSDPQVVMFNGPRLFARLCRIFSRHGFIDILAAAFITHEHYILDTPITVQIPSHAP  
EDYFDIQSALEALNSFIHGHTVAETQSCNRRISRRSYMPIAPSITITPEEDYDPRYSVEITAVNRPLADNAEVEFFAHNVSLRYAKISTLDERVEDSFTVTFDLKNPKIQSSILQAL  
LEQLA

## SEQ ID 5005

GTGCACTTTCACAAACCGAAGACCGAGCATTTATCGGTATCTAGAAAAAGCCTATATCTTCGACGATGTTTGTGTTTCCGCGCATTTCGACCGTGTGCCGCGAGAGCTTAAACTTC  
AAACCAAGCTTACCGCGAAATCACACTCAACCTCCCGCTGCTTTCGCGCGCATGGATACCGTTACCGAGGCGCGCTCGCCATTTTCGATGGCAGAGGCGGCATCGGCATATCCA  
TAAACATATGCGCGCGAAATGACAGCGCGCGCGCTTTCAAAGTAAACCGCACGAAAGCGCGGTGTCAAAGACCGCTAACCGTTGCGCGGACAAAGCTCATCCGCAAGTCTTGGAA  
ATGCGCGCGCAGCGCAACGCAAAATGTCGCGCTGCCCGCTGTTGAAACGCGCAAGTCTGCGCATCGTAACCAACCGCGACCTGCGTTTGAAGACCGCGGTGATTTGCCGCTTTCG  
CCATTATGACCCCGCGCAAGCTGCTGTTACCGTCCCGAAGGCAAGCATAGACGAAGCGCGCAAGTATGATGACACGTAACAGTGAAGCGCGTTTGTCTGAAAGCAAAAAGACGA  
GCTTAAAGCTTGAFTACCATTAAGATATTTTAAACACCGAGTTTCCCAATGCCAACAAGACTCCGAAGCGCTCTGCGCGTGGTGGCGAGTGGCACCGCGCGGACACCGAC  
GAGCGGTCAAAGCTTGTGCGAAGCGCGCGCGAGCTGATTGTCTGATACGCTCCACGCTATAGCCAAAGCGGTGATCGACCGCGGTGATCGACCGCGGTGCGGTCAAAGAACCTATCCGACATCC  
AAGTCATCGCGCGCAACATCGCCACTGCCAAGCGCATTTGGATTGTTGTCACCGTCCGCGCGGATCGCGTCAAAGTGGTATCGTTCGCGGATCGATTTCACACCGCTATCTGTCGCGAG  
CGTGGCGGTGCGCAACTGACCGCATTCACAACTGCGCAAGCGCTCAAAGGACGCGCGTTCGCTGATTCGCGACGCGCGCATCCGCTTTCGCGCGACATCGCCAAAGCGCTTCGCG  
GCAGGCGGTACAGCGTATGCTCGCGGTATGTTTTCGCGCACGGAAGAAGCGCGCGGCAATGCAACTCTACCAAGCGCGCTTCGTAACATCTATCGCGGTATGGTTCCTTGGCG  
CGATGAGCGCAAGTTTCGCGACCGCTACTTCCAAGCAAAACGACGACGCAACAAATACGTCGCGAAGGATCGAAGCGCGGTTCCTTCAAAGCGCGGATTTGTAACATCATCCA  
CCAACTGACCGCGCGACTCGCTTCCAGTATGGGTATTTGGGTTCGCGCAATATTCGCGAATGACGAAAAAGCGAATTTGTGGAATCACTTCCCGAGGTATGAGCGAATCGCAAGT  
CACGAGCTTCAAATACCAAGAAGCGCGCAATTACCACCGC

## SEQ ID 5006

VHLAQTERPSIMRIVEKAYTFDDVLLVPAHSTVLPDVKLQTKLTREITLNLPLLSAAMDVTVEARLAIMAQEGGIGIHKNNPFPQARAVSKVRHESGVVLDVPTVAPTLLIREVLE  
MRAQRKRMKSLGVVVEKGVVGVITNRDLRFENVRDLFVSAIMTPRERLVTVEGTSIDEARELMHTYKVERVLVINEKDELKGLITIKDILKTEFPNANKDSBGRILVGAAGVTGGDT  
ERVKALVEAGADVIVDTAHGHSQGVIDRVWVKETYPHIQVIGNLIATAKALDLVTVGADAVKVGIGPGSICTTRIVAGVGPQLTAHNVAAELKGTGVLADGGIRFSGDIKALA  
AGAYSVMLGMPVTEAPGEIELYQGRSYKSYRGMGSLGAMSGSADRYFDKTDSTDKYVPEIGRVPYKPIVNLIHQLTGLRLSSMGYLCAANLAEHKAEPVEITTSAGNSRSHV  
HDVQITKEAPNYHR

## SEQ ID 5007

TTGAAAGATTGCGTTTATTTCCACCGCGCTTTTAAAGCGCGACGGTATTTCGCGAGACGGGTGCAACCGCGCTTCAGACGGCATTTTCATTCTTTCGCGGTGTCGTCAGAAATGGCTTTGC  
CCGTCGCGCAATCAGCCGTCGCGCTTGCCT

## SEQ ID 5008

LKDCVYFHRRFKGRYSADGVQTAFFRRHFSFGVSVRMALPVRALSPGGLP

## SEQ ID 5009

ATGAAATGCGGTGCAAGCGCGTTTCACCCGCTGCGCAATACCGTTCGCGCTTTTAAACGCGCGGTGGAATAAAGCAATCTTCAATACGGCGCTTCGATGTCGGAATGATGC  
GCCGCGCGCATATCAAAAAATCGCGCGCGCTTCGGGAAAGTATGCCCGCGCTTCCCAAGCGCGCGCTCAGCAITA

## SEQ ID 5010

MMPSERRLHPVCRIPSAFKTAKEINALIYQYGRFDWSEMRPPYQKIGRRLRESMPRPQAAPSA

## SEQ ID 5011

TTGCTTTTCGCTTTTTCGACTTAATCGGAACCGGTTCCTTTCCTTTTTCGCGATTTCGCAACGCGCAGGACGCGCTTTCCTTCTTTCGCGCATCGGCGTGTTCCTTTCGCGCG  
TGGTTTCGATTTCCCTTTCCCGCGCGCTTTCGCGATTTCGCGAATTTGACCTTTCGCGCGCTGCGCTTCTTCGCGCAATAGGACAAGTCGATTTTCCATCATCCA  
ATCGGCAACGCGCGACCGGACGCGCAACCTGTCCTCCCATATTGAAACGATGCGCTGCGTTCGCTTCGATTCGCAATGATTTTCGCGCGGAAATGAAA

## SEQ ID 5012

LPFRPLTLIGTGFAFFPDSATAGTLP/LPLPHRAVFPFAVVPDFPFAAPAGLADANLTFRRLLPSAIRTKSIFPSSKSARATRTATLSPILKRMPLRSPSIAMISGRKLK

## SEQ ID 5013

ATGAATAAAATATTAATCTTAAATTTACGGGAAAAAGACCGCTTTTAAAGTCTGAAAAACAGCGTTATGAACATCTTTGCCAGTGGGAATGGATAATGTAATGTTGGAGCGCA  
AAGGTGTGCTTCAAAAATCGAATCGCTTGCACGCGAGCTGTGATACGGAAGACGAGTATGCTTTTTCGAAACCGCTGGAAGCGATGGCGCGGAGCGTCAAGTTTAAATCAACCG  
CCGAGCGCGCAATTTGCGCGCGGACAAAGCTGGAATTTGTCAAATGCCGCTTCGAGCGCATAGGAACGCTTTCGCTTCGCGGTGCGCTCATGCGGATGACGAAAGGGATTTCGTTTA  
TACGAACGCCAGATGCGTGTGTATGACGCGGACACCGTTACCGTCCGTCGCGGTATCGACCGCAGGCGCGCGCGGAAGGACGCTTCGATATTCGAAACGCGCGCAAGCA  
AAGTTGTCGCGCTTCTATATGATAGGGCGTGGCGATTTCGAGCGCGAAGACAGCGTGAACCAAGCATCGTGTGGAACCGGACGCGGTGGCGCTTTCAAACCGCAATCCG



GCACAGGGCGTGCCTGTTTGAAGCGCCTGCGGGGCGCTGGCTGCACGGGCGCGGGCGGATGTTATAAAGGAATGGCAGGCATTGCGGCTGGCTGTGCGCAGGGGAATCGCC  
CGGCGCAAGTGGCTGCCAATCGGATAACTGAAAGTATG

**SEQ ID 5024**

NFPVPHLSGESRRRLQTLALRPHFVFKARAEDSHKGTFGTLAVVGSAGHSGAPVLAASAAMYLGCCKVRAGFNQDTPPFAVIAGFPETMLQTDAGLTKRQGTINAWTAGCGLGTDAAAVET  
VAAVLARNRDEAVVLDADALNLTDAETRNLRGCKNLILTPHPAEARLLGTGTVAVQVQADRTAAVRKIGAILGATVVLKGHKTLVAASDFTETVYVNESGNAGLATAGSGDVLGGILIGSLI  
AOGVPVFEAACAGAWLHGAAADVIKESAGTAAGLSAGEIAPAARWLRNWTESM

**SEQ ID 5025**

ATGGAAGAAACGGGAAACATTTCCTCCCAATCGGTTAAATTAAGGCTCGAAACAAACCGATTCTACCGCGGAAACCGATTATGAAAAACAAACCAAGTCTGGGACTTCCCCACCCGCTTTTCCACTGGCTGCTTGGCCGATCCCTGCCCTTTATGTGGTA

**SEQ ID 5026**

MENGKHFPNRLKLRLNKPILPPETDYEKQNSLGLPHPPFLAACRI PALYVV

**SEQ ID 5027**

ATGTGGTATAGCGCAAAAGCCGGCGGCATATCTGCAATGGCACACGCGCGTGGCGTGCCTGCTTTCCTGCTGTAFTTCGCGCTCTGCTGGGCAATTTGGGGACGCGATACCGGCC  
GTTCCTCAGTTTCGTCGAGGTGGGCAGGTATACGCGCATATCTGAAAAACGGCAATTCGCCGAACATATTCACGCCCGGACACACCCCTTGGGGCACTGATGTGCTGCGCTTTTGGC  
CGCGCTCTCATTTTCAAGTCGGCACGGGGCTTTTTCGCCCAATGAAAAACCTTCAGCACCAACGGCTACCTCAACCAATTTGGTTTTCGGAACATACGGGCAGCCTTATACGGAATAATCCAC  
CTCAACTTTTCAAGCTGCTCGCGCTTTTTCGCCGATGCACATCGCGCGCGTGGCGCAATACGCATATTCAAAAAAGAAAAAAGCTCGCGCGCGATGATTAACCGGCTTCAATATACATCG  
AAGCAAAAACCTCAATCCGCTTTCGCGGCAAAAGCGCGCTTTCGCGCATATTCGTTTCGCGCGCTTCGCGAGCGCGCATCTGCTCTCTGTC

**SEQ ID 5028**

MMYSAKAGGDMLOMHTTVGLLVLLFLLVFLRCWGIMGSDTARFSSPVVRGWAGIRGYLKNIGPIEHTQPGHNPLCALMVVALLAAVSVQVGTGLFAANENTPSTNGYLNLHVSEHTGSLIRKIH  
LNPFKLLAVFSAVHIAAVAAYRIFFKKNLVRMHTGFKYIEGKTSIRFAGKAALAAALSVAAALAAATILLIS

**SEQ ID 5028**

GTGAATTATTTTCCCAATTTTCGCCAACCTCGCCGGCCGCCCGTATTGGTCGTAGGCGCGCGCCGGTCCGCCGACGCAAAATCAGCCTGCTGCTGAAGCGCGGCGCAGAGGTGGGGTTG  
CCGCAAAACACCTCGAATGCGGAACCTCTCCCGGTTGGCGGGCGGAAACAAAATCCTGTGGCTTGCACGAAGAAATTCGTGCGCGAACACATCGCCACGGTTTCTCTATCATTCGCGCAGCAG  
CGAACAGCCGCTCAACCGCGCGGCTTTTCCATCTTCCGGAAGCGTCCCAAAAGCCGGTCAACGTGGTGGGCGACCGTGACCATCTGCTTCCGTCGGTTCATCGACCGCGACCCCT  
TGTCCAGATTCGCGCTTTCCAGCTCGGCGACGCGCGCTCTCTCGCGCGCTGCTGCGTGGCGTGAAGAGCTGCTGCTGCGCCGCTTTTGGGCGATATGCGCGGAAATTCAGGAAGTGGC  
GCGATGCGGGTTTTTATTTCGCCGTCACATGGTCTGCCGCAAGATGCCGACAAGGCCGACGCGTTTCCGAGGCTATCAGGGCGCATCGAAGCGGGTTCGGTCAACCGTCGGGCAAAACGCT  
CCGCATCGAACCGAAGCGGCTGACCGCGGAAGTGTCCGAAATCATCGCGCGAAGGGGAAATGGCGCAGGCTTTTGGCGGGCAGGGCGGCAACCATCGCGCTGGACCGCGCATCTGAATGTT  
TCGCGCGGGGATCTTTTGTGATAAAAATTTCCCGCTCGCCCCGCAAAACATCCGGAAGCCACCTTTGCTGGTTTGACGAACCGCCGCTCAACACCGCGCGCAAAATACCTGCTCAAGC  
ACGGCACGCAACACCGTGTGGCGAAAAGTCGGGAAATCGGAAAGCGTTTGGATGTCCGACGTGCAACAGAGCGCGCGGGCGGAATCTTAAAGATGAACGCATCATCGCGCAAAAGTCGCAT  
CAACCTTCAAAAACCGGTACCGGCAACGCGCTTATGCGGAGGCAACCGCCCGGCTGCTTTATCTCTGATGAGCAAGCGACATACGGTACTGTTGGCGAGGTATGATTTTA

SEQ ID 5030

VNYFFIPANLAGRPVLVVGCGAVAAKRTSLLLKAGAEVGAAKHLNAELSALAAENKILWLAKFEAHEHRTVPVFLIIAASDDQALNRRVFLHAESQKPVNMGDRDHCSPFPSSVIDRDP  
VQIAVSSSGSPVPLARLLRERLEALLPSPGLDMABISGRWRDAGFYFPVQLVVRQADKADGFRGYQGRIERGSSVTVGQTVRIEPLGLTAEVSEKTIAPKGEVAQAFAGEAATIRLRDLDF  
SRGDLFVDKNFPLAPOKHPEATLCWFDREPLNTARKYLLKHGTQTVSAKVGIEESVLVDRTELEQBAGAESLKMDIAKVRINLQKPVATPYAENTAAGSFTLIDEATYGTVAAGMIL

SEQ ID 5031

TTGTATCAGTTTTTTATGCGCGCTGTTCACAAACCTGCGCGCGATGCCGCGACAATGCCGCTCTGAAGCCAGAATCGGTTTCAGACGGCGCGCAAAAACCAGCGGTTTTCCGCGCGTTTCA  
TCATTATGCCCCGCCCTTCGGGGCGGCAGGGTTCGGATCGGTTTTCGGGGCGCGCAACGGGGCGCTGCAGGTGTGCCGCTGTGTGTCAAACAATTTCCGGCGCATCAAAACAACCATTT  
GACCGACAATGCGGCTCTTTGTGCGCGCTCGGCTCTTTTGCGGTATCCGATGCTGCGGACATATGGCTTTTCCAACCGGCTTCAATGCCAAACCGGCTTCGAGCGCGCTCTGCGCTGCC  
AGCGTCGTTTTTTCGCGGTCCATTTCCATGCCGAAGATTTTGACCTGTGCAAAACATTAAGAGCGGCAAAAGGC

**SEQ ID 5032**

LYQFFMFLFQTLPPDAATMPSEARIGFYTAAKNRRFSAGFIIMPRPSGRQGSDFRAGRRTGPCRCAACVSKHFFAHQNNHLTNAASLSPSVLLPYPMRADIMFPQASHMPNRPSSAVLPA  
SVCFPSISMPKDFDLCKTLKAAG

**SEQ ID 5033**

GTGTGCGGGCTGTCTCGGCTACGCTTTGGGCAAAAGCAGGAAACGGGCAATCCGCAAGGCTGCCCCGCGCTTCAGACGGCAATGCCGGCGGCAGAACCTTTTTCGTAACCGTCTCTTTCCGCTC  
CGCAAAACCGGCAATTCGCAAAATCCGTTGCGCAAAAGCGCGCGGACAGCTGAAAGCGCCCGGCATCCAAAGTCAGGCGCGCGGAAGCTGAAAGGCTACAAAGCGGAAAAACATCGCCCGCGCAAGC  
TCGCTCTGCTGCTGTGTTACGTCACCCAGGGCGAAGGCGAACCCCGGAAGAAGCGCTCTGCTGTCACAAACTGCTGAACGGCAAAAAAGCCCCGAAATTGGACAAACTCCAATTTCGCGTA  
CTGGGTTTGGCGGACAGCTCTATCCGAATTTCTGCGGCGGGCAAAAGATTTGCACAAACGTTTGAAGAATTTGGGCGCAAAACGCTCTGCTGCAAGCGCTGATCGGATTTGGACTTTG  
CGCGCGGCTCGAGACGATTCGACAGCGGCGCAATTTCTGCGCGCTTAAAGAAGAAGCGCTGCAAAAAACGGGCAACGCGCGCGCGCAGGCAACGTCCTCCCGCGCGGCTCTGACAGCGGCATCGG  
AGGGCAGGCTACTGCAAGCGAGACCCCTTTCCCGCGCGCTGCTGGCCAATCAGAAAAATCACGCGCGGCAATCCGA

**SEQ ID 5034**

VSLGSGYAWAKAGNGASAGLPAIQALPAEPPFSTVTLASQTNKASVADKAADSLKAAGIQVRAELKGYKAKNITAGERILLWTSTQGEPPPEAVLHKLLNGKKAPKLLKQFAN  
LGLGDSSYPNFCRAGKDFDKRFEELGAKRLLERVDADLDFAAAAGHTGRIVARLKEAAKNRATPAQATSPRRPSDGIQGVQLGRPLSRPAGQSENRHPPIR

**SEQ ID 5035**

GTGCGCCACATCGAAATCGATTTGAGCGGTTTCGGAATTTGCACTACCTCCCGGGCGACGCGCTTCGGGTTTGGTTTGACAACGATCCGGCACTGGTCCGGGAAATCTCAGACTGCTCGGCA  
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CGATAATGACGATTCGACCGTATTGCTCGCGCAACCCGCTTTTGCAAGGCTTTGTGTCGCAAGCAGCCGATTCGCGGTGTGCTGCACCGCTTCCCGCGAAAATGAAGCGGGAACTAT  
CGCGCGCTGTGCGCGCGCTTTGCGCGCGCTGTATTTCGATTTCTTCGTCAGCGGGAAGCGGGGACGAAGTCGCACTGACCGTCCGCGCGATGGGTTTGTGGAACAGGAAGGCGCGGCA  
GGGCGGGCGCGCATCGGCTTTCTTTGCCGACCGGCTGGAAGAGGACGGCACGCTGCGCGTGTTTTCGGGAACGCAACGACGCGCTTCAGGCTGCCGGAAGACAGCGCGAAGCCGATTTGTGAT  
GATCGGCTTCGGGTACCGCGCTGCGACCGCTTCGCGCGCTTCGTCACAAACGTGCCGCGAGAAAATGCGAAGGCAGAAACTGGCTGATTTTCGGCAATCCGCAATTTTGCGCCGACTTCCTC  
TATCAGACCGAATGCGACGAGTTTGCCAAAGACGGCTTCCTGCACGATATGACTTCGCTGGTCCGCGGATCAGGAAGAAAAATCTATGTGCAGGACAAAATCCGGAACAGCGCGGAAG  
GACTTTGGCAATGGCTGCGAGGAAGCGCGCATATCTATGTGTCGGCGGATTCGCGCAAAATGGCAAAAAGGTGAAGACCGCCCTTCGCTGATGTGATTATCGGGCAGGGCATTCGGAAGA  
AGA CGCGCGAGAGGATATTTGGATATCTGCGCGAAGAAAAACGCTATCGGCGCTGATGTTTAT

SEQ ID 5036

VHRIEDLSSGLHYLPGDALGVWFNDPALVGETLIDLLGINPATETQAGGKTLFVASALLSHFELTONTAPFVKGYATFADNDELDR1AADNAVLOGFVQSTPIAGVLHFRPAKLTABOF  
AGLIRPLAPRLYSISSSQARAGDEVHLFVGAVRFEHEGRARAGGASGFFADRLKEDGTVRVFAERNDFGLRPEDSRKPIVMIGSGTGVAFFRAFVQORAAENABGRNWLIFGNPHFAADF  
YOTENOOFAKDGFLHRYDFANSRDOEEKTYVODKIREQAGLWOLMOEGAHITYCGDAAKAKEVEAALLDWIIIGAGSHDEGDAGBYLWMLREKRYORDVY



## SEQ ID 5037

TTGATTAAATATAATCGGAGGAACACAAATGACCGTACAGGCCAAGACAAAGSTTTGGCGTGGCAAGAAAGCCGTATCCGACAACGAACGTCTGAAAACCGAAAGCAATTTTTTAC  
GCGGCACGATTTTGGACGATTTGAAAGACCGCGTACAGGCGCGCTTCAAGGCGCAACTTCCAATCATCCGCTTCCACAGTATGATGAGCAGGATGCGCGGACATCCGACCGAGGC  
AAAACTCGAGCCCTTGAAATTTATGCTTTTGGCGTGGCGGCGTCCGCGGAGATCATCAACCGTCCAGTGA

## SEQ ID 5038

LIIKYNREHKMTVQARTKGLAWQEKPLSDNERLKFESNPLRGITLDDLKPLTGGFKGDNFQIRFHSYBQDGRDIRTEAKLEPLKPHLLRCRLPAGSSNRPFG

## SEQ ID 5039

GTGCGGAAACCAAGTTGCAGACGATGCCCGCCTCTTGCACAGCCTGGSTTTGGATTCCATCGCTACGCGGCGGATATGAACCGCAATGTGCTTTGCACCTCCAAACCGGATCGAGTCCG  
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CTCCGGAACACGCACTGAAGGCGCGCGAAGCGGTGTAACACGACGCGCACTTTCGGAACCGCAGCCACGCAAAAACGACCGCAGCTACACCATTTCAAAATATGGGCTTGGACAA  
CTCCGCAACGGAACCGCAACCGCTATGGGTATGCGCTTCAAAACCATACGCGCGTTCAGTTTACCGGCGCGGCGACCGCATCGCGCGGTGAAGGCATAGACGGCACTGGCATTG  
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TCGTTGCAATGTGCCGAAGGAGCAAGCGCGATCGAACAGCTGCGCGCTCATACGCGGTGATACCGACGGTGTGACGAAGCTGCGCAAGCTGCGGGAACACGGCACGTGCGGCTTCCTTCC  
GACCTGCCCGCTGCGCAATGGCGGAAGCGCAAGCGGTGTCGCGGACTTCATCGCGAGCTGGAATAGATTATGCGGGAACACGGCACGTGCGGCTTACCGCTTACCGGCTTACCA  
TGCCCGAACCGCTGCGGACGGCGATGTTGGCGAAATCGGACTGCTGCGCAAGCGGTGGGACGCTACAACCTCCACATCGCGCGGCGACCGCAAGCGGTTCGCGCATTCGCGCTTACCA  
AAGAAACATCACCTGCCGGAATCTTTCCGAATTGGAAGACCTGATCGGCAATGGCGGCGGACGCGATACCGACGAAGGTTTCGCGCATTCGCGCATACGACGGCGCATCTGCA  
ACCGGTGTTGGATGCGCGCTCGATTTCGCGACGATCCAAAGCGCTCCGATTCGCGCGG

## SEQ ID 5040

VPKTLITMPLRLHSLGLDSIATAADMNRNVLCTSNPIESLHRQAYEYAKKISEHLLPRTRGYLDMMVDDKKVQSSDDFLQEGEPILKTYLPRKFTAVVPIPLNDVDCYGNLDFVAV  
SDNGQLAGFNVLGGLSTYHNGNTKTYPNISLELGFVPEHALKAAEA VTTQRFNPGNRSHRKNDRTRYTIQNMGLDNFRTEAERRMGMPPKPIRPFKFTGRGDIRGVKIDGNWHL  
TLFIESGRLVDEGGQLITGVLEIAKIHKGFPITANQNLIVANVFBGGKARIEQLARSYGLIRDGVSKLRENAMSCVSPFPCPLAMAEARVLPDFIQLDKIMAEHGTSDOYIVTRITG  
CPWCGRAMLAETGLVGA VGRYRNLIHIGDREGVRIPRLYKENITLPLKLELEDLIGKWAAGRDTEGFGDFAIRTGIVKPLVLDAPVDFWDASKAVPIARA

## SEQ ID 5041

ATGCTCTTTTGGCGCAGCGGTTCCATTCCGCAAAATTCGACTACTGGTATAAAATACCCCTTTTCCACTCTAAAAACCGTACCGGATGCGGCTGAAACAGCCCTGCCCTTTCAG  
ACGGTATAGGCACAAAGAAACACACTATGCCAGAAATCCCGCTCCAAACCTCCACCCAGCGCGCAATATGCGCGCGCGCGCGGATGATGAAACCGGACTT  
CGGCAAGCCCATCATCGCGCTTGCCTTCCACCAATTCGTCGCGCGCGCGCGCTCCACCTCGACAATATGGGCCAGTGGTTCGCGCGGAGATGAAAGCGGGTCAATGCGCAAA  
GAATTCACACCATTCGCTATCGACGAGCGCATGCGCATGGGCGACAGCGGTATGTTACTCTCTGCCGCGCGGATTTGATTGCGGACTCCATCGGAATATATGTTCAACGCGCCACTGG  
CCGACCGCTGCTGTGCACTTCCAACTGCGCAAAATCACCCCGGAATGCTGATTCGCGCGCATGCGCTGAACATCCCCACCATCTTCGCTCTCCGCGCGCGGATGGAAGCGGGCAAGGT  
CATCGCGCTGGCAACATCCAAACCGAAGCGGCTTGGACTGATTGACGCCATGATCGAATCGCGCGGACGCAATGTCAGCAACCGGCAAGTTCGAAGAAGTTCGAACAAACCGCTGCGG  
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CGGACGCTTCTCGGCGGCGCATCATGAGGTTTGTCCATCGGACACGCGTCCGCGGAGCGGCGGAGCGGCAATCGGTTTGGTACACGAAGCGGATGAAATCGACATCCCAAA  
CGCAGCATCCGCTTGTCTATTTCCGATGAAGAGCTTCCGCGACCGCGTCCGCAATGGAAGCTCGCGGCGAGCAAGCGTGAAGCGGAAACCGGACCGCTACGCTCTCCGCGCATTA  
GGGCTTACGCGCGGATGCGGACTTCCGCGGCAAGGCGCGGTGCGCGGACGATTCGCAATTCGAGAGA

## SEQ ID 5042

MFFFAARVSTPQNSDTWYKIPPPPTLKNRTRCLKQPCLSDIGITRKHMTPEYRSKSTSHGRNMAGARALWRATGVMETDFGKPIIAVANSPTQFVPGHVLHNNQGLVAREIEKAGAIK  
EFNTIADIDGDIAMGRHSMLYSLPSRLDIADSIYMVNARCADALVCI SNCDKITPGMLIAAMRLNIPTIFVSGGPMRAGKIVGVANIQPERRLDIDAMIESADDNVSNRQVEVEQNA  
TCGSCSGMFTANSHWCLTEALGLSLPGNSYLATHAGRKELFLEAGRMIVETIRYBQDDETVLPRSIATKAFENAMTMDIANGGSTMTILHLAVANEAGVDFKMDIDRLSRVVP  
CKTAFNNHDIYNEVDRAGGTFALLKELDKAGLHTDVYTHAPFLKDAIEKWDVTPNENTRAIERFKAAPGGVTRTQAFSPNRIWTLDLDRKGCIRIDVAHAYSQDGLAVLFNIAER  
GCVVKTAGVDESILKPTGRARVFESQEAABGILGNQIVAGNI VIIRYBPGKGGPMQEMLYPTSYLKSGLGKACALLTGRFSGGTSGLSIGHASFEABGGAIGLVHEGDTIEIDPK  
RSIRLVI SDEELAARRAEMEARGSKAWKPNRDRYVSAALRAYGAMATSADKGAVRDVQSIR

## SEQ ID 5043

GTGCAAAACATTAAGGCGGCAAAAGGCTGAAGATTGACACCGTTACGCAAGCAAAACGGGTTTTCGCGCAATGCGCGCGCGGATTGCCACTGACCGCTGCGGAGCAGCCGACCGC  
GCCCTCGCTGTGGTAAAGCGCGCTTACGCCCAAG

## SEQ ID 5044

VQNIKSGKRLKIDVVTQSKTGFCPNAGADLPITAAEQPDRRPSLSVKPPPTPK

## SEQ ID 5045

ATTGAACTCTCTGATCTAAAAATCCAACCTATTTCGCGCAAACTATATCTATGATAAACTGGTCGGAAGATTATACCTAGCCCTATTATAGCCAGTGCACCTCCATAATCCAG  
ATTTCATATCTGCTTAAATCTCCAGCTCCAAGCTATTATCGATATCTTATCTTGGTCTCCGCTAGCGTATCCATAGATAAATTCAGATAGTGAACGCTTGAATTTAATTTTA  
CCAGCTCTGTGTAATTTGGGTAGGGCAAA

## SEQ ID 5046

IEYLLI\*KFQLYFPANYIYDKTRKIIPTPY\*CCQTSIIQDFIILL\*FSKLGIIIDIFLVLRSVSIKPKQIAELLFNFYFVCVIVCRAQ

## SEQ ID 5047

ATGCCGATGCCGTTTGAAGGCGGTCGCGCGGATCGCCCGTCTGTTGGGTGGCGGTAATAAAAAACAAACCGGTGTTTACAAACCGGTTTGTGAGGTTAATGGTCAGCGCGCTCTGC  
GTGCCATTGTTG

## SEQ ID 5048

MPMPFEGRSGLIARRLGGNNKKQTVGLVTGLSGFNQGRVLRCHLL



## SEQ ID 5049

ATGATTATTACAAATTTACCTGGGCGATGGCGTATTTTCGCAATTTTGGCCCTCGTTATCGGCAGCGGCTTACCGCGCTCGAGTATGTAAAGAGCCGCTGCCGCCCTTATGCTG  
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CAGGATACGCTGACGGAAGGCGAGCAGATACCGTTTCCATCATCGGCGTGGCGCA

## SEQ ID 5050

MTINKFTWAMAVFSAILALVIGSGFTALEYVKEPPAPYAVSAPKTAGVKPRRLPERNPCCRLTVQTPRPFQTPAMRTDRLRLTERQQIPFPSSGSA

## SEQ ID 5051

ATGCATAGCATATTTTGGTGGTTTGCACATTTTTCGGCGTACCGCTTCGTCAACAGCGTACCTTATGCGCGGACCCCGATGATGGAACCGGTATCTGCTGCCCTTTCGCTCAGCGSTA  
TCCGTGCTCGCATCGCGGTGTT

## SEQ ID 5052

MHSIFWFAHFFGVPPSSNSVPIAADPDDNGICCLSVRRILSVRIAGV

## SEQ ID 5053

GTGCAACCAACCAATATGCTATGCTATTCGAACCGCTCCGCATACGGGAATACCTTCCGACGCGGGATTCGACTACCTCAGCTCGCAACCAACCAACAGCAACGCGTTCGGCGCGC  
AAGGCATCAGCGCAACCGCAGCAACCTTTACGAAATGAACATCAATATTCGGGCATCGAAACAGGTTTGAAACCGCCATCTTGAAGAAACCGCGTGAGATACGCGTTCGCTCCTT  
CGCCCCAACCTTCCGCGCGTCAACCTGAACGATTACGCAAAATTCAAAATCTGATTCGGAACCAACCAACCAACCAACGACATCGTATTGTGATGTTCCACGCGCGCGCGGAAGGAA  
CAGGCTGAACACCTGCCGTTGATACCGAAATCTTATGCGGGAACAGGGGCAACGTCGTGAGTTTCCGCGCGCTCGCGCTGATTCGGCGCGGATGTCGATTTCGGCGCGGCGCGC  
ACGTTACTCGCGCGCTCGAATCTTACACGACCGCTTCACTCTTACAGCGCGGCACTTTCGCACTACGCGCATCAGCGCGATTGCGCGGATTTCGCAAAATATCACCAGCAACAGGG  
GCGGTTGCTTTCGCGCAACATTATCCCATCACTCAAGTCGCGGATAAATCCCAAAATCGACCTGAAACCACTGTTATTGAGCGGATTATTATCTGAACCATAGCGACTTCCCAAC  
GGGAACGCGATGATGTCCTCGCGCGCGGACATCAACGCGCG

## SEQ ID 5054

VQTPKICYAFRTPSAYQYLADAGFDYLSLANNHNSGFAQGITATAGNLDENIKYSGIENRFETAILKKNVRYGVFSFAPNLAALKLNDYAKFKLIRKTKQKTDIVIMVPHGAEKG  
QAEHLFPDTEIFYGNGRNVVEFARLAVDSGADVVPQGAHVTRAVELYHDFRISYSGNFATYGISGIAPIFKLIITDKQGRFVSGNIIPIQVGDKIPKIDPERFVIERIILYLNHSDPFH  
GNGLDVSFGDITER

## SEQ ID 5055

TTGACGATTGAAAAAGCGCTCGAACTTGAATCGCTCGAAACCTGAAAAAGGCTTTCAGACGGCATTTGTTCCGACGGAATTTCCAATATCTTTTACCGCGCGCTGATGTCGCG  
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CTGCTCGTCCGATCCCGGTGTTTGAACGCGCGCGGTTTGAACCGTCAATCGCGCAGCAGCGGGGATTCCGTTCCGCGAGGATGCGCGGAGGCT

## SEQ ID 5056

LTIKCRKLEKRLKPEKRLSDGICSDGISNIFLPARDVAAGRDIQSVFVEVAVQINNPNNSFVRVDFDIADLSGDHNVAGNEPPLFVGDNFENRRNRADAUVGKVAAAVRDEAVV  
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VACRCRDLRAEAVAVVUCEAEVVESESRVGVLPVCGGRSECIATPGLHIFSAIRLRQYAYLMPPTPMETVSAAPPSGVSCPSASPVEGAGFEPISGTSVDPAGCAEA

## SEQ ID 5057

TTGCCCGCTGCGCGGCACAAAGCGGAAACCGTTTGCCTCGTATTTTCAACAGCGTTACACTTGCCTCGCTGTTTTCAGCCATTGATTACCGCAACCGCGCTCATTCGCGCGGCG  
GTTTGCCTGTCAGCGTATTCGCGCGCTG

## SEQ ID 5058

LPGCAAQRRKNRLPRIFKRVTLAAAVFSLITRNRHCAGGLPVSIVLAPL

## SEQ ID 5059

ATGCCGCTGAAAGCCCTTTAGACGGCATTTCCCGCTGCGCGGCACAAAGCGGAAACCGTTTGCCTCGTATTTTCAACAGCGTTACACTTGCCTCGCTGTTTTCAGCCATTGATT  
ACCGCAACCGCGCTCATTCGCGCGCGGTTTGCCTGTCAGCGTCATTCGCGCGCTGTAATAACGAAAGAACACATTATGACCGTATCCCCCGTTCGCGCTGAGAACCGAGTGCA  
GCTCATCCACCGCGCGCTATTGGAAAAATGCGATGTCGAGGACATTTTCGCACTGCGCTTTTGAAGACTTGTCTATCAGGCGCGCAGAACTCCACCGCAAAATTTCAACCGCGCGAA  
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AACTCGATTTTTCGCGCGACAGCTGTTGACACAGCAATCTGATGAGGACGCGCATAGAACTCTGATGGAAGGCTTAACCTGATTCCTTGCAGTTTTCGCGGGAAGCGGAGGTGCG  
CCGAGTGGAAAAAGCCTCCGGATTAAAGCGGATTAT

## SEQ ID 5060

MPSESPLDGIARLGRKAEKPPAPYQFRYTCRRCPQFDYPPQPSLRRRFACQHRCAAVNTKEHINTVSPVALRRKTECKPHPTARYWKKCDVEALFGLPFLPLVYQAEVHRQNPFR  
IQLSTLLSIKTCGCPEDCAYCQPSAHNTNLGKEQMDVDEIVEKAKIARSASRFGMAAWRGPKPDVETVSAI IKAIVKLGMECTGTFGLMEGMAEDLKEAGLDIYNHLDTPDR  
YNDLIHTRRHERMDTLGKVRNAGLKVCCGGIVGMNTRAEAGLIASLANLPQPEVSPINRLVKVBTFLADAEDLDWTEFVETVSVARITMPQSVRLSAGRSNNPFAHQACPHAGA  
NSIFYDKLLTIGNPDEDGRILMEKLNLYPLQFEPEGEVAEVEKASGLKADY

## SEQ ID 5061

ATGAAACACATCCACATTATCGGTATCGCGCGCAGTTTATGGCGGGATTCGCGCATTTGCCAAAGAGCGCGGTTCAAAGTCAGCGGTTGCGACCGGAAGATGATCCGCGATGAGCA  
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GGCGATTTCGAACCGTGGCTGCTTATATTTCCGCGCGCAATGCTGCGTGAAACGCTGCTGACCATCATTTGGGTACTCGCGGTGGCAGGAGCGCAGGCAAAACGACCCCGCTCC  
ATGCTCGCGCTGGGCTTGGAAATATGCCGACTCGCGCGCGGCTTCCATCGCGGTGTACCGGAAATTTTCGCGGTTTCGCGCGCTTCCGCGCGCTTCCGCGCGCTCAAGACCGGACAGCA  
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TTGCCGAAGCCCTCGCGCTTTGGGCTGCAGGCTGCAGGCTCGGCTGAAAGATTTCGATACCTTCGTTGCCGAATTTGTGAAAAACGCCGCAACCGCGGACCATATTTTGTGATGAGCAACGG  
CGGTTTCGGCGGAATACACCAACTGCTGACGCTTTGAGA

## SEQ ID 5062

MKHIIHIGIGGTFMGGIAAIAKEAGFKVSCDARNYPMSTQLEALGIGVHEGFDAQLEEFQADIYVIGNVARRGMDVVEAILNRGLPYISGPQWLAEVNLHHHVLVAGTHGKTTAS  
MLAWLEYAGLAPGFLIGGVPEFVSARLPQTPRQDENSKSPFFVIEADEYDTAFPIKRSKFVHYRPTAVLNLEFHDADIPADLGAIQTPHHLVWTVPSGLIVCHGQQSLQDTLD  
KGCWTFPEVKFGTGHGWQIGEVNADGSPDVLDDGKAGHVANDLMGGHNRMLALAVIAARHAGVDVQTACEALGAFKNVRRMEIKGTANGITVYIDFAHEPTAIETITQGLRQRVGARI  
LAVLEPRSNWMLKGTMSALPASLKEADQVPCYAGADWDVAEALAPLCRLRVGKDPDPTFVARIKVNARTGDHILVMSNGGFGGIHKLKLDALR

## SEQ ID 5063

ATCAGTTAAGCAACCATTTATTTTAACTTAATCCCATTCGGGCCAGTCTCTGTTTCAATTTGGAATTCCTCTTAAATACCTTATTTGTTGATGTGCCATTAAATCACAATTTCTCCCCCTTTT  
TTTGTAAATACGTCTGCTTCGGGAAAATAATCCAT

## SEQ ID 5064

IS\*RTIIF\*P\*SHSGQPCFIWNS\*ILIV\*CAINHNFPSPFFCWTCCPGKLIH

## SEQ ID 5065

GTGTTTGACCGTTTGGCAATGGCTTGAATTTATTCGCAAAACGGCCGATGTTTCTATGCGCATGCCCTTTGAAGGCGTTTCGGCGGCATCGCCGTCGTTTGGGTGGCGTAATAA  
AAAACAAACCGGTGTTTACAAACCGGTTTGTGAGGTTTATGTCAGCGCTCTCGGTTGCCATTTGTTGTAGTAGTATTCGTAATCTTCATCAGACCCCGGATTCAATCCAATCA  
TCGTATTCGGGCTGTTTCAAAGCTGTGACAGATTATCCGTACCTCGTAAATGGGT

## SEQ ID 5066

VFDGFGKWLLELYRKTAGMFLCRLKGVRAASPVVWVAIVKPKFVYKPVQGLMVSASCVAICSSIRNLHHDRIQSNHRIKRCFQSCQTLVPRKMG

## SEQ ID 5067

TTGCACAGGTCAAAATCTTTCGGCATGGAATGGACGGCGAAGAACAGAGCTGGCAGGAGGAGCGGCTCGAAGGCGGTTTGGCAITGAAGCCGGTTGGAAGGCCATATGTCGCAC  
GCATCGGATACGCAAGGAGGAGGAGCGGCGACAAAGAGCCGATTTGTCGTTCAATGGTTGTT

## SEQ ID 5068

LHRSKSFQMENDGEKQTLAQTALRFGIEAGWKHMSARIIGYKRTDGDKEAALSVMKLF

## SEQ ID 5069

ATGCGCGTATCAAAATGATTGGAAGTATATGCTTGTTCAGCGGTTTCAGACCGTATTTTCGGCAATGTTTACGAGTCCCGCATTAATGGTAAACCACTTACAGTCAAACTCCGGAA  
AAGATTGTACCAACGCGGTTTGGGGCGGATCGGTTGACAGTTCGGTCAGGCTCGCGTGAAGACAGGCGGAAGACGCGAGTGTGGGATTTATTCGGACACGGTGAGGAGCAAGC  
CGTCCAAATCCGAAGGGAATGCACAGAAAGCGGTTTCGGATGCCGCGATCAGACCGCAT

## SEQ ID 5070

MRVSKMIGSILLVAVQTVFSANVYECRHNGKTSYSQTPGKDCNTAGLRDRVYSSVRPAVKDRAEDAGVDYSDTVRDEAVQNPKNAGKQKDSAGIRPH

## SEQ ID 5071

TTGATTCGGTTTCAATCAATCGGCTCTGATGCCGCGCATCGAAGCGCTTCTCTGTGCATTCCTCTTCGGAATTTGGACGGCTTCGTCCTCACCGTGTCCGAATAATCGCAACTCCTCGG  
TCTTCGCGCTGTCTTTCACGCGAGGCTGACCGAATGTACACCGGATCCCGCCCCAAACCGCGTTGTGACATCTTTTCCCGGAGTTGACTGTAACTGGTTTACCATTATGGCGGC  
ACTCGTAACATTTGCCGAAATACGCTGTGAACCGCTGCAACAGCAATATATCTTCAATCATTTTGTAGTACGCGCATATTAACCTCTTTATGTTCTCTTCAAAAAAGGAATGTAT  
TTCAATAGAACTTATCTAATCTTTCATCTCTGCTCA

## SEQ ID 5072

LIRFQSMRSDAGIRTVFLCIPRILDGFPVHRVRIIANSVFRPVFHRPDRTVHPIPPQTRVGTIPSRSLTVTGTITMAALVNICRYGLNRCNKQYTSNHPFYAHIKLLYCSSSKKGM  
FNRTSSNSFIPCS

## SEQ ID 5073

TTGCTGAATTTACCTTGTATTATGACGAGTTTGGAAAAGCGGAAATACCGTTTCGGCAACAGGAAATGATGACGATATGGACAAAGTTCGCGCCTTAAGCGGAAGTTTAAAGACA  
TTTCTGAATCAAGTAGGGGATGTTGGGAATACCGGTTCAATTATGAGCAAGGAATGAAGAATTAGATGAAGTTCTATTGAAATACATTCCTTTTGAAGAGGAACAA

## SEQ ID 5074

LNLPCYYDEVLEKRIKIPFKQEIIDDNDKVSALKRKFKDISIKVGDGWEYFPNTEQGMKELDEVLLKYIPFFEEQ

## SEQ ID 5075

TTGCAAGCTGCCATAAAAACCGATTGCTGCCAAGCCGACACTTGTGTTAAAGATGCCGATAATGCCGCAACTCTTCGCTATTTACCGCAAAACGCCCTATTGCT

## SEQ ID 5076

LQAANKNLPAKPTLLVKDADNAATLPLYLPTNALFA

## SEQ ID 5077

TTGTTAAAGATGCCGATAATGCCGCAACTCTTCGCTATTACCGACAAACGCCCTATTGCTTAGAGCTGTTTGTGTTTTCACAAAATF

## SEQ ID 5078

LLKMPINPQLFRYRQTPYLLRAVLFFTKL

## SEQ ID 5079

TTGAGCAATATCTGTCAAAACCATTTCCACCATATCCAAAAACAAACCGCCCGCCACGGCATTTGACATAAGATGAGTTTCCACTGCCGCTCTTCGCAATGCCGCTTCTTGGGCT  
TCAAAGCACCCGCA

## SEQ ID 5080

LSNICQNHFRHIQNKTAATAALDNKMSFHCPSFRNAFLGFKAPA

## SEQ ID 5081

TTGGATATGCTGGAATGTTTTCAGACATATCTCTCAAAATCGTCTAATGGAATCCGAACAAATAAGAAATTTGGTAAAAAATTTGTTAAATCAACGGAT

## SEQ ID 5082

LDVEMVLTDLAQNRANGIRTNKEFGKFPVKSTD

## SEQ ID 5083

ATGCCGTCTGAAAAATCTATTACGGCGTATTGATTTTCTTATGATCGCTTCTATGCTGCTGTCACCGTTTATGCGGGTCTTTGAAGCCCAAGAGCGGCATTGCGGAAGGAGC  
GGCAGTGGAACTCATCTTATTGTCAATCCGTCGGCGCGCGGTTTGTGTTGGAATGTTGGAATGTTT

## SEQ ID 5084

MPSEKIYYGVILFLICIASMLSPFFYAGALKPKAALRKDGQWKLILLSNAVAAVLFWIWKKF

## SEQ ID 5085

GTGAAACACATCAGTTCGACCAATATGAACATATCAGACACCTGCACCCGCTGTGTGCGCAAGGAAAGTTTCAGACGCGAGTATGCCCAAAACCGTTTGGAGGGCGGTGCACTGCTTCAGG  
TTTTCTCGCAATTCGCGCAGAAAGCGGTGCGGGTATATATCCCGAAGCTAAAATGCCGTGGAAGAAAGTCTTAAATTCAGACGCGGTTTTTCGCGAAGCAGGATTTTTCTCGGTTCAGA  
CGGCATATTGAAAAAATCAGCAGCTTGAGTTGTGACAGCATATACCTTACACTGATGATATCCATTGGGCGGAACCTTTCGCGGACAAAGGCGAGTGTGGGTTTTGGACGCGGTGCA  
GATCCGGCAATGTCGCGACCGCTTACGAGTTCGCGCGCGCAGGGGTAGGTACGGTGGTTTGGGCGAGGGTTGTGCGGACGCGGTGCGCCAAAGGTATTACGCGCGGTATGGCG  
CGCATTTCTTGTGGACATTTATTCGACGCGGATTGGAAATATGGTTGGCGCACTATGAAGACCGGTGTGTGCCACCGCGTTGCGCGAGGAAAGCAGCGCGTTTGTACGCGGAGAA  
TTTGTGCGAACCGACAGCTTGGGTGTTGCGCAACGAAGGTGCGGGTGTGCGTAAAGCAGTTTATAGCAGGGCGGCAAGTGTGTGAGGATACCGATGACAGTGCACCGAGTCTTTAAAT  
GTCGCGATGGCGGACAAATCGCTGCTTTGAACAGATGCGGCAACGGCGCGGTAT

## SEQ ID 5086

VKHISSTNNEHRLHRLHLLSQKFRQYATVLEGVHLLQVFLQSGRRKPVVGTIPEAKMPESEVLKLTAVLPEDGIFSVSDGILKKISSLSCADDILFLIDIPLGGLTPDKGDAVLDDVQ  
DFGNVGTVLRSAAGVGTVVLGRGCADAWSPKVLRAHGAHFLDIYSQADLEIWLAHYEDRVFATALREKQAVLYGEDICEPTAHVFGNEGAGVGAVALDRADKCVRI PMHDATESLN  
VMAATICLFEHQRRAAY

## SEQ ID 5087

ATGCCGTCTGAACACGCGCTGCCGAACCTTATCCGCGCTTGATATTTGCCCTGGGTTTCATCTTCTGAACCGCTGTTCGGAACAAACCGCGCAACCGTTACCTGCAAGGCGAAACGA  
TGGGTACGACCTATACCGTCAAAATACCTTTCAAATAATCGGGAACAACTCCCTCCCTGCCAAAATACAAAAGCGCATTTGATGATGCGCTTAAAGAACTCAACCGCGAGATGCCACCTA  
CCAGACCGATTCCGAAATCAGCGGTTCAACCAACACACAGCGCGCAAGCCCTCCCGCATTTCAAGCGATTTCGCACACGTTACCCGCGAAGCGCTCCGCTGAACCGCTGACTCAGCGC  
GCACTGGACGTAACCGTCCGCGCTTTGGTCAACCTTTGGGGGTTCGCGCCGCAAAATCCGTTACCGGTGAACCGTTCGCGGAAACAAATCAACAGCGGCGCATCTTATACGGGCATAGACA  
AAATCATTTTGAACAAAGCAAGATTACGCTTCTTGAGCAAAACCCCAAGAGCTATTGGATTATCTTCGATTGCCAAAGGCTTCGCGGTGATAAAGTTGCGGCGCAACTGGA  
AAAATACGCAATTCAAATTTATCTGGTCGAAATCGCGCGGAGTTGCACGGCAAGGCAAAATCGCGACGCGAACCGTGGCGCATCGGTATAGAGCAACCCAAATATCATCCAGGCGGC  
AATACGCGATTATCTGCCGTGAACACCGCTTCCCTTGCCACTTCGCGGATPACCGTATTTCCACGTCGATAAAACCGCAACCGCTTCCACATCATCAATCCCAACAAAC  
GACCATACGCGCAACCTCGCTCCATCAGCGTGTCTCAGACAGTGCATGACGCGGACGCTTATCCACAGGATTATTTGTTTGGCGAAACCGCAACCGCTTAAAGCTTGCAGACA  
AGAAAACCTCGCTGTTTCTTAATTTGCCGGGATAAGGACGCTACCGCACCGCATGTCTCCGAATTTGCCAAGCTGCTCCG

## SEQ ID 5088

MFSEFRLPNLIRALIFALGFIPLNACSEQAQTVTLQGETMGTITTYKVLNNRDLSPAKIQKRIDDALKEVNRQMSYQTDSEISRPNQHTAGKPLRISDFAHVTAEAVALNRLTHG  
ALDVTGPIVLNWFPGPKSVTRPSEPIKQAASTYTGIDKILQOGKDYASLSKTHPKAYLDDLSIAKFGVVDKVAEGLEKYGIQNYLVEIGGELHKGKNAHGEFWRIGIEQNTIQQG  
NTQIIVPLNNRSLIATSGDYRIFHVDKNGKRLSHIINPNKRPI SHNLASISVSDSAMTADGLSTGLFVLGETEALRLAEQELAVFLIVRDKGYRTAMSEFAKLLR

## SEQ ID 5089

ATGCAGTTTACTTCGAACCGCAGCGCAGTTTACTTACTTGGCGGTAAACCGCGCTTACCGACAGCGAGGGCGCGGTGCGGCTGCTCGCGAGCGGTGAGTGGCAATCCGCGCGCG  
CATTCGCGCAAAAACCGCTTTGCTTTCGCTAACCGTGTCAATCTTACGCTTTTTCGCGCTTTTAAATGTTTGCACAGGTCAAATCTTTCGCGCATGAAATGGAAGCGCGCAAAACAGAGC  
CTGCGAGGCGAGCAGCGCGCTCGAAGGGCGGTTCGCGATTGAAGCGGTGGAAGCGCATATGTCGCGACGATCGGATACGCGCAAGAGGAGCGAGCGCGCAAGAGCGCGCATTTGTCGG  
TCAAATGGTGTGTTTGTATGCGCGGGAATGTTTGCACACAGCGCGCACACTGACGCGCCCGTTCGCGCGCGCGCAACCGATCCGAACCTGCGCGCCCGCAAGGCGCGCGCA

## SEQ ID 5090

MQFYLQPAQFTYLVGNNGFTTSEGRSGCSAAVSGKSAPAFGQKPVLLCVTVSIFSLPLMPCGTQNLNANKWTAKNRRWQAGRRSKGGLALKPVGKAICPHASDTAKGRATATKPHCR  
SNGCFDAPGNVLTTHRHCTAPCAAPQTDNPAAPKGA

## SEQ ID 5091

TTCCTTTTCTTATCGGGATGAAGCCGTGCTGACTTTAGATCGCTTTGAGCAATGCTTGAAGGATTGTTTCTCAAGGTCTGAATGGAACAAACAGCAGTGGCATTAAGCGCGCGCT  
TGGATTCCGTCGTTTTCGTCATCTGCTGGTTTGTGCGGGAAGCGGCGAGGATTGTGCGCGAGGCATTGCACATCCATCAGCGCTTGAGTCCCGAGCGGAGATTGGCGGATTTCG  
CGGAATTTATCGCATATGCTAGGGGTGGGCTGGAACCGTTAAGGTCTGCTGTGGAACAAACAGTTTGGGATCGAGGCGCGGCGGCAAGGCAAAAGCTTATGCGGAGTTTTCGCAAA  
GGCTTTGAGTTTGTGCTGTGGCGCACACAGGAGCATCAAATCGAACTCTTATGCTGCGAGCTGCGCGCGGCGGAGGTTTTCGCGCTTTGCGCGCTTTCGCGCTTTCGCGCTTTGG  
GGGAAACCGCATTTATTCGCGGCTTTGCTGCTTTTTCGCGCAAGACATATGGGATTATGCCGAAACAGCGTTTTCGCGAATATCGAGGATGAAGCAATACCGATACGCTTATTT  
GGGAAACCGCTTTCGCGCACGTTTTCGCGCACTTTTCGCGGAGATTTCCTCATTTTCGCGGCGCATGTGCTGAACAAATGTCGCGCTTTTCGAGAGATTTCGCTTGTGGAAGAGTCT  
GTGCTTCAAGACTCGCTTGGGTTTTCGCGGCGGCTTATTTGATACGCGCGGCTGCTGACGCTTTCCCGCGCGGCAAAACCCATATTTTCGCGAATTTTCTAAAGGAAACCGCATCC  
CCGTCGCGAATCAGAACCGCATTTGCGGACATTTGCCGCGCTTTTTCGCGAGGCAAAACCGGAGCTTGAAGCTTGAACGCTTTGAATTCATCATTTATGAGGAGGCTGTTGTTGCTTTC  
GTGCGAAGCTTTGCAAAACCGGCTTTTCTGAAGATGCGGACGATAAGCGGAACTTCAAAACAACTACTGACAGAACATAGATTGTGTTTGAAGCGGCGATCCGTTTCGAGCTTTCCTGAAGC  
ATGTTGGAACAGGACGGGATTTTGAAGACGCTAGCGCATCGGATACGTTGCTGTCGCGGCGCATCCTAAACAAATGTGAAAAAATCTTCAGGGAACCGGCTTTCGCTTTCCTGCGC  
CAATTTGGCGCTGTTGCGGACAGCGGAAACCGTCCATTTGCGCTTGCAGAACTGTTGTCGAGATTTCAAATCTCGGTTTCAGACGCGCATTTTTCGCGTACATCTGACTTTCCTATTTT  
ATTT

## SEQ ID 5092

LLFLYRDEAVLFLDAFQCLKDCFPQGLNGKKTAVALLSGGLDSVLLHLLVCAGKRAGFVPEALHHLHGLSPRADWDADFCRNYCDMLGVGLVETVVKVCEKNGLIEAARQKRYAEFAEK  
GFDVLALAHHRDDQIEFFMLAVARGGGLRALAAMPVRLPGENGIIWRPLLPFSQDIWDYARKHGLPNIEDESNTDTAYLRNFRHRLPELSAQIPHFGRHVLNNVRLQEDLALLEV  
VVQDCRWVCGAGYFDTARMLTTPRRKTHILRNFLKENGIPVFNQNALADIARVLTEAKTRWNILGPELHYAGRLVFFASEQLAKPAFLKDTISGNLKKILT EHRFVLKRHPFGLPEA  
MLEQDGLIRTVASDTLAVGGIHKNVKILQGKRVLPFLRPINPLVADSGNRLALANCCADPQISVSDGILPVHPDPPIIF

## SEQ ID 5093

TTGGATTTTGAACAAACCATAGCCGAACCTGACCAACAAATCGATGAGCTGCGTTTCTGTCGAAGCAGGCTGCGCTCGATATTTTCGAGCAAGAAATACACCGTTTTCGAGAAAAAGCAACG  
ATTGACCAAAATCGATTTCGCAAACTCACACCGCTCAAATTTACAGGTTTCCCGGATCCGCGAGCTCCCTATACTTTGGATTACATTGACCGGCTGTTTACCGATTGGAAGAGCT  
GCACGCGCAGCGCATTTTCGCGAGCATCATCGGATTGTCGCGGATTGCGCGGTTTCAACGCAACGAGCTGTGGTCTGTCGCGGATCAGAAAGGCGGACACCAAGAAAAATCCCG  
CGCAACTTCGCTATGCCCGCTCTGAAGGCTACCGCAAGGCGCTGCGCTGATGAAACGCGGAAAAATTCGGCTTTCGCGCTCATGACCTTTATCGATACCGCGGCGGCTATCCCGCA  
TCGCGCGGGAAGAACCGCGGCGAGTCGGAAGCCATCGGCAAAACCTGTACGAACTGACCGGATGCGGCTTTCGCTTTTGTGTACCGTCATCGCGGAGGCGGTTTCGCGGCTGCGTTCG  
GGTCCGCGTAGCGATTACGCTCAATATGCTGCAATATTCGACCTATTCGCTTATTTCCCGCAAGGCTGTGCTTCGATTTTGTGGAACCGCGGAAAGGCGGCTGATCGCGCACAGGCT  
TTGGGTATTACTGCGACCGCTGCAAAAGCTGGAAGTTCGCTGATACCGTCATTAAAGAGCTTTGGGTGTCGCGATAGGAGTTTCGCGCAACCATGAAACGTAAGAACCGCTTTTG  
AAAAACACTGCAAGGCGCAAGCATCCCGCTTCCGATTTGCTTTCGCGCGTTTCGACCGCATTAAGCTTACCGCAAAATTTTCGGAACAA

## SEQ ID 5094

LDPEQPIAELTNKIDELRFVQDESAVDISDETHRLQKKSNDLTKSIFSKLTPAQISQVSRHPQRPYTLVDYIDALFTDFEELHGRHFAADHAI VGGARFNGQSVVVVHQGRDTEKIR  
RNFMPGRPEGRKALRLMKTAERFGLPVMTFIDTPGAYPGIGAEERGQSEAIGKNLYELTRLRVPLCTVIGEGSGGALAVAVGDIVNMLQYSTYSVISPEGCASILWRTAEKAADAAQA  
LGITADRLQKLDVDTVIKEPLGAHRDFGQTNKNVAVLEKQLHEAQSLPIADLLSRRFDRIMAYGKFSQ

## SEQ ID 5095

TTGTTCAAAATCAAAAAACAGGTTTCATAAAATGAAGCTCTCATCAACAGATTCTCGCGCTATCATACGCTATTTGTGCTATTTCCGAGT

**SEQ ID 5096**

LFKIQKNRFHKMLSSSTDSAAIIRYLCTFRS

**SEQ ID 5097**

SEQ ID 5097  
ATGAAGAGCAAGCACGATCTCTCCGCATCGGGCTGGACAAATGGCTTTGGCGGCGACGTTTTCGAAGACCCGTTCCCTTGCACAAAAGCATATGCAACTGGGTAGGGTTCAAGTAAACG  
GCTCGAAAGTCAAAAACAGTAAAAACATAGACATCGGGCATATTAACGACTGACGCTCAATTCCCTTCCCCATAAAATCAAGGTTAAAGGTTTGAACCAACACGCCGCCCGGCACCCGA  
GGCGCGGCTTCTGTATGAAGAAGACGCCGAAAAACGGCAGCATTGAGGGAAGAGTGCAAAACAGCTCGACCAATTTCAGCCGATCACTTCGCCCATCCCGACGGCAGACCGACCAAGCGCGAC  
CGCGGCCAACTGGACAGGCTGAAAAAAGGAGACTGG

**SEQ ID 5098**

SEQ ID 5098  
MKDKHDSANRLDKWLWAARFFKTRSLAQKHIELGRVQVNGSKVKNSITIDIGDIIDLTLNSLPHKIKVKGLNHQRRPAPPEARLLYEEDAKTAALRECKQLDQFSRITSAHPDGRPTKRD  
RRQLDRLLKKGDM

**SEQ ID 5099**

SEQ ID 5099  
TTGCCAAGCTGCTCCGCTAAACATACAAACCGATTAGGAACACCATGAAAACCCCTGCTCCTCACCTTCGGCATCTTCCTGACCGTCATCATCGGTATGGCGGTCCGGCTATATTTTCTCCA  
AACGCACCATCAAAAGGCAGTTGCGGCGGCATTACCGCTTAGGTATGAAAAAATGTGCGACTGCACACACCTTGCACACCCCTGCAAAAAAAGCTGGATGAAGAAAAACAGGCAGGCGG  
CATACGGGTTGACCGT

**SEQ ID 5100**

SEQ ID 5100  
LPSCSAKHNTNRLGNTMKTLTLLTFGIFLTVIIIGMAVGYIFSKRTIKGSCGGITALGMKKMCDCTPCTDLOKKLDEEKQAGGIRVDR

**SEQ ID 5101**

SEQ ID 5101

ACATCCCGCCTCTTCCAAAACCGCGCGCGGCCAAATCCGCCGTATCTTTTTCACACGAGGTGCAACGCCGCCGAAATCCTGTGTGACGCGCGCAACCTTATCGGGGTGTTCTGACCAAG  
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CATAGACTAGGTGACGCGCGGAAATCTGTAGCTGTATGCACCATCGGACGCTTGCAACAACGCCACTTCAAAGTCGCCGTACCGGCTGTTACCGACACCGCATCCGCCGCCCTGCAACACGGT  
TTACAGACTCTGTCTGCGTTACCGTAGCGCCAATCCGCGCAAATCCGCCGCTGCAAAATCTTCGCCAAACGCCGCTTCTGCTCGCTTCGTTGCGCGCAGGACAGGAAAGCGCGCGCGGTA  
TAGCGTTTCCAACAACAATAATGCGCTGTGAAAAACACCGCGGCCATATAGATCGATTTCGCTGACGCGGCTGCCCGGACAGCGGCGAATGCGGGCATGCGGAGATGCGCGCTTCCGCGGCTT  
TCCGCGCGCTTTCACGGTCGCTTTCAAAGGGCATAAGCTGTGCCATCGGATGACCAGCAAACTCCGACACAGCTGCACATATGACAGGGTCGGAATGCCGCCGCTTTCAGCTTTTCCGCCACACCGAGATTA  
CGGGTTGACCTGATGCACGATTTTGCCACCAGCTTTCGCGCGCGCACGCCCAACCGCAGCGACTGCACATATGACAGGGTCGGAATGCCGCCGCTTTCAGCTTTTCCGCCACACCGAGATTA  
AAATCCGGGCGCATCGATACCGACGAAGACATCAGGTTTCAACGACAGCAAATCCCGTACCAGTCTCCTGCGTATCGGTAAATTTCCCGCAGCGCGCTGACCACTTCGACAAAGCCGCGCA  
CCGCGACCGCTCTGTATCATAAAGGCTCTCGAAACTTCCGCCCTTCATCAGTTCCCGCGGATGCCGGTTAACCGTGCTGCGGGCAACGCTTTCGATGGCGCGTATCAGGTGCGCCCC  
CAACAGGTGCGCCGACGCTTCGCCGACACTGACGCGCAATCAAAGGGCTTTTTTTATCAACCATATTCGTCTGTCCCGACATATAGTGGATTAACAA

**SEQ ID 5102**

SEQ ID 5102  
 TSLRFQNRARGQIRRIFFQQQVQRPETLLQRGNLIGVFPVVRQCRQQFFRFCEFLQ\*FRHGLLTQQDIRQADMRHDFAFHISIGQRENLVADHRTLAQRHLSRRTARYQHRIRKPAHR  
 FRLSVGYQRQRSGKLRPLQNFQTPQLRLKRCGRQQEAGGGIAFQQ\*CRLKXHRHRLVDPADAAGQQGEYGDADIRAQSFPRRFTVVPQGHKLCHRMTDKLRTSARTEIKRLRHEQAQH  
 AVDLMHDFAHAFAPPRNRRTDIMQGRNARPOLPFRHTQIKIGRIDTDKDIRFORQQIPYQLPAY\*NFROPDPDHDKAAHRQPLLIKALETFRLHQFPADAG\*PCLRATLSDGAYQVRP  
 QQVARRFADTDGNQRAFFINHRLSPHIVD\*Q

**SEQ ID 5103**

SEQ ID 5103

GTGCTTCCTGTTTGCAGCGGGGAATGGTTTTACCAAGTCTCCTTTTTTCAGCCGTGTCCAGTTGGCGGGCGTTCGCGCTTGGTCGGTCTGCCGTCGGGATGGGCGGAAGTGATCGGGCTGAATTGG  
TCGAGCTGTTTGCACCTCTTCCCTCAATGCTGCGGTTTTGCGGCTCTTCTCATACAGAAGCCGCGCCTCGGGTGCCGGGGCGGCTTGGTGTTCAAACTTTAACTTTGATTTTATGGGGAA  
GGGAATTCAGCGCTCAGGTCGATAATATCGCCGATGTCATGTTTTACTGTTTTGACTTTTCGAGCCGTTTACTTTGAACCCCTACCCAGTTTCGATATGCTTTTTCGCAAGGGAACGGGCTCTT  
GAAAAAAGCTGCCGCCCAAAGCCATTGTCCAGCCGCATGGCGGAAGAATCGTGCTTTGCTTTTCATACGATTTTGTGTTGAAATAATTGAATTTGTTTCGAGTTTAGCA

**SEQ ID 5104**

SEQ ID 5104  
VLLFAAGMVLVPSFFQPVQLAAVALGRSAVGMGSSDAELVELFALFPQCCRFRVFFIQKPRLGCRAALVVQTFNLDPMGKGIERQVDNIADVYGFVTFDFRAVYLNPTQFIMLLRKGTGL  
EKTCPKPFVQPHGGRIVLVFHTILFELIEFVSSLA

**SEQ ID 5105**

SEQ ID 5105  
ATGAAATGGACCGATACCCGGCGCATCGCGAAGAAGCTCTACGACCTGCACGGCGAAGCCATCGATCCAAAACCGTGGCGTTTACCCAAGTGGCGGACCTGATTATGGCATTGCCCGAAT  
TTGACGACGATCCCGCCCGTTCCGGCGAAGCATCTCTGAAGCCGTGCAGCAGGCATGGATAGACGAGGCGGAA

**SEQ ID 5106**

SEQ ID 5106  
MKWTDTRRIAEELYDLHGEAIDPKTVRFTQLRDLIMALPEFDDDPARCGERILEAVQQAVIDEAS

**SEQ ID 5107**

SEQ ID 5107  
ATGTTGCCCGTCCAAATATTGATACAGTTTGCCTATCAGCAGAATCAGCGCGTCAAACCTCCTCCATCTCCGACAGGGAGTCGGGATGGTCCGAAGCGGTATAAACCAAGTCTCGGACAATTTT  
GCGGCAACAATATATTGTTTCATCAATCTCCTTATCGGTGTAACCCCGCTCTCTCAGGCGGGTAGAATCAGATTGTTTGGGAGGGGTAACCTCTCCCGGATCAGGACACACATAAGGTGGT  
GCTTGATGTGCCGTCCGCGAGTTGAAACATTAGCCATCTCTCAGGGCGGCGAGTTTTCGCGAAACATATCTTACACGGCTTCAATGCCGACGATAAAGGAAATTTATA

**SEQ ID 5108**

SEQ ID 5108  
MLPVOYLIOFAYQONQAVKLLHLRQGVGVGSGINQFQCGKHIVHQSSLSVETPLFRAVESDLFGRGNSSRIRTTHKVVLLDVPSELKHSAILKGRQFCRNIFTTASMPDDKRFY

SEQ ID 5109

SEQ ID 5109  
TTGCGGAACGCCCTTCCGAGTCGGTCGGCGGCTTCACGGTTGCGGCAGAAAGCGTGTCCCGCGCTGCCCGAGCTTGAAGGACGCTATCTCGACCTTGTCGCCGCGCGCCGCTCTCTT  
TCGGTTTCGCGCAGGACAGGCAATCCGGCAGCGGGCAGGAAGAAACGCAAGCGCGCTCAGATGCCGTATCCGGTCGTTCCGTCAAAAAACCGTAAATAATCAATATAGAAATCGAAAGT  
TCCGCTTCACAAACGCTCTGTTTTTCGG

SEQ ID 5110

SEQ ID 5110  
LRNAPPSRSGGFTVAAESVSAACFELEGRYLDLVRRAAVSFGFAQGANPAGGQKETQAASDAVSGRSVKKPIKINIESKVPSSQTSVFR

SEQ ID 5111

[illegible]

CCAATACCGTGG  
SEQ ID 5112

SEQ ID 5112

**SEQ ID 5114**

**SEQ ID 5115**

**SEQ ID 5116**

SEQ ID 5117

SEQ ID 5118

**SEQ ID 5119**

SEQ ID 5120

SEQ ID 5121

SEQ ID 5122

SEQ ID 5123

SEQ ID 5124

SEQ ID 5125

ATGATGGGAGGGAAAGCGGATTTTATCGGTATTTCGGCGTAGAGGGCAATTTCCGCGCGCAGCGCCCAATCTCTAGCGGTTCGTCTAACTATCGCGCAAAATCTGTTAAATGCCGCCTT  
CCTTCCTTTACACACCGCAGCAGACAGCGAGCAATTTAFGGCTCTTTTTCGAGATTTACAGAACCGGGTATGTCCGCGCCCGCAGCGGCAGATGTTGGCGGAGGCATCGATTTGGGTACGAC  
CAACACGTTGGTCGCCACCGTCGCCAGCGCAGTCGCCCTGCTTCGCCGACGTGCCAGCGGGCGGTATACCCTGCTTCGGTCGTCGCTATCTGGAAATCGCGCGGCATTTGAAGTCGGCAGCA  
ACGCCCTGTTCGCCCAAAAAACGACCCGCTGAACACCGTCAGCTCGCCGCAACGCCCTATTCGGCGCGACTCTTCGGCATCTGCATCAAAATACGACATTAACCTGCCCTTACCCTGTTCGGCG  
ACAATCAACGCTTTATCGAACTGCATACGCGGCAGGGGTGAAAAACGCTGTGCAAGTGTCGGCGGAAATCTCAAAACCTCAAAATGCGTGCCGAAGAAACCTTTGGCGGCGGATTGGT  
CGGCGTGGTGATACCGTCCCGCTTATTCGACAGCAGCGCAACGCCAGGCCACAAAGATGCGCGCGGTCTTCGGCGGTTGAACGATTTAGCGCTGTCTCAACGAACCTACCGCGCGCGCA  
ATCGCTCATCGGCTGGCAACCGCTCGGAAGGCAGCTTTGTCGTACGATTTTGGCGCGCGGCACGTTCAAGCGTTCCTGTTCAACTGACCAAAAGGACTGTTTGAAGTCAAAGGCCACCG  
GTCGCCAAGACGGTGTGGCGCGCGATGACTTTCGACATCTGTTTGTGTTCTGCTACCTGTCGACACGCAAAACAGTCTCCCACTCAACGAAACAGACGAACTGCTCTGCTGCTGTGTCG  
CGCGCGCAAGAAACAATTGACCAACGCAAAACCGAAGCGCGCATTCAGCGCAGCGCTTTCAGCGGTATGGCAATCGACACAAAGCATCAAGTCGCGCGGAGTTCCACAACCTGACGACGCAATTTG  
GTGATGAAAACGCTCGAGCCGGTCAAACAGCGGTGTGAAGATGCGGTTGTCGGTAAAAACGAAGTCAAAGGCGTGGTTATGTTGGCGGTTTCGACCCGATATGCGCGCAAGTCCAAACAGGCAG  
TCGCGACCTTTTTCGGAACAAACCCCGCTGAACAACTCTCAATCCCGACGAGAGTCGTCGCGCTCGCGCGCAGCCATACAGGCAAAACGCTTCGCGAGGCAAAAGACCGCGAGCGGAATGCGCTCT  
TTGGACGTTACCCCTTTCGCTCGGTTTGTGAAGAACTACCGCGGCTTCGCGGCAAAATCATCCCGGCAATTCACCATCCCACTCCCGCGCGCGCGAGGACTTTTACCACCTTTCAAAGAC  
GGTCAAGCGCGATGACGATACACGCTGTGCAAGCGGAACGCGAGCTCGTTTTCGCAATCGCGCAGGCTTGCCTCAATTTACCCTTCGCGGCAATTCGCGCTATGCGGCGGGGTGGCGCGGCT



TCCGCGTTACCTTCCAAATCGATGCCGACGGTTTGTGTCCGTTTCCGCCAAGAACAAGCACCGGGGTACAGGCGCAATCGAAGTCAAACCTCTACGGTTTGGACGATGACACCAT  
 CACCCAAATGCTCAAAGACAGCATGGGCAACGCCCGGAGATATGGCGGCCGCCCGCGCGGAAGCGGTGGTGAAGCGGAAGCGGTGACCGATGCCGTCAACGCCGCCCTCGAGTTG  
 GACAGCGATTGTGCGTGAAGCGGAGATTGCAAAATCCAGCGAGACATCGCGGATTGCAAGCGCGGTGAAAGACGCTGAAGACATCCGTGACGCTGTGCGCAAACTCAGCC  
 GCAGCAGCGCAATTTCCGCCCAAGCGCATGAACCGCAACATCCACGTGCGCTGACAGGTGAGGTGTCGATAATATT

## SEQ ID 5126

MMGGKGGFYRYLAVBENFGGTAQSLAVCSITIGANSVKMPFSLYTPHROAEFMALQISEPGMSAAPHRRHLAAGIDLTSTNSIVATFVRSGSAACLEPDADGRVTLPSVVRYLENGGIEVGK  
 TALSQKTDPLNTVWSAKRLIGRTLADLHQNTHYLPYRFQDNQRIELHTRQGVKTPFEVSAEILTLKLRABETLGGDLVGVVTPVPAFYDDAQRQATKDARLAGLNVLLNLEPTAAA  
 IAYGLDNASEGTFVYVLDGGGTFDVSVLQTLKGLFEVKATGGNSALGGDDFHRLFCYLLLEQNRLSOLNEQDSOLLLSLVRAAKEQLTQTEARIQATISDGMADTSISRAEFHNLQRL  
 VMKTLRFVKQALKDAGVGKNEVKGVMVGGSTRMPHVQQAATFFGQTPPLNNLPDEVVALGAAIQANVLGNKADGEWLLDVTPLSLGLETTGGLAEKIIIPENSTIPTARAQDFTTFD  
 GQTAMTLHVVGGERELVSDCRSLAKPTLRGIPPHAAGAARIVTFFQIDADGLLSVSAQEQSTGVQAEIVKPSYGLDDDTITQMLKDSMGNAAEDMAARARAEAVVEASLTDVNALEL  
 DSDLLDAEFAQIQRLADLQRLKDGKAEDIRAAVAKLSRSTDNFAAKRMNRNIQALITGQSVNT

## SEQ ID 5127

GTGAAGGACTCGCATATTGCCGCAAAAAGCAGAGGAAGCCGCTCCAGTTTGTGCGGCTTCCGTTTCTGACTCAGGAAAAACAGGATGCGGTAAAGGTTCTGTATGCCCTTTGGC  
 GCGAATGGACGATGTGGTTGACGAATGTTCCACCCCGATGTGCACAGGCAACATGAACTGGTGGCGCGCGATTGGACAAATGCGTTGCGCGCGCGATGCGCGCAACCCCGTCAA  
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 GCGCTGTTGAACGAAATCGACCGAGACGCGCGCAAAACGCTCTCAATACAAATTCGCCCTCCCTTCCGCGCGCAAAAACGCAATTGCCCTGAAACCTGGTTATTTCGGAATCAACCGC  
 GCGCGCGCAGCGCGAAGCGGCA

## SEQ ID 5128

VKGLDYCRQKAESRSSFLSGFRFLTQEKQDAVTVLYAPCRELDDVDECSNPVDAQATIANWRRGLDNAPGGAMPEHFNQALRVKETFPLPKYLEALIDGMQMDLVQARYGSFEELK  
 LYCRVAGVVGCLIRIILGPSDGKLTLEYADKMLGALQLTNIIRDVGEDARRGRIYLPMEEMQRDVPASVILQCSPTGNFAELWAFQIKRARETYREAVSLLPDADKAKQKVLVMAAVYY  
 ALLNEIDRGAQNVLKYKIALPSPRKRILALKTWLFGFKPRGTPERA

## SEQ ID 5129

ATGCCGCTGAAGCCCGCGCGCGGGTTCAGACGGCATGCGCGCTTACTTCGATCGGTTTATACGCAAAACCGCGCTTCAGGAAATAAATCAGATTATTCCTCCAGACGCGCTTCAGGCTCC  
 TTCGCTGCCACCGTAACCATAGCGCGGCGCAACACAGGTCGACAGGGTAAACCTTCTTCATACACCAACACCGGATTTGGGTTCCTGCTCAGTGGCCACCGCTGCATCGCTGAT  
 GGATATTCGATCGAGCTTATCGCGCGCTTAGGATTTGATTTCTGATTTCGCTGGCATCAACGCGCTTCTGCAACTCATTCAAAGTCACTGCGACACCATTTTCAGCGCATCGAATTT  
 ACCGCTCTGATCCAAAGCGCGCATTTCCAGATAATCTTGACCGGCAACATTTCCACGGCAAACTTCTGTCGCGCAACTTGTGCGGTAACCTGTCGCTATCGGCAATTTCTGCTGGTGGCGCGCGCGCAG  
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 CATTTCTACTGTCGCGAGGTTTCCACCGCTCCACATTTTCAACCGCTTCTTCACTGTTTTCGCTGCTGTCGTCGTCGCTATCGTATCCCTCAAAACAAATTCGGAATCAAAATCC  
 GGTATTACCGGAGCAAGATAAGGACATTTTCAAGAACTTCAAGCAAGGAGGAAATTTCAATCCGCGCGCGAATACCTTACCGCAAAACCATATATAACGG

## SEQ ID 5130

MPPEARPAGSDGIAALLRSVYTONALQEQINLIIPQTPSGFLPCHRNHSRAQHTVGQGITLHHTNHGIGFLITGHRHLRLMDIRIELIARFRIDFLDLRGLIKRLQLIQSHLHTHFQRIE  
 TALIQKRHFQILDRQHFHGLKLSGLVLRIGNFLVAAQVLLVCQAQLFVFLRFLQNLPRQLIILSRGLSFLFYTVRISYCLDGFHRLHIFNRFPTVLLLCPLAHIVSLKTNWKS  
 GYPSKIRTFSRNFKRQRLSHPPNTLPQPKYKR

## SEQ ID 5131

TGTGTTTTAATCTCGGCTTCTTTGACCGGATCGTACGATCCGAACCCCAAGCATATGGCGTGCAAAACAGCGATAAAACAGATAATGTTAATAGATTAAACCGACCGCTTGTCTTCTTC  
 AGTGTCATGAGAAATTTCTCTTGTCAAGTGT

## SEQ ID 5132

LFLISASLTGSYASEPQAYGVQNSDKTDNVRNLRPLACFPQCHEKFSFVKC

## SEQ ID 5133

ATGATGAACACCGCGCATCGCGCGCGGAAATCGCGCTCATCGGCGCAGGCTGGCGCGGCTTGTCCGCGCGGTCACCTTGGCGCGGCACGCGGAGCTTACCTGTGTTGAAGCGCGCGCGC  
 AGGCGGGCGGAAGGCGCGCACACTGGCGCGGAATACCGACGCTTTCGGTTTTCGGAACAGCGGCGAGCATTTCGCTGCGCGCATACCGGGCGGTGTGCGCGTGTGAAACCATCGG  
 TTCAGACCGCGCGTGGCGCTTTTTCGCGTACCGCTGCATCGGCGATATGCAAGCGGTTTTCAGTTTCGCGCGCTCCCGCTGCGCGCGCGCTGCATATTTCGCGCGCGGTGCTGCTTGC  
 CGCGCGGTACCGTCCGATTCAGAGCCAACTGCTTGCAGATATGTCGATTTCGAGAGTTCGCGCGCGCTTTCAGCGGCTTCAACGCGCTTTCGGAACCGCAAGCTTTCGCGGTGTTGTCGCAACGTTTTCGCGCGCGGTGTCGACGAAAA  
 CGCGTGCAGCGGTAATGCGATTTCGAGCGCTTGTGTCGCGCGCGCTTTCAGAGCGCTTTCGGAACCGCAAGCTTTCGCGGTGTTGTCGCAACGTTTTCGCGCGCGGTGTCGACGAAAA  
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 AACACCTTCCCGGACGGAAGTCTCTGTCACCGCGAAGCTTTCGCGCGCAATGTCGCGCAACCGCTTTCGCGCGCGCTTTCGGAACCGCAAGCTTTCGCGGTGTTGTCGCAACGTTTTCGCGCGCGGTGTCGACGAAAA  
 CGCGCATATCAAAACCTTTCGCTACCCAGCGCATCACACCGCTTATCTGCGCTACCGCGAAGCTTTCGCGCGCGCTTTCGCGCGCGCTTTCGGAACCGCGGCTTTCGCGGTGTTGTCGCAACGTTTTCGCGCGCGGTGTCGACGAAAA  
 CGCGGCGCGGCTCGGACTGCGCGGAAACGAGTCTTCGCGCTTATGCGCTTTCGCGCGCGCTTTCGCGCGCGCTTTCGGAACCGCGGCTTTCGCGGTGTTGTCGCAACGTTTTCGCGCGCGGTGTCGACGAAAA  
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 CGGACTACCTCCACCGCACTACCCGCGCACGCTCGAAGCTGCGCTACAATCAGGTTTCGCGCTGCGCGGAGGCTTTCGCGCGCGCTTTCGCGCGCGCTTTCGGAACCGCGGCTTTCGCGGTGTTGTCGCAACGTTTTCGCGCGCGGTGTCGACGAAAA  
 CGGACGCTTTCAGAGGTGCGCGCAAAACGCTAAATACAT

## SEQ ID 5134

MMNTPHPRPKLAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLDNGQHILLGAYRGVLRIMKTTIGSDPRAAFRLRVPLEWHEHGLQFRALPLPAPLHILGGVLLA  
 RRVPSAFKAKLLADMSDLQKSARLQPDITVAQWLKQNVPRAAVMQFWOPLVWGAINTPLETASLRVLCNVLDGVLTKSGSDYLLFPKQDLGATVAEPALAEQLRLGADIRLETRVCR  
 NTLPDGKVLVNGEAFDAALATAPYHAAALLPEGTPEHVQTAYQLRYHAIITVYLYAEFVRLPAPLTGIADTAQWLLCRGLGLPENEVSAVSVSDRVGAPANRAWDKAHADLKRI  
 LPHLGPRAVRVITEKRAFTATDAPPDLSWLHRRHIFPTGDYLEHPHYATLEACRTIRFRVGGSLPAKPERCRLKTPAGITGLYKVRQNAKTH

## SEQ ID 5135

ATGCCGACACTGACGCAAAAACCATCTTAGTTACCGCGCATCGCAAGGCTTGGGCGAAGAGGTCGCCAAAGCTTACCGCGCGGAGAGGGCGACCGTAATTCGTTGGCAGCGCATCAGA  
 AAAAATCGGAAAGGCTATGACGCGATTGTCGAAGCGGACACCCGAACTTTCGCGCATCGCTTTCGACCTGATGAGTGGGAGGAAAGAAATTCGAACGCTTTCGCGCGCAACCATTCG  
 CGAAGCCACGCAAGGCAAACTGACGCGCATGTCCTACGCGCGCTATTTTTCGCGCTTTCGCGCGCTGAGTTTTCGAACCGCTGCGCGAATGGGTCAACCAATACCGCATCAACACCGGTC  
 GCGCGGATGGGCTGACCGCGCGCTTTCGCGCTGTCGAAGCAGTCCGCGACGCGTCCGCTATCTTCGTCGCGGAAAGCCACGCGCAACCTTCCTGCTCCCGCGCGCATCAATTCGCGCGACGATCAAAATC  
 CGTCCAAAGCGCGTTGAATCTGTCGAAGTCCGCGCGGAGAAATGGGAACGCTTCGCGCAACCTTCGCGCGCAACCTTCCTGCTCCCGCGCGCATCAATTCGCGCGACGATCAAAATC  
 CCATCCGCGCGAAGCGGAGCGAAGCGCAAAAGCTACGCGGACGCTACGCGCGCATTTGCTGTTGGGCAAGTCCGCGAAGCAAGGCGGAGCGCGGAAATCGTTTACTCT

## SEQ ID 5136

MPTLFDKTLVLTGASQGLGEQVAKAYAAEGATVILVARHQKLEKAYDAIVEAGHPPEFAIRFDLMSAREKEFERFAATIAEATQGLDGIHVCAGIFYALSPLDFQTVAEVWVYRINTV  
APMGLTRALFPLKQSPDASVIFVGEHGFEPKAYWGGFGASKAALNVLCKVAADWERFNGNLRANVLVPGPINSQRIKSHPGEGASERKSYGDLVPAFVWASAESKGRSGEIVYL

## SEQ ID 5137

ATGCGCGCGGAAGGTACGGATATTTTCAAACGGAAGCGCGCGCGGGGATGCTGCTTTTCCGGATTTAGAGGTAAACGATTTCGCGCGTCCGCGCTTTGCTTTTGGCACTTGCC  
CACCAGACAAATGCGGGCAGTACGTCCTCCCGTAGCTTTTGGCTTGGCTTCCGCGTTCGCGCGGATGCGATTGATGCGTTCGCGGGAATGATGCGGCGCGGACGAGGACGTTGGCGCGCA  
GGTTCGCGAAGCGTTCCCATTCGTCGCGCGGAGCTTTGCACAGGTAGTTCAACGCGGCTTTGGAGACGCGCGGAAGCGCGCCCAAGTAGGCTTTGGGTGTTTCGCGCTGGCTTTCCGCGCA  
GATGACGCGACGCGTCGCGGAGTGTTCAGCAGCGGAACAGGGCGCGGTCAGCCCATCGGGGCGACGCTGTTGATGCGGTATTGGTTGACCACTTCGCGCGAGGTTTGAATTCAGC  
GGCGAGAGGCGCTAAATAAGCGCGCGAGTGGACGATGCGCTCCAGTTTGGCTTGGCTGGCTTCGCGCAATGCTGGCGGCAACCGTTTGAATTTCTTTCTTCGCGCACTATCAGGTCGA  
AACGGATGCGCAAGGTTTCGCGGCTTCGACAAATCGCGTCATAGGCTTTTTCAGTTTCTTCTGATGCGGTGCCACCAAGATTACGCTGCGCCCTTCGCGCGGCTAGGCTTTGGC  
GACCTGTTCCGCCAAGCGTTTCGATGCGCGGTAAAC

## SEQ ID 5138

MRAEGTDIFQNGSAARAGCLPFPDLEVDPAAPFFAFGTCPDKCGYVVPVAFASGFARMGFDALRGIDGAGDEVDGAQVAEAPFVGGDFQVQVRGFGRAEAPFVGCPFAVAFAD  
DDGRVGRLLQREQAGQPHRGDGVDAVLVDPFGDLEIQRREGVKIAGAVDDAVQFALRGFGNGGKPFEPFFFRTHQVETDGEFGVSGFDNRNVIQFPQFLMACHQNYGRPGVGF  
DLFAQALRCAGN

## SEQ ID 5139

ATGAAAACCGTTTCCGCGCGCATCGCTTTTCCGCGCGCTGCGGTTCCTGACCGGCTGTGCGACCGAGTCTCAGCGAGCTCGAGGTTCGAAAAGTCCGCTCTCGCAATACGCAATATC  
ACGGTGTTCGCAACCGGATTTCCGTCGGAACATTCGACACCGCTCCAGCTTCCAAAAGGCAATTTTTCGCGACAGTGAAGACCGCTCGGGCAGCGAGGCAAAACCATCTCGGTAACACA  
CCTGCAACAAACCAACCGCTTCAACGTACTGAACCGCACCAACCTTAGCGCATTTGAAACAGGAATCCGCGCATTTCCGGCAAGCGCAGAACCTGAAAGGCGCAGATTATGCTTACCGCG  
GATGTAACCAAGTTCGAGCGCAGAGATGTCGGCGATCATCAGCTTTCGCGCATTTTGGTTCGCGGCAATCGCAATCGCTATGCAAAAGTGGCTCTGAAATATCGTCAACGTCATATCTT  
CGAAATCGTCTATTCACACAGGCGCGCGGAATACGCACTTTCACACCGGAAATCATCGTTTCGCGCGCACTTCGCGCTACGATCGCACTTGAACGCGCAAGTTTATAGCTTGGC  
AATCCGCGAAGCGCTGACAACTTGGTTCAGGCTGTCGACACCGCGCATGCGCAATCCACCGT

## SEQ ID 5140

MKTVSAALAFAAAVSLTGCATESSRSLEVAKVASCNTQYHGVETPI SVGTFDNRSSQKGI PDSSEDRIGSQAKTILVTHLQQTNRNFVNLNRNLNLSALKQESGISGKAQNLKGADYVVTG  
DYTEFGRRDVGDHQLFGLIGRGKSQIAYAKVALNVLNVTNVTSEIVYSTQGAAGEYALSNRELIIGFSGTSGDATLNGKVLDLALREAVDNLVQAVDNGAQNSNR

## SEQ ID 5141

TTGCGGAAGCGCCCAACAAAAAATGAAATCGCGCGCGGGTGGCAGCGCCCATTTGGGACTGCTGCTTTCCCGTTCCGGAGACAAAGAGGCGCGCTTCGCGCAATTTGAAGAAGAGAAAA  
GGCTGTTTCCCGAATCGCGCGTATTATGGAATCTCTGATGAAACCGGTAAGGAGGCAAGCA

## SEQ ID 5142

LRKPPTTKKNAAPGAHAHLGLLLSRSGDKGAPRQFEKRLFPESGVFMDFLMTGKGGKR

## SEQ ID 5143

ATGAGAAATTTCTTTTGTCAAGTGTAAAGTTATAATGATTATATATACACTACATCGCAATGAAAAATCGGGAAAAACAAAAACCCCTCCGCGCTCATTCGCGGAAAGCGG  
GAATC

## SEQ ID 5144

KRNFPLSSVKVIHIIYITLHREKSGRTKNPSAVIPAKAGI

## SEQ ID 5145

CATTTTCGTCGCTTTTCCAAACATCACCGCAAAATCGCGCGCGGCTCCGCTTCAACACACGCGGCTACCGCTGAGCGGATGGTTAGGTCGAGCTCGGACGCGTGCAAA  
AACATGCGCTTCAAACCAATTTTCGCAACGCGGTCGCTGATAATCGCGTAGGCTTCGTCGCGCGCAATCGGACAGCTTGAGATTTCAGATGACGCGGATTTGGTTCGTCAGGC  
CGCTTTTCAGCGTTCGCGCGCACCAGAGTCAGGTGCGACAGCGCGACACCGTGCAAAATCGCGCTCTGAGAAACGCGTTAACAACAGAACACGATGCGCGGAGTCCCGCTCTCGCTGAC  
GCGTACCATCTTTTCGCTTGTGCGCGCGGTATTTGAACAGGGGAGTTTGACATGGAATTTGCTGCTCCGCGAGTTTGCCACCCCGCAGCGCAAGGTAGATTTTTGGGGTGGTCTGTTA  
CGGATAGCTTTCGTCAGTTTTCAGCAGCGCGCTGCTGTTCTTCGCCACCATCAACAAGCGGCTGATCTCTGTCGCAACAGGTGGACCACTCAAATACTTCGCTTCGCGAGCGGCGCGG  
GCACTGTTTCGATACGACCGGAACTCACGCGCTGCGACCGGTACCGCGCACCGGGAAGGCTTATTTGACCAACAGTAGCGGCTGCTCTCATACACCACTCAAACGCGACGCGCGGTAC  
GGCGGCGACGCTTTCAGACGGCATTTCTTCTCGCCACGCGCACAGCGGGAATCGGACCGGTATCTCCCTCCGCAATACGGCTGTCGGGTTTCAGCGGTTTCTGTTTAAACCGCACCTCG  
CGCGCGCGATTAATCGGTGGATATAGCCCTTGGGACGCGCTTGGAGATTTTATCAGATAGTTATCAAGGCTTGACCGCGCTCATGTCGCAACCCCTATCAGGCTGACCGAACCTT  
TGCTTATTTCGTCGCTTTTCAT

## SEQ ID 5146

HFRPVQPHRLQIRRLRLQRLTRERMVQVQGRVQKHALQTOFLQTPVRLIIAFAVARNRTRALRLQMHADLVRTARFQRCPHQSQVRQPDVQNAV\*ETA\*HTEHRHRLPVLAD  
AYHLFALCAGIFEQGFIMEIVVRQFAHPQRKVDFFGVVTDSPVQPDERAFLRHQQAARILVQTVQDQLQILRLRTGAALPDAETHAAATVYRHTGRLLIDQ\*RVVLIHLHRLKTRRY  
GGTPFRRLHRLHARRNPHRISLNTAVGPAFLVQPHLAGADNAVDIALGHALEDYQIVIKALTRLMFGNPNYQADRTFATPVRFH

## SEQ ID 5147

TTGGAGATGTTCAAATGAGTCGTGAAATGTTACAGCTGGCAGAGCACTGGCAAGCGAAAAAGCGTTGATGCGGAAGTCGTCCTCAAGCACTGGAATTCGCACTCTCTACCGCGGCA  
AGAAAAAGGCGAGACCGCGAACACATGGACGTGCGCGTCCAAATCAACCGCGATACCGCGGAATACCAAACTTCCGCGCTGGCTGATTGTCGCGGATGAAGACTATACCTATCCGATGT  
CGAAAAAACCATCGAGGAATCCAGAGGAATCCCGGATACGACCATCCAAATCGCGGAATACTACGAGAGCAGCTGCCAACGAAAGCTTCGCGCGCAAGCGCGCAAACTGCCAA  
CAATCATCTCGCAACGATCCGCGATGCGGAGCGGAGCAGAACTGAACGAGTTCTCGCGCTCAAAGAGACATCGTGTCGCGGACGCTCAAACCGCTCGAACCGCGCGGATCATCG  
TCGAATGCTTTCGCGGCAACTGGACGCGCTGATTCGCGCGACCAATGATTCCGCGGAAACTTCGCGAGCGCGGACCGCATCCGCGCTCTCTGCGCGTCGAAGAAATCGGCA  
CACCGCGCGCAAAACAAATCATCTGAGCGGTACTTCGCGGATTTCTCGTCAAACTGTACGCGCAATGAAGTACCTGAAATTCGAGCGCATGCTTGAATTCGCGCTGTCGCGCGGAC  
CGGCGCAACGTGCGAAAGTCCGCGTCAAAGCAACGACGCGCATCGATCCGCAAGGCACTGTATCGCGCTTCGCGGTTTCGCGGTTCGCGGTGTCATGCGCTGAGCAATGAATTCGCGCGGAGC  
GCATGAGCTGCTTCTTGGTTCGCGGAGCTGCGCAATTCGTCATGAGCGCGCTCTCACCGCGGAAGTCAGCGCATGCTATCGACGAAGAACACGCGCTGATGTCATGCTGTC  
CGAGGACCGGCTTCGCGCTCGCATCGCGCGCGCGCTCAAAACGTCGCGCTTCTGTCGAGCTGACCGGCTGAGCTCAACATCATGACTTCGCGGAGGAGCAGACGCAATCGCGGCA  
GAAGATGCGCGCATCCGCGCTGTTTATGAATCACTTGAATGTAGATGAAGAAACCGCGAGCTACTGGTTTCAAGAAAGTTTTCGCAACTTGAAGAGAGTTCGCTATGTTCTGCGCGG  
AACTGCTTGCATTTGAAGGATTTGACGAAGAAATCGTCGATATGCTTCGCAACCGTGCAGCGGATGCCATCTGACCATGGCGATTGCTGCCGAAGAAACTGGGCGAAGTGTCCGCGA  
TATGCTTAACCTCGAAGGCGTAGATGCGGATATGCTCTCAGCTTTCGCGAAGCAGGATTAACACCGCGAGCACTTGGCAGAGCTTCCGCTGGACGAACTGATTGAATACCGGTGTA  
AACGAAGAACTGCAAAAGCGGTATCTGACCGCACCGCAACACTGCTTATCCGAAGACAA

## SEQ ID 5148

LEMFMSREMLQALAEALASEKNVDAEVVQALFALSTAAKKKADREHMDVRVQINRDTGEYQTFRRWLIVADEYTYPDVEKTIIEIIEIPIPTTIQIGEYEBQLNEPFGRAAQTA  
QIIILQRIRDAERQNLNEFLAVKEDIIVSGTVKRVERHGIIVVAGKLDALIPROQMI PRENFRSGDRIRALFLRVEEIGNTRKQIILSRSTSGDFLVKLYANVEPIADGMLRRAVARD  
PGQRAKAVKANDQRIDPQGTICVGRGSRVNAVSNELSGERIDVVLWSPEPAQFVMSALSPAESRVIDEDKHAVDVIVAEDRLALAIGRGQNVRLASDLTGWQLNIMTSAEDERNA

EDAAIRRLFMNHLNVDEETADVLVQEGFATLEEVAYVPAEELLAIEGFDEEIVDMNLNRARDAIL/TMAIAAEKLGESDDMRNLEGVADMLLSIAEAGITTRDDLAELAVDELIEITGV  
NEETAAXVIL/AREHWFTEK

**SEQ ID 5149**

ATGCCCTTCTGCTGCCGAACCCCTTGACCTCGCTGACGGTACGCCGTAATGCCGATTTCCGTCACCGCTCGCGCAGCTGTCGAGCTTGAACGGTTTGACAAATCGCCTCGATTTT  
TTCATAAAATTTCTTTGAACAAACAAATACAAACACATCCGAAAAACGGGAACCCCGCTCAGATTGTCAACATTTTAAACCAAAATACCAAGCAATACAGCCCCGTTGCGCATATAAT  
GACAGCTTTTCAACCGCATTTGAGAGCGGAATCCATGTCTGTGTTTTCGCCCTTGGCGCGCTTACCCGCTTTCCGATTTCGCTGTCGAAAACTCTTGCAAAAAGCCCGCAGCTCGG  
CTGCCCGAAGTCAAATTAAGCAGCAATTTTGGTATTTCCGCCGCGAGAGAAAGCACT

**SEQ ID 5150**

MPLPAEPFDLADGHARNADFRQLAHVVELERFDNRLDFFHKISFEQTIQTHPKNGNPPSDQHFKPKYPSHTAPVAHMTAFPTAFESRIHVCCFALARRYRPFPRPCRKTLAKSRRT  
PARSQIKQRLVFRQREST

**SEQ ID 5151**

TTTGAACACCGCTTTAAACGGCTTGATCAGCACTTCGCTGTACAGCGCGCATGAACATAGGGATCGTCTTCAGCCCAAGCTTGGCGCGCATCCAAGACTCGAACTGTGCCCAATCAAG  
CTGCCGAAACACGCTTCGGGATTGTCCGCGCAGCAGTTTGGGCTTCCGCTCAGCAGACGCGCTTCGGAATTCAGCGTTTCAGCGGTTTAAAGTGTTCGGGACGTGCCCGCATACGCGCT  
CATGCACATCTCCCGCTGTGTGCCAGCAACATAAATATCCACAGTCAA

**SEQ ID 5152**

FEHRFKRLDQHPVAHAGNIGIVFSPSLRRIQRLELCHNQAARNTFGIVRQVWACRQQTAFRQRFQPPKVFCTCRHTRFMHILFVCCQKHIFHSQ

**SEQ ID 5153**

TTGGCGGAACGCGCCCTCTTTGTCTCCGAACGGGAAAGCAGCAGTCCAAATGGCGCTGCGCACCCGGGGCGGCATTCATTTTTTTGTGGCGCTTCGCAAGTATTTTTCCATCTT  
TTCGCTCTGCTTGGCCACAGAGTGTCTGCTGTTTTTCAAACCTTCATAGACGATATCGGATAACCGCGCTAATAATACAGGTTTTATGCCCCCGCGCGCAGCGGTGAGAGCAAGAG  
CGCGCACACAGCGCAACACGGCCCAAGGTTTTTCGGATTTCATTTCTCTCT

**SEQ ID 5154**

LAERALFVSRTGKQSQMGVTRGGIHFFCWRLPQSIFFPSFSACPTKCRFRSNLHRRYRDNRRNNTGFYARRRQAVRAKTAHSDKRPKVFPIISP

**SEQ ID 5155**

ATGAACCTTTGATTTTAGGGCTTGCCGCGCTTTGGCTCTGTCTGCCAGTTCGAAAAGCTCCGACCTCGACTACAGTCAATCAAGAAAGCAACCGGCTTCAATTTTGGTG  
TTCGCGCGCTGAACAGTTCGCTGATGTCAACGGCACTTGGGGGATGCTGGCTTCGACCGCGCGCGGATTTCCGAAGCGGCTATTACGCTTTCCGCGCGAGTCTGGAGGAAACCTT  
CAAGAAACCGGCTTGACCAATGCCCGCATATTCACCGCTCCGGCGGAAACACTGCATCAAATTTCCGCAATGATGCGGTTTTGTACATTACGTTACCGAATACGGCACTTCATAT  
CAAATTTTAGACAGCGTGACGACCGTATCCGCCAAAGCAGCGCTGGTTCGATTCCCGCAACGGGAAAGAGTTGTGGTGGGTTCCGCGCAGCATCCGGAAGGAGCAACACAGCAACAGCG  
GCTCTGTGGGGCTTTGGTCCGCGCAGTGGTCAATCAGATTGCCAACAGCCTGACCGACCGGTTATCAGGTTTCCAAAACCGCGCATACAACCTACTGTGCCCTATTCCCGCAACGG  
TATCTTGAAGGTCCGAGATTCTGCGAAGAGCAGCCAAA

**SEQ ID 5156**

MKPLILGLAAVLALSACQVRKAPDLDTYSFKESKPASILVVPPLNESPDVNGTWMLASTAAPISEAGYVFPAAVVEETFKENGLTNAADIHAVRPEKLEQIFGNDVLYITVTEYGTST  
QILDVTTVSARLARLVDNRNGKELWSGSASIREGSNNNSNGLLGAIVGAVNVQIANSLTDRGYQVSRTAAYNLLSPYSRNGILKGPFRFVEEQPK

**SEQ ID 5157**

ATCGAATCTTGATATCTGCAAGCCGACCGCCCAAAATCAGCGCAGCGGTTTCAATATCCGAACAAGGTTCCGGTTCTGTATTTTCAGAACCCGAACCTTTTATTCAAATTTAACTTA  
ATTCCGGCGTGTGTATGG

**SEQ ID 5158**

MRILILASRTAQNGATGNIRTRFGFCILQNFNLLFKPLNSGVVVW

**SEQ ID 5159**

TTGCAAGCCGACCGCCCAAAATCAGCGCAGCGGTTTCAATATCCGAACAAGGTTCCGGTTCTGTATTTTCAGAACCCGAACCTTTTATTCAAATTTAACTTAATTCGGCGTGTGT  
ATGGTAAATTA

**SEQ ID 5160**

LQAAPPKIRRPVSISEQSGSVFCRTTFFYSNLNLIIPAWLYGKL

**SEQ ID 5161**

TTGTTAATCCACTATAACAGCAATATGCCCTGACCGGCAAAACTTCCCAAACTTCATCAAAAATCAACTGTACCCGCTTTTTCAGACGGCAT

**SEQ ID 5162**

LLIHYNQYALTGKTSNFIKKSTVPVFFRRH

**SEQ ID 5163**

ATGGGAATCTCTTACGGTATCAATGCCGCTGAAAAAGACGGGTACAGTTGATTTTTTGATGAAGTTTGGGGAAGTTTTCGCGGTACGGCATATTGCTTGTTA

**SEQ ID 5164**

MGNLLRYQCRLLKKTGTVDFLMPKGEVLFPVRYCLL

**SEQ ID 5165**

ATGCAAAACCGCAACCGAGCTTTATTCACCGCGCTTGGCTGTTGCAGACCTTATTGATGATTACCGCGGCTCGGCGGTGATTCTGTTTTTCGCGCGCAACACCGCTTGGGCGGG  
AGTTTGCCTATATCTGCGCTTTGCCGTGACCCGAAAGCAGCGTCAAAGTATGCTGCTGATTACGGCAATGTTACGCTGCTGTTAACCGAAGTCCGGTTGAATGTGTGAGTACCTT  
CATGTCCAAGGACTTTACGATTTCGATGCAGGATTTGAATGCTTCGGCATTTTGGATGTTTCAGCGATGAACCGCGCGTGGTACTGATACGGGCTTTAAACAAGCTGTTACGACTTT  
CTCGAT

**SEQ ID 5166**

MONRQTELYSTPSWLLQTLIMITAASAVILFFARNWRLGREPAYILRLCTPKSTVKVLLITAMVTLILLFEVRLNVLSTFMSKGLYDSMDLNASAFWMFAAMNAGVVLIRAFNVNVNDP  
LD

**SEQ ID 5167**

ATGAAAAAACCATTTGAACACAACCGGTTTCGACCTCTGGCACACCATCCGCGAAGAAACCGCGCGCTGCCCGCGCAACCGATGCTGGCAAGTTTTTTCACCAACCGGTTGTC  
GCCAGAGTCCCTCGGCTCGCTCTTGCTTACCACCTTCCAGCAAACTCCGCGAGCCGATATTGAGAGTCCGCGCGCTGTTTGAATTTTACCAGCAGCATTTGGGACGACACCCAAAT  
CAGCAATGRTGTCGAAGCAGACTTAAAGCCATCTACGAACCGGATCCCGCTCCGAGCAATATTGCTGCGGCTTTTATATTTCAAAGGCTTCCAGCGATTCAGGCAACACCGCATCAAC  
CACCGGCTGTATCTCGACGAGCAAAAACGCTGGCGTATTTCTTACAAAACCGTATGTCGGAAGTATTCGCGTGGACATCCACCGCGCGGCTTTAGGATACGGGCTGATGCTCGACC  
ACGCCACCGGCTTTGTGCGGAGAAACCGCGCTGTGGGCAACAAATATTCGATTTTGCACGGCGTAACGCTCGCGGTTTCGGGCAAGAAGGCGGCGACCGCACCCCAAAATCGGCGA  
CGCGGTGATGATCGCGCAACCGCTTCGATATTGGGCAATATCCGATCGGCAGCAATGCCAAATCGCGCGCGGCGAGCTGCTGTTTCAGAGCTGCCCGCTCCATCAGGTTGTGCGGC  
GTACCGCGCAACCGGTCGGCGGATCGCTCAAACCCGCTCGCGGATATGGATCAAATATCCAGTTTCCGCAATCGACTTTATGATT

## SEQ ID 5168

MKNHLATTFGLMHTIRRETAATAAAAEPLASFLHQTVLRHRSLSVLAHYLSSKLSGSPIMDVRLFEIYQALGSDTQISKVEADLKAIERDPACDEYSLPLLYFKGFHAIQAHRIH  
HRLVLDGRKTLAYFLQNRMSSEVPVGDHHPAARLGYGLMLDHATGPAVGETAVLGNISILHGVTLGGSGKEGGDRHPKIGDGMIGANASILGNIRIGSNARIGAGSVVSDVPPSITVVG  
VPAKPVARSILKTPSADMDQNIQFARIDFMI

## SEQ ID 5169

TTGAACCAAGAAACATCATCGCCACACCCCTCCGAAAAGCGGTATTGTACAGGCAAAACCGCTTGGGAAACGTGATAAAATCAGGCGGA

## SEQ ID 5170

LNQENIIAHTLPKSGIVQANRLGNVKSOG

## SEQ ID 5171

TTGGCGATTAAATGGTGGGAACGGCTCAATGAAGTTTGTACTTCGCGCTGGCTTGGCGCAAAAATACTACCGCTGCAAAATGCGCCGCCACGGCCGGACACATCGACCAGCGTATCC  
AACAGGATGCGCAGGAATTCATCGCTTCGACCATCGAATTTGTGCGCGCATGGTCAATTCGTCGTACTTCTCTGGAATTTGCCGTTGTTTG

## SEQ ID 5172

LAIKWSERLNEVLTSRWLADKNYRLQMRHAPDNIDQRIQDQAEFIASITIEFVRGMVNSVVTSLFAVVL

## SEQ ID 5173

GTGCGGAATGTGGAAGCCGAACACGGTCAGGATGCTGCAAGCCCTACAAAAACAACGGCAAAATCCAGAGAAGTAACGACCGAATTGACCATGCCGCGCACAAATTCGATGGTGAAGCG  
ATGAATTCCTGCGCATCTCTGTGGATACGCTGGTTCGATGTTGTCCGGCCCGTGGCGCGCATTTGACAGGCGTAGTAGTTTGTGCGCAAGCCAGCGCGAAGTCAAAATTCATTGAGCC  
GTTCCGACCATTTAATCGCAAGCCTTAATCGAGAAAGTCGTTAACGACGTTGTAAACGCGCGTATCAGTACACGCGCGCTTCATCGCTGCAAAATCCAAATTCGCGAAGCATTCAA  
ATCTGTCATCGAATCGTAAAGTCCTTTGGACATGAAGTACTCAACATTTCAACCGCACTTCGTT

## SEQ ID 5174

VRNVEAEHQDQACQALQNGKFORSDRIDHAANKFDGRSDEFRLILLDTLVDVVRVAHLQAVVVFVGKPARSONFIEFFRPFNRQALIEKVNDVVRFPYQYHAGVHRCKHPKRSIQ  
ILHRIVKSPGHEGTQHIQPHFG

## SEQ ID 5175

TTGGCAGGCATCTGACCGTGTTCGGCTTCGACATTCGCGACGGCATTTGTTGGTTTGTCTTTATTTTCATGATTTTGGCGATCTTTATCGCCATGTGGATAGGCAACCCCTTGATTGCTT  
ACAATTTGAAACAAAAAATCAACGGGACTACCGTTATTCCTTCATCTCTGACGACACCGCGAAAGCGTGGCGTTTACAGCGCGCAACACGACACCGCCCGCTTTCCGA  
CGCTTTAAAGCCATTTATTCGCAACCGTTGGCGCATCGCGCGGCAAGCGTCTGCTTAAGCGGCTTTAACGATATGTTTACCAACGGGCATCAAACTCTCTCTGATTATTTGCAAGCTCCG  
CGCTGTTTGGCGGCAAAATCAAAATCGCGGACATCCAGCAGACCGTCCAAAGCTTTCGGCGCATGCAAAACCGCGCTGCTTTCTTCGGAATGTTCTACAAACAAATTCACCGCTGCCAG  
CCGACTGGAGCGCTCTGTCGTCCTTTTGTCTGAGTACCGAAGAACACACGCGCGCAGCAACCCGAGATTAGCGAAGTTTCAGACGGCATTCGACTGGAAACGCTCGCCCTGCTTCGCGCA  
CAACGGCGAAGTTTATTTGGACGGCATCAACATCAAACTCAAAAGCGCGGATTCCCTGCTGATAGCGCGCGCGCGGCT

## SEQ ID 5176

LAGILVVFQFDIPHIVVFVIFMILAIPIAMWIGNPLIRYNYENKKLNGDYRSLILVRDHAESVAFYSGEQHEHGRLSDFKAIIRNRWRIARQSVCLSGFNDMFTNGIKLFLITLQAP  
RLFAGQIKIGIDIQTQVAFARLQNALSPFRMFYKFTACHARLERLVFLSTEBQHAQQPEISEVSDGIALENVALFRENGEVLLDGINIKLSGDSLLIRGPSG

## SEQ ID 5177

ATGAACACCTGCGCGCTTGGTTATCTGATTGACAAATTTGGATAAAACAGACGGCTGGCAGCACAAACTCTCCCGCGGCAACTGCAACGCGTCCGCTTCGTCGCGCGCTGCTCTCCAAGC  
CCAAATCGTCTGCTCGACGAAGCGCGCGCGCTTGGACGAACCGCGCGAAGCC

## SEQ ID 5178

MNTCLGYLIDKLDKTDGQHLSPGELQVAFVRALLSKPKIVLLDEAAAALDEPAEA

## SEQ ID 5179

ATGCCGCTGAAAAACGGCTTCAGACGGCATGTTTCAGCCGACGGCAGCGTTGCCGACATCGAGGTGCATATTTCGGAACGCGTTCGAGCGTACTTCGGTGTCCGATACTGATGATGCTGTG  
GGCAGTTTTGCTT

## SEQ ID 5180

MPSENGFRHRSAAGSVADIEVHLAERVERTSVSDTDDAVGQFL

## SEQ ID 5181

GTGCTTTTCAATTTGAACGATGCGCTGAAAAACGGCTTCAGACGGCATGTTTCAGCCGACGGCAGCGTTGCCGACATCGAGGTGCATATTGCGGAACCGCTTGAGCGTACTTCGCTGTG  
CGATACGATGCTGTGCGGCGAGTTTTCGCTTTAAGGCGCGG

## SEQ ID 5182

VSFQFERCLKTPASDGIQVQALPTSRCLRNALSVLRCPIILMLSGSPCFKAR

## SEQ ID 5183

TATTAATAACGCACTCCGCAAGCAATTTCCCTGCGCTGTTCCAGCCGGCAGGCGCAGACGTAGTCAAGTTTGAATTTGATTTTCCGCTTTCGGCGCGGAAGTAAGACGGCAGCGGAGC  
CCAA

## SEQ ID 5184

Y\*KRTFQSIFPAPVPSRQANVVKFELILFFRRGSKTAAEPQ

## SEQ ID 5185

GTGAACACGCTTTGAACCAAGAAACATCATCGCCACACCCCTTCGAAAAGCGGTATTGTACAGGCAAAACCGCTTGGGAAACGTGATAAAATCAGGCGGATAAAACAAATCGAATAAATCTT  
TACCGCAAAACGGAGGCAAAATGCTCAAAATCCATCGAACTCAATTCACACATCCGCAACCGCTTGCAGCATATCTGAAAGCGAGGGGTTTGGATTTTCAGACGGCAATGCAGGAAGAAGA  
AGGCAACAAAGAAATCGCGGCATCGTCCACAGCGGTGCCCCACTCTGGTCCGCAAACTGTATTCCGAACAAAAATGCAGAAGTTTTTTTGGGAAAAGCGGATTTGATTGCCGACTAC  
ATCAGCCGCGGATGCAGGA

## SEQ ID 5186

VKQLEPRKHHRPHSEKRYCTGKPLGKRDRIIRINKSNKSLPQNGKMLKSTBLNSHIRNRLAAYLKGRGLDFQTAMQEEGNKEIAIVHSGPLTVLRKLYSEDKMKQKFFWEKRLIADY  
ISRRMQG

## SEQ ID 5187

GTGAACACGCTTATTTTGGACTTTGGCGCACACGACTATCCGAGTTTCGACAAATTCCTCGGCACGGAATAACCGGAACCTGGTCTATGTGTACAGCATAAACACGACCGCTTATCTAAG  
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GTTTGAAGGAGAAATACCTCGCGTCGATCAAGTCGAAAACTGGGCAACGAAGAACAAGCCCTGCTTTTTTCCATCTTCAACCGCTTCCGCAACAGCGCGCAAGGCTTTTTGCTGCTCGGT  
TCGGAATACACGCCCCAGCAGCTCGTCATCCGGAAGATTTCGGACGCGTATGGCATACTGCTCGTTTACGAAGTCAAGCCACTAACCGACCAAGAAAAATCGACGCGCTCGCCAATA  
TGGCGCGCGCACGCAAGTAACCGTCGATTCGAAATTTTGAATACCTGCTCAAACTCGCGCGCGATATGGACAGCTGATGATGATGCTCGACAGCTGGACAACTACGCGCTAAC  
CATGGGCAACGCACTCACCTCGCGCTGCTTCGCCAGCTTTTGAACACAGGAACCCAA

## SEQ ID 5188

VNQILFDFAHDYPSFKPLGTENALVYVLQHKHDPFTYVWEGAGKSHLLQAWVAQALEAGKNAAYIDAASMPLEDAFEAYLAVDQVEKLGNEBQALLFSIFNFRNSGKGFLLLG  
SEYTPQQLVIREDLTRMAYCLVYEVKPLTDQEKIDALANMAAARQVTVDSSEIPEYLLKHWRRDMSIMMLDLDNYAVTMGRITLPLLRQLLQOQETO

## SEQ ID 5189

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ACGAAAAATTCACCGCGACTACCAAAACGGCTGCCCTCGACATCGACGCATTCTCAAACCTCCACCTCGCCCGCTCGCCCGTTACAGCAAAGAAGAGCTGGCGGAGTTTCACCGCGAATT  
TATGGCGGAATACATCATCCCCACATCTCGCTATGACGCTATGCTGGTGACAGGCCACCAATGGCAGGCGACGAAACCTCGTGATTTCCTCAACCAACGAGTTTCATCATCACCCCC  
GTCTGCGCGCTTTTCGGCATCGCCAAACATGATCGGCACACAACTCGAAACCGGTCGCGACGCGCTACACCGCAATTACATCGGCACGCCAGCCCTCAAAGAAGCAAAATCACCCGTC  
TGAACCAATGGCTCGCCGAACGCGGAAACGCTCGAAAGCTACGCGCAAAACCTATTTTACAGCGACTCCAAAAACGACCTGCCGCTGCTGCGCTCGTCAGCGAACCCGTCGCGCTCAA  
CCCCGATCGCAACTGGAAGAAAGCAAGCAAGAAAGGCTGGCCGCTTTTGAATTTCAAA

## SEQ ID 5190

MKNLAIFLDNLTINTSDHAWPQYLKKGVLDAETEAQNEKPYRDYQNGCLDIDAFLKLHLPLARYSKEELAEFHREFMAEYIIPHSFMRQLVQSHQMGDETLLVSSNEFLITP  
VCRLPGIANMIQTOLPGRITGNVIGTSPSLKKGKTRNLNQLAERGETLESYKTYFYSKNDLPLLRVSEPVAVNPDAELEKEAKEKGVPLNPK

## SEQ ID 5191

ATGCGCTCGAAGCCGATTCCGCGTTCAGACGGCATTGAGGCTGAAATCCCAAAACCAAGCCACAGGAATTTCATCGGGAACCAACAACTTTCCACCGTCATTCCACGAAAGTG  
GGAATCTAGGACGTAAATC

## SEQ ID 5192

MPSEARFQVQALRLKSQPKATGIHREKQSFHRHSHESGNLGRKI

## SEQ ID 5193

GTGGGAATGACGAAATTTCAAAGTTATGGCGTTATCGGAAAAACAGAAATCAAAGCCGAGAAATTTATCCAAACCAACCGGATTTCAAAAAACCAATTCGCGCGGGAATGACGGATT  
TTAGGTTCTGTTGTTGTTCTGTTGCTCGGAA

## SEQ ID 5194

VGMTKQSYGVIGKTENQSRRIYKQPDFKTKFPAGMTDFRFLMFLFARB

## SEQ ID 5195

ATGCGCGCTTTGGCGGAAACCTGTTGTGCGGTTCTGTTTGGGGTTTCGGGCAATTTCTAAGTTGTTATTCGCGAGCAAAACAGAAACCAACAGAAACCTAAATCCGTCATTCCC  
GCCGGGAATTTGGTTTPTTGAATCCGGTTGTTTGGATAAATCTCCGCTTTGATTCTGTTTTCGCGATAACGCCATACTTTGAAATTTGTCATTCCACGCGCGGGAATCC  
AGACCTGTGCGCACGAAACTTATCGGAAAAAAGTTTCTT

## SEQ ID 5196

MPALAEHLFVRFLFLGFRAISKLLFPKQKPKQKPKIRSRREPGFPFIRLFWINSPALIFCFSDNAILTKFRHSHAGGNPDLARKLIGKRF

## SEQ ID 5197

ATGGAGTTTGAACATATTTCCCGCCCGGACAGGCGGATCTCTGCGGAAGCACTGCCCTACATCCCGCGTTTTCGGTTCGGTTCGGCTCATCAAGTATGGCGCAACCGCATGA  
CCGAACCTGCCCTGAAAGAAGGTTTCCCGCGATGCTGCTGCTGAAGCTGGTCGCGCATTCATCCCGTCATCGTTACGCGCGCGCGGCGCAGATCAATGCGATGCTTGAAGAAAGTCGG  
CAAAAGGGCGAATTTGTCAGGAATCGCGTTACCGACAAAGAGACGATGGATATTTGTCGAATGGTATTGGCGCGGCACGTCAACAGGAATTCGTGTGATGATTACACATATGGA  
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ACGCTGATGCGGATGCTGCCGAAATCGCTCTGCGGTGCAAGCCGCGTCAACGGTGTGAAGGACGCGACATCATCGCGGAGGTTGCCAACCGCGCTTTGCTGGAATCTTTTA  
CCGATGCCGATCGGTCGATGATTTAGGCAGAGGGGAAGATGCC

## SEQ ID 5198

MEFENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVLLKLVGIHPVTVHGGGPQINAMLEKVGKGEFVQGMRTDKETMDIVENVLGGHVKNKEIVSMINTYG  
GHAVGVSGRDHPKAKKLLVDTPQNSVDIGQVTVESIDTGLVKGLIERGCI PVVAPVGVGKEGAFNINADLVAGLAEBELNAEKLMMTNLAGVMDRTGNLLTKLTPKRIDGLIADG  
TLYGMLPKIASAVEAAMGVKATHIIDRLPNALLLEIFTDAGISMLGRGEDA

## SEQ ID 5199

ATGATGTTTCTGGTTCAAGCTGTTCACTTGTTTGTGCTATTCGTTGTTGCGAGGCTGTTTACCTGCCGAGGATTTCTGTAATATGGCGATGATGATGCGCGCGCGGCAATC  
CCGAGTATGTCGCGCTGTCGGGATGGCGGTGCGGTTGACCGTTTATGTCGCTTTGGGTTTCGCGCGGCGATACCGTTTGCCCGCGCGCGGTGGGCGAGCGG  
CTGGTTACAGTCAAACTGTGTTGGGCTGATGCTCTGGCTTATCAGTTGATTTGCGGCTGCTGCTGCGCGGTTTTCAGGATTACAGCAATGCTTTTACACCGCTGTTACCGGCTG  
TTCAACGAAATCCCGTCTGCTGATGTTGCGCGCTGATCTGCTGCTGTTCAACCGTTT

## SEQ ID 5200

MMFSWPKLPHLFPVVISWFAGLFYLPRIFVNMAMIDAPRGNPEYRLSGMAVRLYRFSPLGFGAVVFGAIPFAAGRWGSGWVHVKLCLGLMLLAYQLYCGVLLRRFQDYSNAPSHRWYRV  
PNEIPVLLMVAALYLIVFKPF

## SEQ ID 5201

AAAACGCACTCCGCAAGCATTTCCCTGCGCTGTTCCAGCCGCGGACGCGCAGAACGTAGTCAAGTTTGAATTTGCGGTTTCGCGCGGGAAGTAAGACGCGAGCGAGCCCA  
GCCCGCAACGCAACCGCCGCAACACAGGCATCAGATAAAGAGAACCGCGCCCATTTTCCGACCGCAGCGTTGGAACCGCGCAGGACAGCCGCGCATGATCTTTATAGC  
CTTCTTTATCCGACCTTCCGCACACGGTTCCCGGAACGTGCATCCCTCGGATTTCACA

## SEQ ID 5202

KTHSAKHFPACSQPAGAERSQV\*IDFAVSARK\*DGSGAPSPERKPPENTGTTITRRSRPFRPQRSEGRQTAASIFIAFFIRPFRFPFGTCIPADPQ

## SEQ ID 5203

TTGTCGGAATCAFTGCCGACTCCGCCGTTTACAAGGAAACGGTTATTTCCGGTTGCGTGGGAATCGGCGTATCGAATAAAGGCAATTTGTCGACTGATAAGTCCGCGCATCGCG  
GCATATTAAGCGCAGGCTTGAAGCGGCAATGCCGTC

## SEQ ID 5204

LSLSLPDSARLQGNRLFPVAVESGVSNKRHFVRLISAGIGGILRRRLRLEAGNAV

## SEQ ID 5205

TTGTTGACAATTTCCGCTTATGTTAACGCCAAACCGCTGTGAACAATCTTCAGACGGCGTTGGCACACCTTCGGCAGGTTGAAGCCTTGCATACGGCGG

## SEQ ID 5206

LLFISAYVNAKRRLKQSSDGVWHTFGQVEALRYGR

## SEQ ID 5207

TTGAAGCCTTGCATACGGCGGTAATTCGCGTTTATCCGTTTCGAGAAACCGCGCAGCAGCAAGGACTTTCCCATGATTAATAACAGCACCGGCTTCGATGCCGCTCGTCTGTC  
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TGAAACACGCGCAGAACCCGCTACCCGAAAGGCTGGGAAGGCTATCAGGCGTGTGCTCATACGACCCGCAACTGGTCCGCGTACCGACTTCTACGAAACGCGCTACTGACCGTC  
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GCAGCAGCGTGCAGGCGCGGACATCAATCTGCTGACCATAGGCAACCAAGTCGAAGCGACATGAAATCTGGATTACCGCCCGCAGCACC CGGAGAAACCATGCGGAATGGTTTGT  
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CGTACCAACGCGCGCTGCGAATCTAACCCGGAATGGGAAACCCGACTTTGGGAAAGAGCCCGGAAGTGTCTTCTGCGCGGGAAGAAATGCTGGAACCGCGGTGGATTGTTTGTG  
ACATCCAGCGGATGAAGGTCTGCCCTTTGTCTTGTGTCAGGAACGGAAGGTGTGCCGAATCAATCCGCGCATTTCCGCGTGGAGCGCAGTTCAAACCGCCCTTTTGAACCGCAG  
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## SEQ ID 5208

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NHTPLNSVYYAYFPYSEEQHLNLLGDAQSGSLCRIIDLGSTVQGRDINLIITIGNQVESDMKIWTARQHPGETMAEWFVEGLLRLLDSQDPTARTLLDRATFYIVPMNPDGSLGHL  
RTNAAANLANRWEWENTLEKSEPVFVRGKMLETGVDFLFDIHGDBGLPFVVFAGTEGVPNYNPRISALEAQFKTALLNASPDFQDEYGEKADPGKANMTLATNWNVRNFCILAYTLEP  
FKDNANLDDDFGWNQSRSLRLGEAVLSAILNVAGDLR

## SEQ ID 5209

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TCGCGCAAGGCTTGTCCGTTTATACCAAGAAATCGCTCGACGACTTCTGACATGGGCACTTTTGGCGTGATTTTGGCGGACGCTTGGGCTATGCTGCTTTTACAAATTTCTCGGACTA  
CCTCGCCCATCCGCTGATATTTTCAAGGATGCGGAAGCGGAATGTCGCTCCACGCGCGCTTTTGGGTGATGTTATGCCATATGTTGTTTACGCGCAAGCAGGCACTCGGCTTCTC  
AACTGATGGACAGCGTCCGCGCGCTCGTTCGCTGGGTCTCGCTTCGCGGACATTCGCAACTTTATCAACGCGCAACTTTGGGAGCGCATTAACGCAATTAAGCAATTTTGGCAATGG  
GCTTCCCGCAAGCGCATTAAGAGATGCCGAAGCGCGCGCACAATCCGCTTTGGCGAGAATGGCTGCAACAATACGATATGCTGCGCGCTATCCCTGCGAGCTTTATCAGTTGATCCGCT  
TGAAGGCTATTCGCTGTTTCGCGCTGTTTGGCTGTTTTCAAAAACCGCGCGCGCAGCGGCACTTCGCGCGCTTTTTCCTCGCGGCTACGCGGTGTTCCGCTTTATTGCGGAATTTGCG  
CGCAACCGCGAGCTATCTCGGCTGCTGACCTTGGGCTGCTGATGGGCAATGGTTGAGCGTCCGATGATTGTTTGGGTATGCTGCGCTTGTCCGTTTCGCGATGAAAAACAGC  
AC

## SEQ ID 5210

MI THQFPDVLISIGPLAVRWYALSILGFLPFTFLRRRIAQGLSVPTKESLDDFLTWGILGVILGRLGYVLFYKPSDYLAHPLDIFKVBEGMSFHGGFLGVVIAINLPSRKHGIGFL  
KIMDTVAPLVPLGLASGRIGNFINGELWGRITDINAFWAMGFPQAHYEDAEAAHNPFWAEWLQYQMLPRHPSQLYQFALEGICLFAVWWLF SKKPRPTGTALPLGGYGVFPIAEFA  
RQPDVILGLLTLGLSMGQWLSVPMIVLIGVGVFVRGMKKQH

## SEQ ID 5211

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GCCATTCGCAAAACGCGCTTCGATTTCGGAACCTTCGCGCGCGTAAATTCGATTCGTCGCAACACTTCGCGGACGAGTCGAGCGGTGCCAATTTGTCGCGCGCTTCAACAGCG  
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## SEQ ID 5212

MEIRFQAFRLIVQMKTNASILTATRLVFPAAARTGIVPAGFPFPADGLRFVDDRLEPVAVDVQGRVQFGRKFRQLAFGELQADSAVFLFVUNAACHGEGVKQLFRFPIGGFKPIGRH  
NVQTVKIGVAPSVKIAAALAVVVEPQIGQLFIRHRCGFHRHCNQFPDFTGTTGGKILRFVQHPQVPERCQFVRPAQRRHKTLLNLVATHRVALFAPGIG

## SEQ ID 5213

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AAAAACCGCGAGGAAACGATCCCTGCTGCGCGCGCGGAGGAAATACAAGCGGTGTCGCGTAAGAT

## SEQ ID 5214

LKRMMDSRKFTASKRRLGELLDAKSEQNTMRCEVQGFMTALLSGPDRKLAFLDWLEPEVLGDSEQFTAAERSEIERLVLANAMETTAAMSDKKLPDLWLYDDGEGSDFTYTCNAYLYG  
LDIVPTDWFADDEAFBELFYPVMALEGGIYDEEENGATRLQFTGELAEASELPYALADIYRWQAVINKPQTVRRBEGTGRNDPCPGSGRKYACCGRN

## SEQ ID 5215

TTGACGAGCATCTTATGCCGATAGAAATGCAACGCGCTTTTGTATGAAACGCAAAATGGCGGCAATACGCGGATGAGCCGCTGCTGCTGAAACAGGCGTACCTGCTGTTGAAAAAG  
AACGCACCATTCGCGATCCGCAATTCGCGGAAACGCGCGTGGCTGACGCTGAAAGGCTATATTTTCGAAATCAGCGCGAGGTTGGAATACGAAATCCGCTTCCGATGCGGAAAGAT  
GATGAAACGATGTCGCGTTTAAAGTGAAGAAACGCGCTTATCCGCTCAGATGGGCGCGCAGCTGTTTGAAGTCGATGTTTCCCTTGGCGAAACTCGCTTGGCTGCGCGGAAATC  
GAGTTGCCCGCGGAAATGCGGATTTTACCGTCCGACTGCTGGGCGCGGAAATCACTTCAGACGATGTTTACCAATGCTTATGAGCAACATCCGTTCTCAAGCTGGAAGAAATG  
CCGTC

## SEQ ID 5216

LFEHMLPIETERRFLIENDKWRQYADEPLLLKQYLSVEKERTIRIRIAGKRAWLTLKGYISEISRSEFEYELPLADEKMMETMCPFKMKRRYPVRNGSLFEVDVFLGENSPLVVAEI  
ELPAENADFLRDPWLGREITSDGMPNTAYLSKHPFSSMKNV

## SEQ ID 5217

ATGCAATATAGATAGACCGTCTGGTCCCTATTTTCGCGCGGCTGAAACGCGCTTGCAGAGCGTTGAAACGCGCAGATCTCGAAATGCCGCGACGACCGCGCCATCTACAAATGGCGCA  
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GACACAGGCAACCGCTTATTTATTTTCGACACACCTTGCAGGACGCGCAACATCGCCGCGCGCTATGACCAAGAGGAAAAATTCGCGCTGCGGCAATTTGGAAATTTGGGC  
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CGGCAACCGGATTGAGCTTGGGCAATTTGTCGCGCGCAACGCTTCAAAACCAAGCTGCGGATTGCGCATCGAGTTGGAAGCGAAGAGGCACTGAACCGGCAATTTGCAACGCTTCAA  
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ACCGCGGAAGAGCGCGCGCCGACATCGTGTTCGCGCATCAAAGCGAAGAAAAACCGGCTTCCGCAACCGGCTCCGCGCCTGTTGATGCAATTTTCAAAGCGATTGAGAGCGTGGCGCAAA  
GCGCGCGGACTTTGAGATTATTCGTCACCGCGTACCGAAGTACGGAAGCCAAAGCGAAACCGGCTCCGTTTGGCGCGCGCAACCGCGTCTCAACGGTCAGGCGCGGATAC  
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**SEQ ID 5218**

MQLDIDRLVATPGVNALAEALKRHPENAATTAATYKWRTRGSLPLAQIQLTALAESQGRPLDLNAPLQKNSLERTENTQANRVIIIDTTLRDGEQSPGAAMTKEEKIRVARQLEKLG  
ADIEAGFAAASPFGFAVNAIAKTITKSTVCSLSRAIERDIRQAGKAVAPAPKKRIHTFIATSPHMETYKLMKPKQVIEAAVKAVKIAREYTDVFEPCEDALRSQIDFLAECGAVIB  
GATTINIPDTVGSIPYKTEEFRELIAKTPNGGKVWSARHNDLGLAVANSLAALKGGAQVECTVNGLGERAGNASVEEIVMAKVRHDLPGLETGIDITQIVPSKLVSTITGYFV  
QPNKAIVGANAPSHESGIHQDGVLKHRETYEIMSASVGSANRLSLGKLSGRNAPKTKLADLGLIESEKALNAAFARFKELADKKREIFDEDLHALVSDMGMMNAESTKFSQKISTE  
TGEPRADIVFGIKGEKRASTGSGPVDALPKAIESVAQSGATLQIYSVNAVITQSTESQGETSVRLARGNRVNVQGDITDILAAATAKATLSALKLEPSAARPKAQSGSTI

**SEQ ID 5219**

TTGCCGCTTGTACCGCGAATTTGCCCTGTTCGTGCGCAATGTCAACAATCACCGGCATCTGCAATAAATAGACAAAATGTATAAAATTAATAAAATTTATAGCACTTATTGAGAT  
TTTTTCAAATTAATATTGCCCTTTGTCCAAAATGCGTATAATCTGTCATATTTCTGCTCGCGGCTGATTTATTT

**SEQ ID 5220**

LPPCTAEFALFCRNCQSRRIKNDKMYKINKIYSNLRFPQINIAVLSKRIILSIFLIRADLP

**SEQ ID 5221**

ATGAATAACAAAGAATCGTATTTAAGTCGGCACATCTTCGATTACCGGTCGGACGGCAGCCTCTCGCGCGCAAAATCCAAACCATCACCGCGCAGCTTGCCGATTGCATCATGCGG  
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GCTGATGAAGAATAATACGGAACCTGTCTTCAGACGGCATCTGTGTCGACAAATCTGCTCAGCGGTGCCGACTTTGCGGCAAAACCGGCTACCAAAATCGCGCGCGCAGCTTTCC  
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GAAGCGCGCAACATCAGCGGACGGCTCGTTTTTCGTCGCCCGTCCAAAGGTTTCGGGACACAGAAGCAATGGCTGGCGTCTATTCGGAAGCGCGGGCAGCGTTTATGTGGACGAAG  
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**SEQ ID 5222**

MKYKRIIVKVGTSITSDGSLSRGKIQTITRQLAALHHAGHELVLVSSGAVAGFALGPKRPVKIADKQASAAVQGLMEETANLSSDGIVSAQILLSRADPADKRRYQNGAGLS  
VLIQRRAIPINENDTVSVEELKIGDNDTLSQAAMIQADLLVLLTIDIGLYTGNPNSNPDAVRLDKIEHINHEIEMAGSGSANGTGEMLTIKIAATIAESGVFVVICSSLKPDSLA  
EAAEHQADGSPFVPRAGLRTQKQWLAIFYSESRSVYVDEGAHEALSEQKAC

**SEQ ID 5223**

ATGTCGGGCAATGCGGAATCGAAGGGCATTTTCCCGTATGGACACCGTAACCGTGTACAGCAAGGCAACCAACAGCCCTTGGGCAAAAGGGCGGCTCTTTTCGGCTCCGCGCGCGCGG  
AAGACCTGCTCAAAATCGCGTAAGGCGAAGAGCGGTGTTTCATCATCGGACGATTGGATTTCATCACACCGCAAAATACGCTGCTTCTGACCGCAATTT

**SEQ ID 5224**

MSGIAGIEGHPFRMDTVTVYSKATQPLGKGRVLFGSAAAEILLKSRKAGVFIHRDWDISITPEIRILLTFE

**SEQ ID 5225**

ATGTCAAACACAAAAACAGCTTGCCCTTGCCAAAGCGGCAAAAAATCCGTCACACCGCGGATCGGGAAGAAAAAACCGCGGCTGCTTGTATGCGGACAGCTCTGGAAGCGGCGG  
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**SEQ ID 5226**

MSNTQKQALALAKAKSVNTADAEKNRALLAMADSLERAAEDILANRLDLKAAAGKIPDSWTRILLDGRICANADGIRAVAAALPDPVGEILETSTLPNGLEIVKRVAMGVIGIYE  
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VYNAKTRPSVCNMEVLLVHEGIAADFLPKLERLLVGRIEAGLPPVFRIDPQAARYIGGEAAGADDFTEFLDYILAVKTVASVEEAVGHIEARGTHESGDIVTENRHAADYFTTHID  
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**SEQ ID 5227**

TTGATTTTTTGCAAATAGAAATGCCGCTCTGAAGACTGTTTCAGACGGCATTTTATAGTGGATTAACAAAAATCAGGACAGGCGCGAAGCCGACAGATACAAA

**SEQ ID 5228**

LIFLQIEMPSDCFRHFYSGLTKIRTRRSRRQYK

**SEQ ID 5229**

TTGGAAATCATGTTAATGCCGCAAGATTAAAGGAAGGGCGGCTATTATACGTGTCGGCGGGGCAAAACCGAAGCGCAATCGTTTCGGCAGAAITGCGCGCGGTTGTTTTTTTGG  
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**SEQ ID 5230**

LEHNHGAARKIKRGCGYYTVGGGKPKAESVSAKLPAAGCFPLGNKHVKINSVNRSLSCGRHMFVIVLIVLILLALAGLFVRAQSEREMREVSAMQKKKGKQAEPLPKDGMDFPPEPSLIL  
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TRALSSAALRETKKRYIDAFEKNGTAVPKVRVSDTPMEGLQITGLDDPVLQRTYSRMPDADKEAPSESADYGFEPYFEKQHPAPSAPSAVKAENARNAPFRRHAGQKRGQAEKSPDVSQQQS  
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EVHRVVEYLKQFGEPPDYVDLISGGGSEELPGIGRSGDGETDPMYDEAVSVLTKKASISGVORALRIGYNRAARLIDCHEABGTVSAPEHNGMRTLVPLDWA

SEQ ID 5231

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SEQ ID 5232

MLFNATQAEELRVAIVDGNLLDLDIETFLGKQDRKNGYIKGIITRIEPLSEACFVDYGTDRHGFLPFKEVSRSYFLGYEGGRARIQDVULKEGHEVTVQVEKDERGNKGAALTTFIISLAGRY  
LJLMPNNPRGGVSKRIEGERQELKAAMAQLDIPNGMSIARTAGIGRSABELEWDILNYLKQJWQAIERAGKAHHDPYLLPFHSSILLIRAIIDTYPFDIGEILLVNDQEVYDQVAEPFSYV  
MPGNAGRLKLYEDHTPLFSRFQIIEHQIESAFSRSVSLPGSGAIVIDHTEALVSDVNSARATRGADIEDTAFKNTMMSAAEEVARQMLRLDLGLGVYVDFIDMENPKHQRDVENVLRLDALEK  
DRARVQMGKLSRFLGELLESRQRLKLPALGESSHAACPRACTGVIRGIBESTALHVLRLMVQEEAMKNDTGEVRAQVPFVDVATFLINKEKRAELFAMEERLJUNVVLIPIHLENPHYEINRIET  
DDVEEDGEPYSYKRAEPEEDESAPFGGGEKAARPEPAVKGVHTSPAPTAAPKEKTSWWDSPKAWLKRIFGGSETQAPVAAETSEKRSSTANRSGSRANNRRQNPRRSKREGSKIEVREA  
AGKTAQKARADAKETRANNGNRRNRNEDGRATERANEAEIQSRNVQAPAVDAADAPPETGQTGKRRRSGSRNERGQTAPETAVAETAQTAENTPPPEPTYAEDKGSKPASERNRRERDS  
DAKERRERNRQADRRGKKKRNIPSAKIEQYLIINHDTADVRSAAAHVFGSTDNAPETQVSTADPLIATPVQTATSSAVSNGDALIYDAEKIRRAAADIPEGAAPKAAQXMPSETAT  
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SEQ ID 5233

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SEQ ID 5234

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SEQ ID 5235

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SEQ ID 5236  
LWRKYAQNHNHNGVCGKPVHRGGQCYALAHPRRFRIPQSLYLGTTHRYGAENVGIPARQTPTATEEHRHQPAGGLLRGRGNGGKPGGGIGIVRRRGRSRHYGRADIRTSDAISRFDN  
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SEQ ID 5237  
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GGCATCTGAAGCCCGCTTTGGATCAACACTTTCGACGACAACCGCTATCTGAAGTCCGAGCGCGGCATATGGCTG

SEQ ID 5238  
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 VNRLSRELVNRLPPNPIFIFVNGFLASAGILLTGLNLIGILDAANAPPSEKILMTVALPVFILLAMAEAFLSGISTAIFFVALKPHWNTVTDNRYLKSERGTWL

SEQ ID 5239

ATGCTTTCCAACATCCTCCCCCTTTCCATCGGTGCAATATTCCGCACAACGGCGCGTTGGCTGCTCAACTCGCCGTCGCCGCATCGTTGTCTCCCGCCACAGGCAACCTGTTTGCCAAC  
GGACGGGCGCGTGTCTATCGGCATCTTTGCCGAACCGCTCAGCCATCGCAATGGAAGCTGCTGCTGATTACCGGTTTTTTCGGCAGCCTGACCAACGCTTTCCGGATTTTCACTGGAAAC  
CGTAACCTGCTCCAATCGAACCGTCCCGCTTCGGCACTTGCCAAATATTTTCTACACACGGCAGGTTGCTGCTGCTGACTTGCTCGGGCTGAAGATAGGGACGGCAGTCAAA

SEQ ID 5240  
MLSNILPLSIGAIGTTRARWLLNLAVPASLSPATGNLFAHWTGALLIGIFAETVSHPEQWKLILLITGFGSLTTLSCFSLETVTTLQSNRPASALANIFLHTAGSLLILWLGLKIGTAVK

SEQ ID 5241

ATGTCAAAACCAAAGGAAGCAATTTTTGCGGTATTATTGACTGCCGTCCTATCTTCAGCCCGAGCCAACTCAGCAGCAGCGAACTGCCGTGTGTAGGAAAAATTATGGCAAGTGC CGGAAG  
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AAAGATCCCGATGAGCAGCGCGCCCGTCCAGTTGGCAACAGGTTGCCTGTGGCGGGAGACAAACGATGCGGGGACGGCGAGGTTGAGCAGCCAAACGCGCGTGTGCGCGAATATTGCGACG  
ATGGAAAGGGGGAGGATGTTGGAAGCATGGTTTGTGCTGCCTATGCCGTC

SEQ ID 5242  
MSKPKEAIPCGYLTAVPPIFSPQSSEPAVCRKILASAEAGRFDWSRVTVSSENPEVRLPKPKVLSSSFHCGWLTVSAKHPSSAPVQLANRLPVAGNDAGTARLSSQRAVVPNIAP  
MERGRMLESMVL SAYAV

SEQ ID 5243  
ATGAATATCTTCGTTACTGATTTTCTTACTGGTTTATGAGTTTATTAAAGCTTTCCTTATATACCGTCCGTTCAATCATCGGATGATGATATTGATTTTGGCAAAAGGATTATGACGGTTA  
CTTTTTCGCAATTT

SEQ ID 5244  
MNIFVTDPSYWFNSLLTLSYIPSVHSSDDDDIDFGKRIMTVTFLHP

SEQ ID 5245  
ATGACGAAAAGTTCGTTTGGTCCCGCAGTGGCGTTATCGCGCAATCAGCGACATTGGAACTTCTCGCGGCAAGCTGGATGTGGCGGGCAGGATATGGCAGCGTGTGGCGCTGCAG  
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CAGTACGCTTTCTAATGATGAAGATGAAATAACGGAAACCGTGCTGATGTCGAAAGATGAAGTCGTCAGGCATTGGCAAACGATGAAATTAAAGACGCTAAACATTAAATCGGTTTGCAA  
TACTGGCTGATGAAGGAT

SEQ ID 5246  
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YWLKD

SEQ ID 5247  
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CGGGCGAGGATATGGCAGCGTGTGCGCTGCCAGAAATTGGCGGAGGAAGACGCTTTATGTTGCCAGACAGCGTGGCGCTGCTGTACAGTTTTTATACGGCGGTCTGGTTTTTGCAA

SEQ ID 5248  
VDLREVKLGGETTYEGGFVSI~~SR~~DKVRLPNGNEGQ~~RI~~VRHPGAACVLAVTD~~DE~~KVVLVPAVALCGKSDIGTSCGQAGCGGRGYGVS~~CA~~ARIGGGNALCC~~Q~~RAPAVQFLYGGRLQ

SEQ ID 5249  
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TCTCGGACGACGATATTGCCAATAACGGTGCAATTATCGCGAGGTATCGGAAACGCTGCGCCGACATCTGAAAGAACAGGATTCTCTGCTTTTGGAAACGGTTGGCGGAATATATTCCGCAATTT  
GGTTTTCGGGATATTTCGCGCGGGTGTGGTGCACGTGAAATCGTCAAGCCGGGTATTTTGGAAAGCGGTGCGCGAGGTTGAGATGGAATCGACGCGCGCAAGCGTGAAGAT

SEQ ID 5250  
MDKIFLHGKADTLIGVYGNERRRLQTLIVLDIGVPEKAGSDDDIANTVHYAEVCETLRRLKEDQFLLEALAEYIADLVLGYPGAVVHVHKIVKPGILECVREVGVETERCKRED



## SEQ ID 5251

ATGACCGTCAGCGGTTTCAACCAATTCATATATAAAATCCGGAATACAGCATTTATCGGACAATCAAAAAATCTTACCGAGCACATAGCCCATAAAGGCAATCAGCAACCCGAAACCAGC  
GGTTTGATATATGCGGGCGGCTCGGTTGCCAATACNGAAATATCATCTTCCCGCCCGCGTGAAGTTCAAGATATTCGGGCATTTCCCATCGCGCTCTCTCTCGCCCTCCCGCT  
CTCCGGCGGACGACCGTTTCCAACCTCATATACGGGTAATAATATCAAAACCCAAA

## SEQ ID 5252

MTVRRPNHFIYKIPNTAFIQSKNLTEHIAHKNGQPNQRFDIAGRLGLPTYXNIIFPPAVKFKIFGHFPIRASSFALPLLRREDRFLHRIIVISKPK

## SEQ ID 5253

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AACGTGGGAATCCCTGCCCGTCAAAACCCCTGCCCGGACGAGGAACATGTCATCAGCCGCGCAGCGGATTTATGCGCGGACGGCGGAAACGGTGGCAAGTTTGGAGGTGGCATTTGGCA  
TTGTGCGCGCGCGGGAAGAGCCGTCATTATGGCGCGCGGAGATATACGGAACCGATGCCATTAGCGACCGATTTCGGGATAACCGAAGTGGATTGTCTGTGGAGGAGATGCAAT  
TTTTCCAGAAATAGACCGGACGCATTTGGAGAGAAGCAGAGCGGACGGAACCGCGTGCAGCAGAAAGCGCTTGCATATACATTTCGTGATTACCTCAAGGGA

## SEQ ID 5254

VETQMVRAQVEIFDAECHKMPSEAFRRHPCENMLKITIIAACAENLCIGAGNMPWHIPEDFAFFKAYTLGKPVIMGRKTWESLPVKPLPGRNRIVSRQADYCAAGAEVTSLEVALA  
LCAGAEAVIMGGAQIYQAMPLATDLRI TEVDLSVEGDAPFPEIDRTHWRAERTERRVSSKGVATTFVHYLKG

## SEQ ID 5255

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CGACAGCGCAATCGCGCGCTGCGCATCGCGCGCTGGTTCGGGATATGTCGGCGGTGTTTTCGGATTAAAGGGCGGCAAGGCGTGGCAACGGCATTTGGCGGTCTTCTGGCATCTCT  
CTGCAACTGCTTGGTCTGCGCGTGTATTTGGCTTGTGATGGCATTCGGCTTCAAGATATCTCCCTTCCCGCGCGTGTGCCACAACCGCGCCCGCTTCCCGCACTCTTTTTATGC  
CGCATACTCTTGGATTTCGCAACCTCGCAATCGCATATTGGTGTGCTCGGCATAAGAGCAACATCTCAACCTGATTAAAGGCAAGAAAGCAAAATCGGCGAAAAACGC

## SEQ ID 5256

MPNIPAVAVSYLIGLSFAVIVSKYYGMDPRTYGSGNPGATNVLRSKKKAAALTLGLDAAKGLVAVLIARVLEPIGLSDSAIAAVALAALVGMWPFVFGFGKGGKVATAGVLLALS  
PATALVCAILWMAFGFKVSSLAALVATTAAPLAALFPMPHTSWIPATLAIILVLRHKSNIILNLKKGESKIGERK

## SEQ ID 5257

ATGCTCAAAACACTTCACCTTGTGTTTGTAGTGTCAATATTTCAACCGCAAGACAAAGCCCTACTGGTACATCGACACGCGCGCGCGGCTGTGTACAATCTCGAAGGCGAGGCGCGC  
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CGGCTCTCCGTGGCTGGCGCAATCGCTGACCTGCTGCGGACAAATTCGCGCTGTTGAGCTGCACCCACCGACTTTGTCCATCTGCAAAACAAATATGGGCGAAGCGGGATTGGGCAAA  
CGCGGACAAGTGTTCGCGAAGACGGTTACAAAGGGCTGATTTCCCTGCTGCCCGCCCGCGCGCGCGCGCTCTCATCGACCCGCGCTATGAGGAAAAACAGGACTACCGCGGTG  
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CGACAACCTACCTTTACGCGCGCAACTGCAGCTCCACGCGCGGAAACCGGAGGTTTCGGTATGCACGCGGCAAGGAAATGTTGCTGATTAAATCCCGCTTACCTTTTAGCGCAACAATTTGGCGCA  
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## SEQ ID 5258

MLKHTPLFLVLQYFNKDKFYWIDTHGGAGVYNLEGSEAQKVEYRQGIALLRQAQNLPAELSDFAAHIQKILPSPELYCGSPWLAQSLTCVGDRLFLFELHPTDFVHLQNNMGEAGLEK  
RGQVLRDYGKGLISLLPPPRRAAVLIDPPYEKQDYRRVTETLKAALKRFESGCIYWPCLSRRESKLPPELKKLLPDNYLYARLHVHAPKTDGFGMHGSGMFINPPYLLABQLAA  
NLPAFLTRLLAQDEGARYLLDSKTR

## SEQ ID 5259

ATGAAAACTTAAAAATATTTCCGTGTTGCTGTGTGCGGTTTGTCTGCTGCTGCGCTTCTGAAAAATCTGTAGCCAACTATGCTATCGGGACGATTTCGGCGTAATCAAGGCTG  
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AATCCGTCAAGGTATGGGTACGGCTGCGGTGTGTATGCTGCTGAACGGTGTGTTGTTGTTACCGTGGGTGTAATGAAAAACGCTGTT

## SEQ ID 5260

MKNLNI SVVAVCAVLLAACASENSVANYAIGDDSAVIAKAGNRAEARI SRBELAQHRRQRKNVSEELALEREKANKHDAIRQGMGTAAAGMLLNGVVTGTVGHSVF

## SEQ ID 5261

ATGCGCTGAACCCCTCAGACGGCATCTTCCGTCAAAACAAACAAAACCGGCGGATACACACTCCATATCGTCCGGTTCTGCATAAACACAGTATTCAAAAAACAGAACCGCTTTTCATT  
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AAACATTTTACGTTGACGCGGTGTGCGCGAGTTCGCCACGCGTAATTCGCGCTTCGCGACGGTTACGACACCGCTTATACGCGCGAATCGTCCCGATAGCATAGTTCGCTACAGA  
ATTTTCAGAGCCGAGGACGCAAGCAAAACCGCACACAGCAACCAAGGAAATATTTTCAAGTTTTCATACCTGTCTTATATCTCAAAA

## SEQ ID 5262

MPSEPFRRLHPSKQNRRAIHTPYRFLHRTSIQKSEAFHYTHGNTHTVQHQHTGSRHTHTDCVMLIGTFTFQSQLLNIFTTLAVLRQFRTRANSRFGVTPTSLDYGRIVADSVIGYR  
IFRSAGSKQNGTHSNNGNIFQVFTCPILSK

## SEQ ID 5263

ATGAAATGAAGAACTGATTTTGTGTCGGTGGCTGCGATGTTGGTGACGGCATGTAATACGACAGCCCGCTTTTGTAACTCAAGAACTGACGCGGAAATACAGCGGAAAGTCTGT  
CCATTACAGATAAGCGAGCGTGCCGAGCGTGCCGAATACCGTAAAGAAACGCCGGAAGAAATGATGGATGCGGCACGCGCATCAAAAAGGCAACGAAATTCACCCAATATTTATTTAT  
CGA

## SEQ ID 5264

MMKKLLILLSVAAMLVACTYADRRPVTQESAETQAKSRAIQISERAKRAEYRKERREREMDAARAIIKANENSPNIYFIR

## SEQ ID 5265

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ACACTGCAACAAACCACTGCGGCAAGCACTCGCGCGGCTTTTGTGTCGCTGCTTTCGCGCTGACCGGAAATCAACGCCAAAGTTCGCGCTCGCGGCACTTTCGCGGCTATTTGGGTATG  
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## SEQ ID 5266

MLSLYICIMSLFKNKFGILYFSIRLPRSDLPRAVFSHYNPTRYPAERTKGTPRSNLPFFRRHKPRNEQNDTLTRFLPEHLQWQLEALGGVLLSVVSACTEINAKVRLGALAGVLGM  
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FTLNAENEFVLTKENPKVPESTKEFALNMSNRHMLFPVQYVDELLAGETGTGRKNYNMRWASVMAETHRIILMRGGVFMYLQDKRDPKPKRLMYEANPMALILEBQAGASASNAQQA  
MLDIQFESLHQRAVIMSGSEEDVYLRLHSE

## SEQ ID 5267

GTGAATCGGATCTGCCCGCATATTTCAAGCATACCTCCGGAAGAACAGAAACTGCCTTTCGCAACGATAAAATACCGTCTGAAAAATTTTCAGACGGTATTTAAAAATTAAGCTC  
AAATTTATTTGCCCGCGCTTTTTCAGGATGCGGTACAACTCGTCTTTTCAGTTCAATTTGGCTTTTTCAGCTCATGATGGTTTCGCAACCGCTGGTAACCGGATTTGGCCAGACC  
GGTAATTTTATCGTCCAGCTCGTTATGCTGTCGACAGACGGCGGAAGCGGAATTTTCTGTTCAATTTGGAAATCAAAATCACGGTATTTGGGAACATAATCGCTTTCTCTCTTGG  
TTTACGGTTAAAAAGTCAAT

## SEQ ID 5268

VNPLRRYFKHTLRKNRKLFPRTIKIPSEKPSDGLIKIKAIYLPAAPCRHAYNSSPSFLAPFSSSHVSAPLVTGLLARFVILSSSSLCSSNRRAKREFSCFNLEIKSRYSGNIIAFLSW  
PTVKSN

## SEQ ID 5269

ATGGAGTTGGAAACGGTGTGCGCGGAGGAGGGGGAGGGCGAAGGAGGAGGCGGATGGGGAATGCGCGAATATCTTGAATTCACGGCGGGCGGAAGATGATATTTCTGATGTT  
GGCAACCGGAGCGCGCGCAATATCAACCGCTGGTTTTCGGGTGTCTGATTCGCTTTATGGGCTATGTCTCGTAAGATTTTT

## SEQ ID 5270

MELETVPVPEEGEGGGADGEMPEYLELHGGREDDISVCWQPEPPGNIKPLVFGLLIAPMGTVLGRIF

## SEQ ID 5271

ATGACACACCATTTACCCACAGACGATATTAAGATTAAAGAAAGTTAAAGAGTTGTTGCCGCGGATGGCCATCTTTACGAGCTGCCGATTTTCAAGAGGCTTCGGGCTTGTTTACCCGA  
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## SEQ ID 5272

MTHHYPTDDIKIKEVKELLPPIAHLIELPISKEASGLVHRIQELSDLVHGRDRRLVIIGPCTSHDPKAALEYAERLLKLRKYENELLIVMRVYFEKPRRTTVGWKGLINDPHLDGTFDI  
NFGLRQARSLLSLNNMGPASTEFLDMITPOYYADLISWGAIGARTTESQVHRELASGLSCFVGKNGTDGNLKIADAI GAASHSHFLSVTKAGHSATVHTGNNPDCHVILRGKEPN  
YDAGHVSFAVEQLRAAGVTDKIMIDCSHANSRKDYTRQMEVAQDIADQLBQDGGNMGVMSHVLVEGRQDKFEVYKSTTDACIGWGAETEELLALLAGANTKMRMARAG

## SEQ ID 5273

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GCATAACGAGCTGGACGATAAAATACCGGTCTGCCCAACAATCCGGTTACAGCGGTGCGGAACCATTCGATGAGCTGAAAAAGCCAAATTGAACCTGAAAGACGAGTTGTACGCCATC  
CTGCAAAAAGCGCGGCAAA

## SEQ ID 5274

MRKAEDCQRPYRTVGRFSADGVA VYNKTLDKNIIPVVIINVKIQDFLTVNQERKATMFPYRDLSKLRQENSRFARLFDENELDDKITGLANNPVTSGAETIDELKKAKLKLKDELYAI  
LQKAAK

## SEQ ID 5275

TTGAATTTTATGCCATATTACATACATAAATCAGCATGCTTTGTATGAATTATCAATCAAACTCAGGCGAAGGATGCTTGTAGCTAAACATATTTATGACTGCATGTATAATGTCTA  
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GCAGGTGATTCGAAGTATTTATAGTAGCTCAGCAATCCATTAGCAACAAGCTGGTATGATATCTTAAAGCAAGCGGTAGCGCTGCAGATGCGATGCGGTGGCGGTGCAGAGACA  
CTAAGCTTGGTAGAGCCACAGTCTGTCAGGCTTGGCGGTGTCATTTGTGTTGATTGGGACAATACCGCCAAAACATTGACCACATTTGATGGCGGTGAGACGGCACCGGATGCGTGCAG  
CGCCAGATTTATTTGGATAAAGATGGT

## SEQ ID 5276

LWYLAHLHTIISMLCMNYQNSGEGVLVARTYLLTALIMSMVSGCQVIVHANQKVNINSAVLGADAHTPEHVTGLTEQKVIASDFIVASANPLATQAGYDILKQGGSAADAMVAVQTT  
LSLVEPQSSGLGGAFVLYWNTAKLTTFDGREAPMRATPELFLDKDG

## SEQ ID 5277

TTGCTTGGGAAAAATTTATTTGATACGCCGATCCACTTGGCAAAACAAAGCTTTGAGGTGTCGCCAAGGCTTGCCTCTCGGTTGAGCAAAATCAGCAGCATTTGGCCAGCTATCCAAAAA  
CAGCCGCTTATTTTTCGCAATGGTGTGCCGCTACAAGCAGGAGCTTGTGCAAAAATTTAGAATTTGCTGACAGTGTTCAGGCGTTAGCAGCTCAAGGTGCAAAAGCTCTGCATCTGG  
TAAATATGCCCAAAATATTGTTTCAGTTGTCCAAATGCTAAGGATAACCCCGTCAATTTATCTTGCAGATTTATCTGATTATCAAGTGGTGAAGCCGCCGCTGTTTGTGACTTAT  
CGTATTTATGAAGTATGCGGTATGGGTGCAACCAAGCTCAGGTGGGATGCTATGGGTGAGATTTTGGGATTTTAAATGAATTTTCAACCAATCGGCTGGGATGATGCTGAAGGTTTGC  
GTTTGGCGATCTGATGATATTTGGCGACCGTATTTGTACCACTACCATTTGCCAGT

## SEQ ID 5278

LPWGLFDTPIHLAKQGFVSPRLAISVEQNQHLARYPKTAAYFLPNVPLQAGSLKLNLEFADSVQALAAQAKALHTGKYAQNIIVSVVQNAKDPQLSLQDLSDYQVVERPPVCVTY  
RIYEVCGMGPSSGGIANGQILGILNEFSNPRVGYDABGLRLRIVMYNATLILYQYPPAS

## SEQ ID 5279

TTGGCGACCGTGTATTTGTACCACTACCATTCGCCAGTTGATTTCTAAAGACTACCTAAACATCGCAGCCAGCTGCTTGAAGCTCGGATAAGGCAATTCCTAGCTATCTGCAGGG  
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CTCAACTTTGATGGCAATGGCTACCTGCTGAATATGAGCTGACAGACTTTAGTTTGTAGCCAAATAAGCAGGCAACAGCTGCGCAATCGTGTGAGCTTGGCAAGAGACCCAGCTCC  
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TGGATATCCAAAGATGCCATCAGTGCACCAATTTATTAATCGCTTTGGTATGATGAACCTAGAAACCGGTTACCAACCGGTTCCAGTGGCAACAAACATTAATGATTTGGCTATAAGAC  
TGATGTGCGTGAAGTAAATTCAGGTGTTCAAGCCATTTATTCAGCAACAGCGGCTGGTGGGTGTCGATCCACCGCGAAGGTCAGTGAAGGCTGAT

## SEQ ID 5280

LGPDPFVFPTRILSKDYLRKRSQLLBQSDKALPVSAGDPIHEWASSQAIPLSTSHISIVDKAGNLSMTTSIENAFGSTILMANGYLLNNELTDFSPFPIKQKQVANRVEPKRPRS  
SMAPTIVFKAGKPYNAIGSPGSRIGYVAKTIVAHSDWNMDIQDAISAPNLLANRFSYELTGTAVNQQTLDNLGYKTDVRELSNGVQAIITPESRLVGVDPFRREGRVTGD

## SEQ ID 5281

ATGGCGGGCAGGAAGAAATGTCTTGGCAAGTGGTGTATCAGCGGGTTATGGCTGATAAAGATGTGGTGGTGGTGGTATTTGATTGATTTTGCACAACTGCCGAAATTTACCATTT  
ATGATTTGCTTTGATTAGCTTTGTGCTAAATAAAGTGATGAGACGCTAAAAACCGGCATGTAAATAAATTACCTGATAATGCCAAGAAAAATTTACGCATTATGGGCTATCTGCC

## SEQ ID 5282

MAGQEELSWQVYQVRNADKVVVAGYLIDFAQTAENLPFDVLP LLSLVNKGDETLKTEMLNKLFDNAKENLRIMGYLP

## SEQ ID 5283

ATGTTTTCAAAAGCGTTACCTTCGCAACAATATGACCCCGATTGGCAGCAGCATTTGCCCAAGAACGCCAGCCAGCAAGACCACGTCGAGCTGATTGCTCTGAAACTACGTCAGT  
GCGCGGTGATGAGGCAAGGTTGCAATTTGACCAACAAATACGCCGAAGGCTATCCCGCAAAACGCTACTACGCGGCTGCGAATACGTCGATATGTCGAACAATTTGGCAATCGACT  
CGTAAAGAACTGTTTGGCGAGCCTATGCCAACGTTTCAACCGCCTCCGCTTCCCAAGCAACCAAGCGTATATGCTTCCGTTTTAAACCAGGCGACACCATTTTGGGTATGTCCTG  
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TCCGCGCCATGACCACTCGCGGCTTTAACGAACCGAGCGCTCGCTATTTGTCGAATTTGGTTGCCGATGATTTGGCTAATCCCGAAGCAAGCAACCTCCGCAAGTCCGCGGAC  
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## SEQ ID 5284

MFSKSVTLAQYDFDLAAAIQAEDRRQDHHVELLASENVSCAVHEAQSQLNKYAEYPAKRYYGCEYVDIVEQLAIDRVKELFGAAYANVQPHSGSQANQAVYASVLKPGDTILGSL  
AHGHLTHGASVNIISGLYNATVYGLDENEVLDAEVEERLALHEKPKMIVAGASAYALQIDWAKPREIADKVGAYLVFVMAHYAGLVAGGEYPNFPFCDFVTTHKTLRGPBGVVL  
DNTHEKALNSSIYPSLQGGPLMHVIAAKAVAFKEALQPEFKYAKQVKINAAMAEELVKRGLRIVSGRTESHVFLVDLQPMKITGAARALGAHITVKNKAIIPNDEKPFVTSGL  
SAAHTTRGPNFEDARVLSNLVADVLANPEDEANLAKVRGQVLTALCDKPYVYGT

## SEQ ID 5285

TTGTTTCGGTAACATTTCTCTCCAGCAAAATGACCAACTTTTCAATCTGCGATTCTACTATCTTCTGCTGATCAATTCATCTTTGTCATCCAGCAGCGACCTGAT  
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TATTTGAAATCTGGGCAATCTGGCGCAGCTTTGCGAGATTGATGCGGCTTTTCCCGGCTTCTATTTTGAATACCCGTTAACCGGACATTTCAATTTTCCGCCATCTCTCTCTGCGCT  
CTGATTGACTTCCCT

## SEQ ID 5286

LFSVTLFFLFQNDQLFQYCDFTIFLPDQFILCIQORPQFFIPKHQHIRADNIMVIGIVADREKRSVLLRQQLNHIDIENLGNLAQLVEIDAFFAFYFRI PVMRHFQFFRHLFLP  
LIDFP

## SEQ ID 5287

ATGGCTTTCCACCATCAGCCCATGATATGCGCGCGTCTGTTTCAATTTGGTCGCAATGCTTGTGCCACTTCCATCTGCGCGGTGTAATCTTGGCGCTGTTGGCGTGGCTGCAAT  
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CGGTATGGAATTTGGCGAATGCCCCGCTTGGTTACAGACAAGAAATGATGCGAATGCTGCGCGCACCGATTCGATCGCAATCTTCAAAATGCGCTCGTACCGCTTTTAAAGT  
GACGGGCGAGGACAGACGCGCTTCCCAATTCGCGGTGGACTTTGCTTTCGGTCTGCGCGCGGATTTGCCCGCAAGAAATCAGTTCGCGCATATCTGGGGTGAATCAATATCAAAAT  
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CCACCGCTGTTCTCGGCTTCTCGAAATAAACGCGCATCAGATCAAAAGCTTCTTTCATACCGCTTTCGCGAGTTTCAACAGACGTTCCGCAATTTCAACCGCGCTTTCGATCGT  
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TGGGCAATCGCGCGCAACACTCTTAACTCTTAAATCTTAATATCGTCTGCGGGTAATGGTGTGTCATCTTGCATCTTCTCTGATGGGTTTTATACGCTGCTTAGGTATACATG  
ACCTTGACAAACAGTGCAACATATTACTACAAAGCTATTATTATTTCAAAA

## SEQ ID 5288

MAFHHHAIDIAVLFQVGNVLCFHLPGVILAAVGVAAIDHQLVGYPCTQLPHRLADVSRIIRLFSAAQNDMTVGIAAGMDNGMPLGYRQEMRMARRTDCVDRNLQIAVRVTA  
DGAGTACQPAVDLAFGRPRADCPPRNQVGLILGCNHIQKFRGRHAHIIQGGQQTARLTQTEIDVERTVQMRVNVQTFPHRRSRLLLEINAHDKLVFIPLAEFQQTFRIFQRRFLW  
RTRPDNDQQPPVAVNQIGKFLADAVNQARSLFGNRQLVKMGNRRQQLFNFNLNIVCGVMVCHLASFLMGFYTLRLHRLPCTNKNILLQSYFISK

## SEQ ID 5289

AAGGCTCGCGCGCGCATCTCGACGCGGCTCCACGCGAGTTATCAGCTGCGCGAGTCCGCGCTGCCGTTGCCGCAAAATCGAGCGCGGTGCGGTGATCGACGAGGTTGCGGAT  
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## SEQ ID 5290

KAAARHLGGSLHGSYQAAGVRPAGCRQIERGAVIDGGADKQPQRDVHALPEAVVQHQQLVHVHRYGIRTFEHLRLBQVRRIRAGEVYPPAAQVFERGDNVGVFVSEVSAPAGNI  
EPGD\*DFGI PDAEFVF\*VWQNAADAFNRRLRGGGNVFORQVGRYEGDAQAFAGKHHDLPRAAPFRQIPGVSAEKTACARGVDDAFVQRGNDVAVEN\* NACERGVQKLQHTGWE  
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## SEQ ID 5291

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CCGTATATGAGTGGAAACGGTCTGCGCGGAGGAGGAGGCGGAAGGAGGAGCGCGGATGGGAAATGCCGAATATCTTGAATTCACGCGCGCGGGAAGATGATATTT  
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## SEQ ID 5292

MIEMSKYRNDLYDVVSYPPQVDRGLIRECLKENLGEKAEGLIESLDSKPQVLVEEKCTWAKREELHDYFSYLGLODITRIWSKRSRRRRRAKEEFARMKCPNLLNPAGKNI  
YVGNPSRPAISNRWFGSC

## SEQ ID 5293

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CAATACCATCATATAATATTATCGGCTCTGATGAAATGCTGGTGTGTTGAAAAATGAAAAATGAGGTGCTGCTGGATGCAAGGATGAATTGATCAGGCAGAAAGATAGTGAATCGCAGTA  
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## SEQ ID 5294

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## SEQ ID 5295

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## SEQ ID 5296

LGKRYKNGFHPVNTCADVEARWANGAMRDVRIERLISRNVLRLRIGDAIQNMCMETVNSIRMYRQBCRSSESDFYDEMLBHEHNFIGSSKSFASSLLPLSVTNFTTDMACTPZF

## SEQ ID 5297

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GGGAACATCCGAGTCGATCTACCAAAATCAACGAATACGGTGTTCGTGTCGGCGTGAATTC

## SEQ ID 5298

MKALLALITLALISOTAMAQLPDFLGKEVTVRTDISKQTLKNADLKEKHVKQKNIGFRADMPDDIHHGMRFEVSHSRDKKDMYVVTBSTTKPPGKDVEEKRTDVTYAGYTYTQPISEATK  
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## SEQ ID 5299

ATGCGCTCTGAAAAGTTTCAGACGGTATTAGGGTCTGCTACACATCAAAAACCCCAAACCAAAGGCTTTCGGTTTGTGTCTGGGGCATATCGCCCGAT

## SEQ ID 5300

MPSEKPTVLGSATTSKTANQKACGFVSGAYRRD

## SEQ ID 5301

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## SEQ ID 5302

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## SEQ ID 5303

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## SEQ ID 5304

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SFSKYSEKKAQELAVEAHEHNRFLDKFHAQBEAWIRKIEARRTRNBRVRLBELRQRAERNRVQGVNFKLDSGKSGKIIAELEHASFAYDDRVIMDKFSAIILQRGDKIGLIPNGIG  
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## SEQ ID 5305

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SEQ ID 5306  
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SEQ ID 5308  
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RAFVREHGVIP

SEQ ID 5309  
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LIKTI PAI HSGKTARNIRFPVSTTIKYRTPRCRFLHIRQNFIRKENVENKON

SEQ ID 5311  
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SEQ ID 5312  
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SEQ ID 5313

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SEQ ID 5315

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SEQ ID 5316

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VVPQSRMSMEPTDNPALYRALRTPLNPSPLYFYDFGDPHIVGSSPEILVRREKDDYIVRPIAGTRLRGKTPAEDLANEQDLSDAKEIAEHVMLIDLGRNDVGRISKTGEVAVTKNVIE  
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SEQ ID 5317  
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SEQ ID 5318  
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[illegible]



CAPTTTCGCTTATATGAGCTGGAACAAATTTACAAATCATTGAATTATGAAGACGCTTGGATTGTTTTACATCATGGTCAATGATACGATTAAAGATATTTCCGACCTTCCCTTAG  
ATTGGCATT

**SEQ ID 5320**

MNPLFTQERRIRPHKLLDGNILATNNRGVVSADGSNTRSFNIAKGIADLHSETVSRILPGQTSNFAEIAICSEFVQSAPEKLQHIRPGDWNVQVGSRRNRLEIARYQQYVHL/PALAKAA  
EENPELAAALGSDYITTPDIIVTRNLIADAEINRNEFLVDENIATYASLRAGNGNMPLLHASISCKWITIRSDRAQNARSEGLNLRNRKGRPLPHIVVVTABPTPSRISSIALGTGEIDCVY  
HFAIYELQILQSLNVEDALDLFYIMVNGIRLKDIDSLPLDLAF

**SEQ ID 5321**

ATGAACACACCCCCCATCTCTCCCGCCCATGCTCGGCATCTCGGCGGCGGACAATTAGGCAGAAATGTTGCGCTTGCCGCTAAACCATGGGCTACAAAGTAACCGTTCTCGATCCCG  
ACCGGAATGCGCGGCGGCGGGAATTTGCCGACCGCCATTTGTGCGCGCGGTTGACGACCGGCGCGGTTGGACGAATTTGGCAAAATGCGCGGCGGTTACGACCGGAATTTGAAACCGTCAA  
TGCCGACGCGATGCGCTCTCTGCGCAAGCATACCAACGTTTCCCGCAGCGCGACTGCGTGTCCATTGCACAAAACCGCATTCAGGAAAAAGCGTGGATACGCAAGCAGCGCTTGCAAAAC  
GCGCGGTATCAGGCGGTTTGAAGGCGGAAGACATTACTGAAGCAAGCGCGCAATTTTTCGCCGCGCATCTGAAAACGGCTACGTTGGGCTACGACGCGCAAGGTCAAATCCGCGTCAAAA  
CGTTGGACGAATCAAAGCGCGTTTCCGCAACACGCGCGCGTGGATTGCGTTTGGAAAAAATGTTGGACTTCCGCGCGGAGATTTCGCTGATCGTATGCGCTGGAACGATGAAAAAGT  
GCAAACTTCGACCCCGCGGAAAAATCCAGAAACCGGCATCTTGGCTTATTCATCTGTCGCCGCGCGCTGAGTGGCGACGTCAGCAACAGCGCGCGGACAGCGCGCAACCGTTGGCG  
GACGAATTTGGATTATGTCGCGGTATTTGCGGTAGAAATGTTGTTGTCGCGGACACATGAATTTGCTGCTCAATGAAACCGCGCGCGGACGACCAATTCGCGCCACCATACGATAGATG  
CTTGGCGCGGACAGCAGTTTCAACAGCAGGTACGCATTATGTGCAACCTGCCCGCGCGGACACCAAAATTAATATCCCTTGGCTGATGCGCAATATTTTGGGCGACGTTTGGCAGGAAGA  
TGGCGCGGAACCGGATTGGCTGCCGTTGCAAGCGCGCGGAATGCACACCTGCACCTATACGGAAAAAAACCGCACAGAAAGTGGGAAATGGGACACTTTACCGTTTGGACCGGAT  
TCGACACCGCATTTCAAGAAACAAAAAACTGCATCAGTCCCTA

**SEQ ID 5322**

MNTPILPPMILGILGGQIGRMPFAVAATWGYKVTVLDPDPNAPAEFADRHLCAPFDDRAALDELAKCAAVTFEFENVNADAMRSIAKHTNVSPSGDCVSLAQNRIOEKANIRKAGLQT  
APYQAVCKAEDITBASQFLPGLILKTATLGYDGKQIRVKTLDLKAFAEHHGGVDCVLEKMDLRLGEISVIVCRINDENVQTFDPAENIHENGLAYSIVPARLSADVQQQARQTAQRLA  
DELDYVGLVAEMFVVDTHLIVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLPADTKLLSPCCMANILGDVWQEDGGEFDWLPQSRPNAHLHYLQKTAQGRKMGHPTVLTDD  
SDTAPQRAKHLQSL

**SEQ ID 5323**

TTGAAGATGCTTTGACGCTTTCACGCTGCGCGGCGGTAACAGTGTGACAGGCTCATGGCGGTATGTCGCGCGCTTCAGACGGCATCTGTCGCGTTGCTGCGGATTA

**SEQ ID 5324**

LKMSLQSCVAGNSVSRILMAVCRRLQTAASVPLVGL

**SEQ ID 5325**

TGCTGTTTGTCTCAAAACAAACGCGATTCTAACGCCACAGCGCGCGCGGATGTAATTTTTCTGATTTTGTGACAATCTGCTAGAAATGGCGGTTTACAAAATTTAAACCTGCTTCAT  
ACCGCAT

**SEQ ID 5326**

SCLLQTKRDSNATGARRCKFF\*FC\*QSRMGVYKI\*TLAYRH

**SEQ ID 5327**

ATGTCGGACGAAGCCCTATTATTTTACTGACAGCTGCTGTGCCAAAGTTGCCGATTGATTGCCGAAGAAAAAATCCCGATTGAAATTTGCGGGTTTGTGCAACGGCGCGCGTGT  
CGGGTTTCCAGTACGGATTACTTTTGACGAATCAAAACGACGACGATTTTGAAATTTGAGAAAAACCGTTTGGCTCTTTTGGTTCGATCCGATGAGCTATCAATATCTGTCGCTGCGGA  
AATCGACTATACGGAAGTCTGCGAGGTTCCGAGTTCTGTCATCCGCAATCGAATCGGAAAAACCTCGCGTTGCGGATCTGCTTTTCCGTG

**SEQ ID 5328**

MSDESPIIFDSCAKVADLIAEENNPDLKLRVFNVGCGSGFYQYFTTDEIKNDDFEIEKNGLVFLVDPMNSYQYLVGAEIDYTESLQGSQFVIRNPNAEFTTCGCGSSFSV

**SEQ ID 5329**

ATCCTTCCTTTTTCAGATAGGTACTCAGATAAATACCTGAATAATAAGAAAAAAGCATCAGCGCAGTCGAACCGAATCTTATAGTTAACCCATTGCGCTTCAACCTAGTAACACACA  
AACCAAGTTGGCAATACCCATAAAAAATCAGAAAAACCGACCATATATGTCATTTTCCCATACCGCATCCGGAAGCTGAATCTCCCTGCGGATCTGCTTTCAAGCGGTTTATACCGG  
CAAGGTGGCTGCCAGCAGGAATAACGCCCGCACCAGAACATCTGTCGGCTTCCATATGAAGCGGCTGTGCCCAAAACAAATGTTGCGCGCGGAATACGCAATCAGCACCAG  
TCCGACCCACTGCATCTATCCAGCTTTTATGCTTCCAATAAGGAAAGCGCTGAAACACCGCTGCAACCAAGGCAACCGCGCAGCGCAATCATATTTTGGTAACGGTATAAGTA  
GCAAAAAACAAATGACGGACAAAGGTGCTGACAAATTTTCATATCCAAATGAGAAAGCAA

**SEQ ID 5330**

ILLFQIGTQINTLNKKEKHQRSRTEHLIVNPLRFXPKHKGPNVGNHKNQKTDPHICQFSPYGRKLNLPADTRFQAVPTRKVAQQE\*RPAPQYCRLPHEAAVAQNNGCAAEYDNQHQ  
SDPLHRIQPMFLPIQESRLHACNQGNRRSGNHIFGNIGSSKKQDDGQKQVADKPHIQMRKQ

**SEQ ID 5331**

GTGCAAGACTGCAAGACATCTTCAAAGTCCACCTGCATCCGTCCAAATACACCTGCATCTCAGCTACAACGAACAGCGCCCTAAAGTATGGGAAGGCTTGTAAACACAGAAAGCTACC  
TGCGGACCATTTCCGATCCCGACAAAGCACTTTGGGTGCGGAATACAAAGGCAACATACAGGAGATTTTTCCAAATCGACTGCCAAGAGCACAACCTCGATGCGCTTTACGCTCCACCCCT  
GTTCCAAATCTCGGACTGGGCACTGCCGTGCTCCGTGAGGAGAAACATCGCCACAAATCCGGTTTGAGCTTTCTGAAACTCTACGCATCTCTCAACTCCGCTCCGCTTTACCTTCTC  
AACCGCTACGAATCGCTCGTTGCGGAGATTGCACTTGACCCGACATCAAAATCAAAATGCAACTGATCGCAACACCTC

**SEQ ID 5332**

VQDCKDIFKVLHVSQYTCILSYNEHALKWEGLNTPESYLPITSDPKALNVAEYKNGIQGFPQIDCQEAQLDALYVHPLFHNILGLTALLRQAEITIAHKSGLSFLKLYASLNSVPFYL  
NRYESLGSALVQLDPSIKIKCELMRKL

**SEQ ID 5333**

ATGCTTGTCTGTCGGTTGGTAGATGGGCAACTTTATACGGCTGCTGCGCTTGTGGAATAATGTTGATTGAAGATTATCAGTTTGGTTATAAGCGGGGATTAGAGGTGTTGCGC  
ATCAGTTGCGATTGATTTGATGCTGGGGTCAAGCTGCAATCTGCCGAACCGAGCGATTTCGTAGCGGTTGAGAGGTAAACGGGACGAGTTGAGAGATGCTAGAGTTTCAGAAAGC  
TCAAAACCGGATTGTTGGCGGACAGGGCAGTGGCCAGTTCGGAATGTTGGAAACAGGGGGTGGACGTAAGCGCATCGAGTTGTGCTTCTTGGCAGTCAATTG  
GAAAAATCCCTGTATGTTGCTTTGTATTGCGCAACCAAGTCTTGTGCGGATCGGAAATGGTGGCAGGTAGCTTTCTGTGTT

**SEQ ID 5334**

MLVLSVGRWGFRLSALVEIMFDLKIISFGYKAGLEVFAHQFAPDFDAGVKLQYCRTERFVAVEKVKRDGVERCEVFQKAQTGFVGDGFLTEQGSQSEIVEQGVVDVKRIELCLAVDL  
EKSLYVAFVFGNPKCFVIGNGRQVAFV

**SEQ ID 5335**

ATGAAAACTTACGACAGGCACTCTATACCGACGCTGCTCACCGCTGACGCGCGCAGCGGATTCAAACCATCCGTCGGGACAAATGCCCGGCAATACCGAATCCGACGAAAAA  
ACATTACCTGCTCAATGCTCTATACGATGTGACAGGTATTTTACAAAGAAATACCAACCTTATTATCAAAACATACCAATCCGAACACCCCGGACATCCGTCAGCATCCCAACATC  
CCAAGCGCGCTCAGCAACAGGCATTATCCGTAGCCAAAGCGCTTCAAGCGGATTCGTAACCATGAACCAATCTCCGACATCGACCTGCTCGAAAAAAGGACTGG

**SEQ ID 5336**

MKTYAQALYTAALLTACSPAADSNHPSGNAPANTESDGKNTILLNASTDYTRYFYKEYNHILFKTYQSEHPGTSVSIQQSHGGFSKQALSVAQLQADVVTNNQSSDIDLLEKKDW



## SEQ ID 5337

ATGTTTTCCTTGTGCGAAAAACAACCCCAACAGATCCGCGATTGGAACGACCTTGCCAAAGACGGCGTTAACATCGTCATCGCCAAGACCTCGGGCAACGGAGCTACGCCCTCCTCG  
GCGCATACGGTTACGGTCTGAAAGCCAAACCGCAACGAGCAGGAAGCCCAAAACTCGTCGCATCCATCTCAAAAACACACCCGTTTTTGAAGACGGCGGACCGCGCGCCACCAC  
CTTACACACAGCAACATCGCGCAGCTACTCATCTTTTGAAGACGAAGCCAACTACGTCAGCAAAAAAGTACCCCAAGGACAGTTTGAATTCGCTATCCGAGCTACACCAATTTCCGCC  
GAAAGCCCGCTTGCCTCGTCAACAGCGTCTGTCGCAAAAAAGGACGCAAAAAACCGCCCGCCCTATCTCGAATACCTTTGGAGCGAACCGGCGCAAGAACTCGCCGCTCACTCTACC  
TGCCTCCCGCAACCCGAAGTATTGGCAGCACAAAGCCGACTTCCCGACTTAGACACCTTCCCTCCCGAAGAAAAATTCGGCGGATGGGACACATCATGAAACCTACTTCCCGA  
CGCGCGGCTATTGCAACCGCTGACCCGCAAAAA

## SEQ ID 5338

MVFLVRKNNPKQIRDNDLAKDGVNIVIAKTSNGRYAFILGAYGYGLKANNENBEAQKLVASILKNTVPFENGRAAATFTQRNIGDVLITFENEANYVSKKLQGGFEIVYPSYTTISA  
ESPVAVVNSVAKKGTQRTARAYLEYLWSEPAQELAAASLYLRPNPEVLARKADFPDLDTFPPPEKFGWDNIMKTYTFADGGVFDRLTAQK

## SEQ ID 5339

ATGACCATTATGCGCTTGAACCGCCTTTCAGACGGCATTTACACATCAAAACAGAAAACCGCACCCAAATCATCATCAAGACACAACCGCAACCGGATACAAAACCAACACCGC  
CGCCAAATGCGCTTGAAGCCGTGCGCGCAACCATCTTATCTGGGGCGCGCTCATCAAGGGCGCATTAACCTTCT

## SEQ ID 5340

MTIMPSEPPFRHFTQNRKPKSSQDTTANRIQNPTPPKCLKPSAQPSLSGARLIKGAHFP

## SEQ ID 5341

ATGTTCCGATACGAACCGCAAAATATTTGGTTTGTTCAGACGGCAAAAGCACTGTTTATTTGGCTGTCAAAAGGGATGGTTAAGGAAAGTTATGCGCCCTTTGATGAGCGCGCCCCA  
GA

## SEQ ID 5342

MFRYEPQNIQFVSDRQKHCLFGCQKGLRKVMRPFDEARFR

## SEQ ID 5343

ATGTTTTTTGAAAGTGTGATTGTATATCAAAAAGAAATGCGGCAACCGTCGCGAGTGTGATTGCGCGAAATGCGGGTGGTGAACCGATATGCTGCAACCGCTGATAAAGTTTAAAAA  
CCTGCCTTGGGAGCAGGTTAATGGTTTGTCTAATCTTGAATTCGCGGAAACGCGAAGACCGGAAATC

## SEQ ID 5344

MFPESVIVYQKMRQPSAVLIAGNAGRSNRYARTPDKVLKTLAKQVNGPANLELPETRNTEI

## SEQ ID 5345

ATGAATACCGACTTCCAAAAGATCCTCAAACTGCGGCAACAGGCCAAAAAGAGCGGCAGAAAAACAGGAAGCCGAAAAAACAAGCAAAACAGGATTTGGATTTTTAC  
AAGCAGTCGGCAAGTCTCCCCATTAAAAACCGGCAGCAATATTATGCGCAGTCGCAAAAAACCCCATCAAGCCCGTCCCAAGACACCGCAGCAGAAAGAACTACTTCTACAT  
AGGCAGCACATACACGACCCACCGCGCAGCTTCTGCAAAACGGACAGGAAAAACGACATCCACCGCTGAAAAACGGATATATCCCGTGTACCGATGTGCACTGCACGGCTAC  
ACCCAAGAAGAAGCAAAAAGTCTCAACGAATTCATCGCATTCACCCAAAAACCGCGGTATGCGGCGAAATCATCCACGGCAGCGGATTAGGTTCCAAAGGCTACAAACCGTCTCTGA  
AAAACATGACCGGAACTGGCTGATGCAACACCCGACGTACTCGCTACGTCGAACCCCGGAAGGCAACGACCGGCTGCGTCCGATCTCTGCTCAACGCAAAATTAAGCGCAGCAAGAC

## SEQ ID 5346

MNTDFQKILKQLKQAKKEAEKQAEKKNQKQEQDLDLFSQAVGVSLPLNRQYYAQSDKTPIKARPKDNRTDEZNYFYIGSTYNDPPAPCKNGQKNDIQRLKNGYPPVTVDLHG  
TQBEAQKVLNEFIATQKRGVCGEIIHSGSLGSKGYKPVLRNTRNMLMQHPDVLAYVEPRENGDGVRIILKRLRQDD

## SEQ ID 5347

TTGAGTTTTGCAATTTATGGGGTAACTTTTGGGGTAACTTTTAGGAATCACCTTAAAAATATCTTAAAAATACAAAAGCCATCACGATTTTTT

## SEQ ID 5348

LSFRNLWGNFWGNFSGITLKNILKIQKPSRIF

## SEQ ID 5349

TTGCAGGCGTTTGACCAACAGATTTTCATTAATCCGCAACATACAGTCCGTCTCTCGGCGTATTTTCCCATGATTGACCAAAATCGAATCTCGGTCAATCAAAACCCCTCCATCGAA  
TCCCCCTTGACGGAATTAACAGAGGTTTTTCGTATCTCGGTAACATAATCTCAATCCAATCCCGCTGCAAGCCCAATGTAATACCGGTCTCATGACCGCAAACTGCCCGTATC  
CCGACGCGCCGGAATATCATATCTCGGCACAAAGACAACTCTCGGTATCACTTCAATTTCCCAAGGTATCGTAAGCAAGGATTTTTTTGGGGCTTATCCGGAACCGGATTACCTC  
CCCTGTACAGCCCAATCGATACACCCCTTCACTGCTTAATTTTTTTCAATGTTTCAGACTTCGCGCAGCCGCTTCAFTCCATATCTCTGTAAGCCCGCAATCGTCAATTTCAATA  
TCGGATGCGGATTTTTGCTCGCTCGCTCACTTTTCCA

## SEQ ID 5350

LQAFDQIFINPHIQSVSRRIIPMIDQNRISVIONPLHRIPLDGNRYQVFRISGNIILNMPMSERHKRYFLMTDKLPVSRSPNIIISRHDKLVRINFI SQGIVSKGFFWGFIRKRI  
PCQPIIDTTPQLQLNFPQCFLRLQTAFIGPISABARNRHFNI GDFCLPRFTFP

## SEQ ID 5351

GTGTCGCGCGTACGGTAGCCGATATCCCGAGTCTAACGGCAAGGCGAATACAAAGCTTTTACCGCTTATGTTAAAGGCAAGGCCACTGCGCGCAATTTGAAAGAAAAA

## SEQ ID 5352

VSAVTVADI PESNGKGEYKVFTAYVKKATAGNLKEK

## SEQ ID 5353

TACTTGGTTTATATGCTTTTGGGTACGGGGCTTTTCTTACCCTAACCACGGGCTTTGTCCAATTCGCGTGTTCGGGCGCAGCATCAAGAAATGCTCGCGGGCGCAACAGGGGACG  
ACCTCAC

## SEQ ID 5354

YLVMYLLGTGLFTVTTFVQPRFLGRSIEKLGGRKQGDDPH

## SEQ ID 5355

TTGATTAAACTGTCCGACTTTTTGGGGTGCACTGAGCTTCGGCAATTTTTATCCGTTTGGGGTAACTTGTGTTGAAAGCTGCAAGCCTTATAAA

## SEQ ID 5356

LKLSDFIGCSSAFAFIRLVTCLSECKPYK

## SEQ ID 5357

ATGCCATCCGTTGAATGCTGTTGGGGATTGTCGAGTGCACGCGAGCACTTCTATTACCAATTTGGCGTCCAAATCGGCGAGAAGGCAATATGCGGATTTGAAACGACATATCCATGATA  
TTTATCAACGATATAAGGGAAGATACGGCTACCGGAGGATTGCGGCGAGCAATCCGTACCGCAGGAATACCGGTCAATCACAAGAAAGTCAGCGCTGTATGGCGAAGACGGGGCTGAAGGC  
AGTGATACGGCGCGCAAAATACCGCTCGTTCAAAGGAGAACTCGGCAAGTTGCGCGCAACATCTGCAACCGTGTTCATTCAAGAAAGCCGAATGAGAAATCGGTAACGGACGTATCC  
AAGTTGATGTAGCGGAGAAAGATATACCTTCTCGGATTAATGATTTCTTTAACGGGGAAATCGTCAGTTACCGTATTCAAACCCGCGGACTTTTCGATTTGGCGCGGAGATCTGA  
AAGGTGCGCGGAGAAACCGGGCGCTGTGAAAGCCGATGCTGCATTCGGATCAAGGTTGGCAATATCAGATGTTTTTTTATCAAAAGCAGTTGAAAGGCAACCGGTCTGTTTCAGAGTCT  
GTCCCGCAAGGGAACGTGCTTGGACATGCGGCAATGGAAGTTCTTCGGAACGTGGAATCGGAATGTTTCCATACGTGCAAAATATGATTCGTTACCGAATCGGAAGCGCACTGCAC  
GAATATATCCGTACTACAAACGATAGAATCAAGTTGAAATTAAGGACTGAGCCCTGTCAGTACAGAAATTCAGTCCCTGAAAGCGCT

## SEQ ID 5358

MPSVELLLGIVLPRSTFFYQLAVQSAEGKYADLRHIDHDIYQRYKGRYGYRRIAIAIRHAGIPVNHKKVSRIMAKTGLKAVIRRRKYSRPFGEVGVKAPNIIQRCPHSEKPNKRWIVDT  
KFDVGGKTYLSPIMDLFNGETVSYRIQTRPTFDLAGELKGAPEKPGSEKPNLHSDQWQYQMFYQKQLKGNGLVQSLSRKGNCLDNAAMESFFGLTKSECFHTCKYDSVTESBAALH  
EYIRYNNDRILKLGKLSVPVQRIQSLKAA

## SEQ ID 5359

GTGACGGGGCAGGGAATGTCCCAAAAAGCTGCCGACAGCACTGAATCTGCCGACTGCTCCGTTTTCGCCCAATGGTTGCGOCTCTACCGTTGAATGGTATTACGGTTTAAAGCCCA  
AACCCAAAGGAAGAAGCCCGTGAAAAACAGTATCCGCCGCAACGAAAAAGCCGACTATCTGAAACCAAGGAAGAACTGTTTTCGGGAATTGGCTTACCTTAAAGCGGAAGCGGCTGT  
CCTAAAAAGCTCGATGCTTGAAGAAGTGCAGGAGAAAGCACTGCTGCGAGGGT

## SEQ ID 5360

VTGQMSQKAAADQLNLPDCSVLPQWLRLYLRLNGINGLKPFPKGRKPKVKKQYPQTKKADYLTKEELFAELAYLKAEAAVLKLLDALKEVRQKERNSSQG

## SEQ ID 5361

ATGCCGCTTTACCGTGAATCTGTATCTTGCCACCCATTGCGTACCAATGAATCGAAATGGAATAATATAAGTAAATTAACAAAAATCAGGACAGGCGCGGACCGCAGGCAOTACGA  
ATGGTACGGAACCGGTTCCGCCGCGCTCCATCACCCTTAGGGAATCGTTCCCTTTGGGCCGGGGCGGGCAACGCCGTACCGGTTTGTGTAATCCGCTATATTACGGCAATGCAAAAAAC  
ACCGGCCAAACCGCAGCAACGCTTTACTTTGTCAAGAAACACGCTTTACCTGCGGATTGCGCTTAAAAACCAACAGGCAGCC

## SEQ ID 5362

MPLSPCNLYLATHLRNTESEMEKYSKLTIRTRRTAGSTNGTEPVRPALHHLRESFPLRGGAATPYRLLIRYITDNAKTPAKPQRLTCQETRTGCFALKNKQAA

## SEQ ID 5363

ATGCCGCCAAATCCGATAGGCAAAAACCGGCTCGATATGTGCGGCGCATCCGGAATGCTGTCTGCATGAATCGCCAAACATTGTTGATTGACGCGAGCCGCGTTTGCCATCCGCCAA  
ACAGATGCGGATGCGCGCAAAAAGACCGCGCTTACAAAGGACAGACCCGGCAAGTAACGATATTATTTGACACGCGCGCGGATTTTCGACTGCAACCGCTTTGTCCGGATGA  
AACAGGATTGACGCGCGCTGTTCGCCCTTATGCCGCGAGCTGAAAGGGCAATGGCGAAAGCGCGGATAAGTGGGAAAGATACCGGCGCTTATCGCGGAACACGCGGAGGATT  
TCCAAGGGTGCGGCTCCGCTATATCAGGAATCCAACAGG

## SEQ ID 5364

MPPNRIGKNRLDMSGIRMPVCMKSPNILLVRQPPFAMRPNRCGWRAKTAAYKQDPAKVTHYLTRPAGFSDCQRVCPDETGFDRRLFRPYARSLSKQMAKARI SGKRYRRLSARHABGF  
SKGCGCRYITKSNR

## SEQ ID 5365

GTGCGGCTGCCCTATATCAGGAATCAACAGGTAGAAATCTTCTTTGCCACGCGGCAATTCGGGGCAATTCAGTCGTGCGGGATGTCTTCAAACCTTTGTCGGGGCGGATGCGGT  
TCCGGGTGCGGAGTCTTCTATCGTAATCCAGCCGACGGGGCGGCACATATATTGACCAATTTGTGTTTCTTGTGTTACCGTGTCTTTTTCAGCGCGGCGCGGGGTTTGGTTCGGA  
TGCCGTC

## SEQ ID 5366

VRLPLYHEIQQVEIPFAHAAGFAPFVVGDFVFLCPGDAVFRVAEFFIVNPAAGAAHLSHLCLVCTVLFCSGPPFGSDAV

## SEQ ID 5367

ATGAAGGGGAGCGGAAGGATATTTATGAAACCTTTAAAGACAGACTGGTTTTTTTATGAAAGTGAAGCGGAGGCAAGCAAAATCGCATCCGATATTGAAATGACGATTGCGGGCTTCA  
GCAGATATGGAATGAAGCGGCTCTCGCAAGTCTGAAACATTGAAAAAATTAAGCACTTGAAGGGGTGTAGTATCGATTGGCTGTGACAGGGGAGGGTAATCCGTTTCGGATGAAGC  
CCCAAAAAATCCCTTGTCTTACGATACCTTGGGAAATGAAGTTGATACGCGAGAGTTTGTCTTTGTGCGGAGATATGATATTCGGCGGCTCGCGGATACGGGAGTTTGTGCGTATGAG  
GAAACGGGATTTTCAATGGCGTTTACAGCGGATTTGAGATTATGTATTACCCGAGATACGAAAAACCTGTCTGTAATTTCCGCTCAAGGGGATTCGATGGAGGGGGTTTGAATGAGC  
GAGATTGCAATTTGTCAATCATGGGAAATACGCGGAGAGACGACTGTATGTGTTGCGGATTAATGAAATCTGTTGGTCAACCGCTGCAAAATCGTCCCGCGGGGATTAATCAATGT  
CATTTCCGCCAACGAGGCTTATCTGCTTTTGAATCAATTTGAACGACTTGACCGATGATGTGAGAGATTATCGGGCGTGTGAGTGTTCGCGAGGACGGTT

## SEQ ID 5368

MKSGRIFMETFKDRILVLPWKSEARQAKIASDIEMTIAGFSRIWNEGLPKSETLKKIKQLKGCSDIWLITGEGNPPFDEAPKSLAYDTLGNEDTDEFVFPVYD IRAAAGYQGFVGH  
EPVFTMAFRHWEIENYVTRDTKNLSVI SVKGSMEGVLANDGDSILVNHGEWPPRDGLYVLRINENLLVKRLQIVPGIINVISANEATPAPEINLNDLTDEVBIIIGRVEWFGRTV

## SEQ ID 5369

TTGACGGGTGAAGCGTTGCTTTTGGACAGCGTAGCCGAGCAATTTTTCGCCAGATAACGTTTAACTTGGACAGCTCCAAACCCGCCAGGAAACGTGTGGATTGCGCGCGGTTGG  
GTGTAGGTATAACCGGCATACACGGCAGCCATTTTGCTTATGCGCGGTAGCGATGTGTGATTCCTCTTTTGTCTGTGATCGTTTTCGTTCCGGCGTACTCTGCTTAAACGCA  
TATCGTGGCGTTCTGTAACGAAACCGGATGAGCGGTGCGCTTATTTTCTTCAAATGCGCGGAGTGGCTTTGCTTTAACA

## SEQ ID 5370

LQGEAFAPWTVGAAFFSQITFNLDLQATATETCGFAARLVGVTGSHFAYCAVSDVCIPSPVVCIVPASVGLCKTHIVAFVERKPHDGVRYFSKLEPAVALELT

## SEQ ID 5371

ATGCGCGCGCGCGCTTCAGACGGCATCCGAACCAACCCCGCGCGCGCTGCAAAAAAGCAGGTACAAACAGGAAACACAAATGGCTCAATATATGTGCGGCGCCGCGGCTGATT  
ACGATGAAGAACTCGCGACCCGGAACACGCGCATCGCCCGGGACAAAGTTTGAAGACATCCCGAGCACTGGAATGCCCGGAATGCGGCGTGGGCAAGAAGATTTTACCTGTGGA  
TTTCTGTGATA

## SEQ ID 5372

MRRPASDGRTRKPRRPAKKHGTNKTQMAQYMCPCGWLYDEELGDPHEGSIAPGTFEDI PDDMKCECGVKEDFYLLDFVI

## SEQ ID 5373

GTGGGAAAGATACCGCGCTTATCTGCGGAACACCGCGAGGATTTTCCAAGGGTGCGGCTGCCGCTATATCAGAAATCCAACAGGTAGAAATCTTTTCCCAACGCGCATTCGGG  
GCATTTCAGTCGTGCGGGATGTCTTCAAACCTTTGTCGCCGGGCGGATGCGGTGTCCGGGTGCGGAGTTCTTCATCGTAAATCCAGCGCGAGGGGCGGCACATATATTGAGCCATTGT  
GTTTCTTGTGTAACCGTCTTTTTCAGCGGGCGCGGGGTTTGGTTTCGGATGCGGTGTAAGCGGGCGCGCATCTGCCGCTTGGGCGGTTTGTGCTTCAGACGCAATTTTC  
CGCTGTTTATTTGCGGCTTCGATTGCTGCTATTCTTTGACAGAGGTGTT

## SEQ ID 5374

VGKDTGAYLRNTPRDFPRGAAAASRNPTGRNLLCFRRIRGISRRGCLQTL SRGRCPVGRVLRHRSRRGRITYIEPFVPCLYRAFLQRAAGVWFGRLKRAAASVPPWAVCASDGI  
RLFILRLRLFLCRGV

## SEQ ID 5375

ATGAACGCCCAACCTGCTTGCCAACTGTGCGAACTCGTCAAAACCAAGCTCAAAACCCCTGTCGACGACATCGACCGCAAGGATACCTACCCGAAGCAATTTATGCGCGAACTCGGG  
CAATCGCGCGAGTGGTATAGAAAGCGGAAGCGGCAACGCTTAGGCTTGGCAACAGCAATCGCGCTGTGCGGAAATCGGCAAGAAATGCGGCGGACCTCTTTCAGCGGTGGTGTCA  
GGCGGCTGCGGCTGGTATCTGCACAAACGCCCAACAGCGCTCAAGACAAATACCTGCGGACATCTGCAAGGCAAGATATTGGCGGGCACGGATGTCCAATACCGTCAACAC  
CTTGC CGGCAATTGAAACACAACTTCAAGCGAGTGGTGGAGGGCGGTTATACAGTCAACGGTGGCTGCGGTGGGTGTCACATCGCGGAAGACCAATTTGGGCGGAATACCGGCC  
AAATCGCGCGCGCTACGTATGTTCATCACAGCGGGCAAGGGAAGCGTAAAGCTGCAAACTGCCCGAATTTTTCGCCCTCGAAGGCAACGCACTTCAGCTGAAATTTCAAGA  
CGTATTATTCCGACGAGACATCATGCTGCGCGGCAACAGTTTTCGCCGTACATCAAAAGCATCAAGACAGGCTTCATCTCTGCAAAATCGGTATCGGCGGGCGGTGATTGAGCGC  
AGCCTGCGCATCATCGCTTCGTCAACGCTGTCACGCGGAGTCAACAGCTATCTGACGACAGGCTACGACAGCTCAAGCAAGGCTGGACGGCGGTGGGAGAAACCAACGCGCTG

CCGGATTGGCGTGGGACACACGCCGACCACTCGCCACCTCAAGCTGCGGAGCGCGCGTACTGGCCCTTGCCGCTGCGCAATCGCGCGCTGCATTCGCGCGCGAAGGCTA  
CCTGATGCGGAGTCCGCCCAAGGCGCTCGCGGAGCGATGTTTGTGCCCATCTGAACCCCGCAATCAACACCTCTGCAAGAAATAGCAGCAATCGAAGCGCAAAA

## SEQ ID 5376

MNAQTLLANVAELVKTKLPLVDDIDRKGYYPEAFMRGELGAVGIEABGGNGLGLATRIAVLREIGKECGATSPSAWQAAACAWYLHQTPNQAVKDKYLDILQKVLAGTGMNFWKH  
LAGIEKHNLAECVGGYTVNGALFWVSNIGEDHIANTAQITGGGYVMFTGGQREGVSLQNCPEFCALBHTTFSLAFKDVFPIDEDILAAPQFAGYIQSIRAGFILLQIGIGAGVIDG  
SLGIIRLVNVNAEVNSYLLDDGYDSLKARLDGANAEETERLAGLAWNDTFLDNLATLKLREAAVLALAAAQSAALHSGAKGYLHRSFAQRVRGEAFVATVTPAIKHLCKEIAAIEBAK

## SEQ ID 5377

TTGTTCCTTAAGGTTTTTGGGGGAAATCGGGGGCACGCTGATCGCGGCTGCTTTTCCCGCGCTTGGGCGGCTTGTITTTTGTGAGGGGGTGTITTTGAAAAACCGCTGCATTACG  
GCGGTTTTTGTTCGTTAGGCGTATGCTGCAATTTGGGGTTGATTTGCGTTTGGGCGAGGTTGTGGCGTAGTTGCACAAAGTTGCCAAGGCTACGCCATTACGACTTCGACTGCTGCT  
GCCGTTGTAGCCGCTTCGAGGAAGCGTTGAGTTGCTGCTGCGATACTGCGCTTTTTCGCCATTACGCTTGGGTGAAGCGCGCAAGCGCGCGAGTTGGCATCTGCAGATTAC  
TGCCGCCAAAGCGCGCGCGCATTTGAGGGATTGCTCGGACAGGAGTTTTTTCAGGTTGCGAGTTTGGTGTGCCCTGCCACGCAGAACTGCATTTGGTTGGTGGGACGCGCATGATCCGG  
ATCACTTCGACTTCGCGCGCGCTGAGGCTGTGGCGCGCTGAGCTTCGCCGACTCTCTGTGTAAGCCCAAGCTTTCGGGGCGTTTGCCAATACCGCATGAGTTGGGGATAAGCGGT  
TGTTTTTGGGTAGCGCTTACGCGCGGTTTGGCGGCTTCGGGGCGGTTTCGAGGTTGTGTAAGCT

## SEQ ID 5378

LFPLKVPGGKSGARLMRCFSRRLGGFLFPEGVFLKRLHSGGFVCLGVCLQFGVDFGLGEVVGVAQSCQGYAHYDFDCLLPVVARFEEGVFVVGCAFFPHYGLGEGGKRAEFGIVRFT  
CRQSAGGIEGLGQEFPGCEPVPCHAEALVADGDDPDHFDPAAGQAVGGVELADFLVKRQSPGVCQYADEVGDKAVVFGYGLYARFGGFGGFEVGTG

## SEQ ID 5379

ATGGCAGCTTTAAACGTTACACACCTCGAAACCGCCCCGAGCGCCCAACCGCGCTAGAGCGCTACCCAAAAACAACGGCTTTATCCCAACCTCATCGCGGTATTGGCAACGCC  
CCGAAGCTTTGGCGTTTTTACCAAGAGTGGCAAGCTCAACGCCGCCAACAGCTGACCGCGCGGAGTGAAGTGATCCGGAATCATCGCGCTCGCACCAACCAATGCAGCTTCTGCGT  
GCCAGGCGCACCAAACTCGCAACCTGAAAAAATCTGCTGCGAGCAATCCCTCAATGCCCGCCCGCTTGGCGCGCAGGTAAATCTGACGATGCCAACTCGCGCGCTTCCGCGCTTC  
ACCAAGCGGTAAATGGCGAAAAAGGCGCAGTATCCGACGACGAATCAACGCTTCTCGAAGCGGGCTACAACCGCGCAGCAGGAGTGAAGTGTAAATGGCGGTAGCTTTGGCAACTT  
TGTGCAACTACGCAACAACTCGCCCAACCGAAATCAACCCCAATTCAGGCAATACGCC

## SEQ ID 5380

MARLTVHTLETAPEAAKPRVEAVPKNGFIPNLIGVLNAPALAFYQEVGKLNAAASLTAGEVEVIRILAVRTNQSPCVAGHTKLATLKLKLSSEQSLNAAALAAAGKSDDAKLGALAAF  
TQAVMAKKAUSDDLENAFLAEGYNRQAVEVVGVALATLCNYANLQAQTEINPKIQA

## SEQ ID 5381

ATGAACGAGAACTTTACCGAATGGCTGCACGCGTGGGTGGCGCCATCAACGATCCGATGTGGTCACTATGCTTTTGGGTACGGGCTTTCTTACCCTAACCGGGCT  
TTGTCCAAATTCGCGCTGCTGGCGCGCAGCATCAAGAAATGCTCGCGCGCGCAACAGGGGAGCAACCTCAGCGCATACGCGCTTTACGCAATTTGTAACCGCGCTTGCAGCGCGT  
GGCGGTGGCGCAATATCGCGCGCTGGCAATCGCCATCAAGTCCGCGCGCGCGCGCGGTGTTTGGATGTGGGTAAACCGCTTAATCGGCATGAGTTTGGCGTTTGTGCAATCTTCGCTG  
GGCGAGCTCTTTAAAGTCCGCGCATGCGACACCACTTTTCGGGGCGCGCTGCTACTACATCAGCAGCGTTCGGGCGAGAAATGGCTGGGCGTGTGTTGCCCTGAGCGCTGATTT  
TCTGTTCGCTTTTGTGTTGAAGCGGTTTCAGACCAATACATCGCGGATACCGTCAAGCGCGGTGGGCTGGAGCGCTCATTAATGTCGCGTCCGCTGCTGATTTTAAACCGCGCGAT  
TATCTTCGGCGCATCAGCGCATATCCAAAGCGCGGAAATCGTGTGCGCTGATGGCGGTTTTGTACCTTTTATCGCGCTTTTCATCATTTTGAACCAATATTCCGATGATTCCGGAC  
GTGTTCCGTCAGATTTTTCGGCGCGTTCAAAATTCGACGCGCGCAGCGCGCTTACTTGGCGGTCTGATTTGCAAAAGATGATGATGGGATCAAAAGCGCGCTGTATTCCAACGAGG  
CGGTTATGGTTTCGCGCGCAACCGCGCGCGCGCGGAGTGAACACCTGTTTCGCAAGGTATGATTTCAAAATGCTGGCGGTGTTGTGATACCATCATGCTTTGTCCTTGCACCGC  
CTTCATCATCTTGATTTACCAACAGCTTATGGCGATTTGAGCGGTGCGCGCTGACGCGCGCGGATGTCAGCCAAAGTGGGCGAATGGGCGCGGTTTCCGCGCGCTCATCTGTTT  
ATGTTTGCCTTTTCCACCGTTATCGGCAATATGCTATGCGGAGTCCACGCTCAATTCATCAAAAGCCATTGGCTGATTACCGCGCTTTCCGCTATGCTGTTTGGCGTGGGTCTATT  
TCGGCGCGGTTCGCAATGCTGCTTTTGTGTCGGATATGCGGATATGCGGATATGCGGATATGCGGATCAACCTCGTCCGCAATCTGCTGCTCTGCAATTCGCGCTTATGCTGCTGCG  
CGATTACACCGCGAAGCTGAATAATGGGCAAGACCCGAGTTCAAACTTTCGCAACATCCGGGCTGAAACCGCGCATCAATCCGATGTTTGG

## SEQ ID 5382

MNENFTWELHGWGAINDPMSYLYVMLLGTGLFFVTITGFPVRLFRSRIKEMLGRRQGDDEPHGITPPQAFVTGLASKVGVGNLAGVAIAIKVGGPAGVPMWVTALIGHSSAFVSSSL  
AQLFKVRDCDNDHFRGGPAYIYTHGLGQKWLGLVLFALSLIFCPGFVFAVQNTIADTKAANGWEPRHYVGVVALVILPAPIIFGIRIRISKAAREIVVPLMAVLYLFIALLFTINIPHPD  
VFGQIPSGAFKFDAAAGGLGLISQTMGMGIRGLYSNEAGMSAPNAAAAAEVKHPVSQGMQLGVFVDTIIVCSCTAFIILITYQPYGDLGSAALQAAIVSQVQWAGAGFLAVILF  
MFAFTVIGNYAYAESNVQPIKSHWLIATVFRMLVLAHVYFGAVANVPLWMDMANGIMAWINLVAILLSPLAFMLLRDYTAFLKMGKDFEPLKSEHPLKRRIKSDV

## SEQ ID 5383

ATGCGTTTTAAGCGAGTACGCCCGAAGCAAAACGATGCAGACGACAAAAGAGGAATGCACACATCGCTAACCGCGCAATAGGCAAAATGGCTGCCGTGTATGCCGTTTATACCTACA  
CCCAACCGCGCGCGCAATCCACACGTTTCCGTGGCGGTTCGAGCGTGTCCAAGTTAAACGTTATCTGGGAGAAAAATGCTCGCGCTACGCTGTCCAAAAAGCGAAGCGTTACCTCGCA  
AGCAGATGCTGAATCCGTCAAACCTTGGCGAAGGCTGTTTCTGAAGCTA

## SEQ ID 5384

MRFAEYARSKNDADDKRGNAHANGAIGKMAAVYAGYTTTQPGGESTFRGGLEVRVQVKRYLGEKCCGYACPKSERFTLQADGEIRQNLGEGWFLKL

## SEQ ID 5385

TTGCTGGTTTTCTTCATTTTTCTATCCTTTTTCTGTCAATTCGGGATTAACACTATGAAAAATCTGAAAAATATGATTTGGATAAGAAAAATCATAAATTTAAATTTAGTTTATCATAGTT  
ATTCCGTTTTTGGGATAGCTAATGTAAATATATTTCAATGTTTACTT

## SEQ ID 5386

LIVFFIFLSFFQPGIKPMENLKNYVLDKKNNLNLVYHSYVFGIANVKYISCLL

## SEQ ID 5387

TTGTTTGGCACGCTGTGGCGTGTTCAAAAGAATGTGGGGTTGGGCTGGGATGACGGCGCGATGTTGTTGGCGGTGTTTGGCCAACTGTTTACGGCGACACGCGCGCACAG  
ACTGCGGTTTTAAGTATTTGGTTTGGCGGTTTCCGTCTGGTTCCGCGCAAGGGCAACAGCTTTATGCACGCCACTTTTATCGCGCGCTATACCGAATTCGCCGAACAGTGAAGC  
CGCAACCCCAAGCGCATTTGGCGCAATATTTCCGCGCGCGGGCGGG

## SEQ ID 5388

LFGTWACFKRMWGLGLGTGAMPVLAVFAQLVYGDTPATDSAFNVGLAVSVWFGAKGNSLYARHLISRGYTELPEVVEANPQAALAQYFGRGG

## SEQ ID 5389

TTGTTTGAAGGCTTGGGCGCGCGGCGGATGGGTGTAGATTTTGTATGTTTTCATGCTGTTTCTTTTCGTTGAAACCTGCCCTTTGGGAAGGAGGATCAGACTTTATTTGTGAGA  
CGCGCGCGGTGTGAGACATACGCTGAACATGCCCTCGGGGAAGACAGATCCGCAATCCGCTC

## SEQ ID 5390

LFDDLGRGCGMVDVFWHRVSFVSVELFPFGKVSDFICETRARVQTYGLAMPVGEDRSINAV

## SEQ ID 5391

TTGGCGGTGTCGCCCGGAGCATTTTCGAAATGTGAAAAATTCGAGCGCTGCTGCAAGCGGACGCTGATTGTGATTACGAGCGCGCAATACCGACTGACCGCGGCTCGAACCC  
CCGACGGCAACGATTACGACCGGACATCTGATTGTGAACACCATGCGGATGAACATCATCCAAACCATCAACAAACGAACAGTCTGCTGCCCTGCCCGCTCGACCTGAAACGAGT

TGAAC TGCTGCTGAAACCTTTGGGACGAGAACCCGATTCGGTCATCGGCTCTTCTTGCACTCGCGCGTCCGTTTATAGCGCGGTGTGCAACAACCTCCGGCGCGCGTGTGGTACAGCGCGG  
CCGGCTACACCGAAATGGCGTTGTTCGCCAAATCAACGAGAGCGGAGTGTGGAACCTGCTCAACCATTGGGCATAGACTTGGCGCAGACGCCCCAGAAATCTTGACCAACCTGCAAG  
GTCATCTATTATCAGAAAAAGCATCAAGCAAGACGCGGGCAAGGACATGACCACGCTATTGCGAACACGTCGCCCACTGGAAGAACCGACCGCGCGCGCTTCAATGCCGACCCCGC  
CGCCATTCAGAAAGCCTTCGGGCTCGCGGGCAAGCTGATGGTTTTTGCGCTCCGTTTGGACACTTCCCGCAAGAAAAACAACCCGCGCTGTCTACATCGGCACGAACGACATCAACGAG  
CTGACCGCATCCGCCCGCGCCCTTGGCGCAATTTGAAAGCTGCGCGCTTTCGCGCGAATACATCCACGCCACGCTTTCGACATTCCCGACAGTTCGACGCAAGACAGCTTCTACGTC  
TCAAAAAATTCGGTACGCAACAACTGCCGAAATATTATTGACTTGAAGCGCGCGGTGGACAGGTTTCGGCAAAAAAGCTCAGCTTCTGCCCAACAGTTTCTTCGCAAGGCAATGCAAGTTCGT  
CAGCAATTCCTTGCCGACGACCTGCCCAATTCATGCGCGATTACCGCGACAAATCAAGCAACACCTGATCTGCAAAATGGCGGAAAGGCGTGGATGAGGCGCGCGCTTCTTAAAA  
GAATATTTTTCAACACCGCGCGCGCTTTTTTCGCGTCAACGCGGAGAACCAAGCGCGATGCTGACCGTTTCGCCCTCGCTTCCCGCGCCATCCGCTACCGTTCGCTGCACGAG  
ACGAATGTGAGGAGCTTGGTGGCGCTGATATTCCAGCTGCGCGCGCGACGACCGCGACTGGTTTGA AAAACTGCCCGCGGAAATGCACAAATAAATCATTCATAAATGTATTACGGGCATTT  
TATGTGCGACGTTTTCATCAGGATTACATCATCAAAAAAGCAACGGCTGTATGGCTTGAACACAGAAATGCTACACTCTCTATAGACCAACGCGGCGCGCAATATCCCGCGCAACACAAC  
GTCGGCCATTTGTATGAAGCCAAGCCCGCGCTCAACAGTTTACCGCAAACTCGACCCGACCAACAGCTTCAACCCGGGTATCGGCCAAAACAGCAAAAAGAAAACTTGGCGGAA

**SEQ ID 5392**

EQ ID 5392  
LAVVRPGSILEMWRILQACVEADVIVITQAA NTGLTGGSSTPDGNDYDRDIVIVNVMRMI IQTINNNEQVVCPLPGSTLWLELLIKPLGREPHSVIGSSCIGASVLGVCNNSGGALVQRB  
PAYTEHALFAQINEEGRLELVNHLIGD LGDTPEBILITNLQGHYQKKDIKQDAGKGHDHAYCEHVRCQVDEPTAARFNADPARHYEASGCAGKLMVFAVLDTFPQEKQTAVFYIGTNDINE  
LTDIRRAALGEGFESL PVSGEYIHRHAFDIADVYKGTFTYVLIKFGTHQLPKLFDL KARVDRPFGKVSFLPKHFSOKAMQVFSKFLPDHLPKSMRDYRDKYEHHLILKMGGGKGVDEARAFK  
EYF SHHGGAFFECNAEETQAAMLERHFAVASAIYRSVHDEVEDVALDIALRRDRDWF EKLPPEIDNKILHKLYYGHFACHVPHQDYI IKKGNGCNALHEHLEHLIDQGAQYPAEHN  
VGHLYEAKPALQYFYNKLDPTNSFNP GIGKTSKKKNWAB

**SEQ ID 5393**

SEQ ID 5393  
ATGATGTAATTTTCGCTACGGCTTGGGTCAGGCTGCTGATTAAATGCGAGGCGTTTCATAACACTCTCCTATCGGGATAAGCGCGCGCAAAATCCCGGTACGCGCGGTATGTTCAATTT  
GCAATATTTTGGTGGCGCAAGTTGCAAGCTGCAAATTAATTTTGGTTAAAGAAA

**SEQ ID 5394**

SEQ ID 5394  
MMYFSPTVWVRLINCEAFITLSYRDKRRRKSRYAAVCSTWIFWCGKLHAANYFWLKK

**SEQ ID 5395**

SEQ ID 5395  
ATGAAAAAACTTCTAATGATAACCCCTACCGGTATGCTTGCAGCTTGTTCACAGGTGTCAATGTGCGGCGGTGATGGTTGAAATGCCGACAGGAGAACGCCCTGTTGTGCTGCAGGTTTC  
CCGCGACGAATAAACCCGCTTTCCGATGCGGTGGCTGTCCGAATGATTAACAATCCCGGATCGCCTTCGGCATCAAAATATGATTGAAATGCTCGCGCGGACAAATATCAACGTGCGGCTGGC  
GGGAGGCAGCCAAATGTTTAAATAGGCAGCCGACTTTATTCTTAAACCATGCAAAAGAAATCGGAAATAATGTCAGTGTCTATATGACGGGCGATAGCGAAAGCGACAAGGCCGATTTG  
GAAACCGCGCAATGCCAAAAATTTAAATTACATTATTCTTTAAACAAAAA

**SEQ ID 5396**

SEQ ID 5396  
MKKLLMITLFGMLAACSTGVNVGRLMVEMPOGERPVVVQVPATNPLSDAVAVGMIKTSGSPSASNMTEMLGADNINVGVAGGSMFNKATALYSLNHAQKVGNNVSVYNTGDSSESQKADI  
ENAAANAKNIKLYHFFNOK

SEQ ID 5397

SEQ ID 5397  
TTGAANTGAACCATACTTCCATTTTATGAAGCCGGTCTTCATTGGCCGTGATGGATACATTGTAATGATGCGTTATGGCAAAGTAAAGGAAATGCCGTC

**SEQ ID 5398**

LKLNHTSIFMKPVLHWPVWTHCNDAL#QSKGNAV

**SEQ ID 5399**

SEQ ID 5399  
ATGAAGAAACACAGCAAAATCTTATCTACTGCGGCATTACCTCATCTGCTTTGCCTTCCAAGAAAACGGTTCTGAAGCAAACAGCCCGACATCACTTTATCCGCATCCCTGTGCG  
AACAAATTCACATGCTGAAGCCAAAGATATGGATACAGAACAACTCTCCCTTTCCAAGAATGCGACATCATCGAGTCTTCACACGACTGGGAAAAAGAGTAGCGCAACTTGAACGAACA  
GGAAATGCTCGCCGGCGTCTATGAA

**SEQ ID 5400**

SEQ ID 5400  
MKKTSKYLIIYTAFTSPCFAFQENRSEAKQPDITLSASLCEQFMNLNAKDMDTBQVSLSKCEDTIESSHDWEKEYGNLNEQENLAGVYVE

SEQ ID 5401

SEQ ID 5401  
ATGAGCGGGGTGGCTGTCTATCTCCGCAACAAAAACAGATAGCAATTGCGCTCCCAAGATGCCAACCTAAACTCCAAAGGCGGGTTCGTGAGCAGCGGTCTGAATGTGGGCAAAACAACGTA  
CGGCACTCTCCGGCTAGAGCTTGGACCCATACCTACCGGCACCGCGCAATCCGCAAGTCTGCCGAATTTGTCTCGAACAACCTACCAAAACCAAAACAGACAGCGAAAAGTTTAACGAG

SEQ ID 5402

SEQ ID 5402  
MSGVAVYL R N K N R I A I A S O D A N L N S K G R F V S S G L N V G K Q L T G S L G V E F D P Y Y R H R A I R K S A E F V S N T T K T K T D S E K F N E

SEQ ID 5403

SEQ ID 5403  
ATGCGCTGTGAACGGCTTTTCAGACGGCATCGGTGCATACGGGAACGCCGAACATCGAAGCTCCGGCGTTTCAAATAGGGCGGCGGACCAAAACCCCGGCACTGGCGCATCGGAGTGGCG  
TGCTGGCTTCCGCCCCTGACCCGGTGTTCGGATTGGCATGCGGGGAGACCCGCAACGGAGAAACGGCATTATAACGGGTTTCTGAAAACTCAACCGTTTGTATACGGTCAATACGCCG  
AAACACCGCC

SEQ ID 5404

SEQ ID 5404  
MPSERLSDGIGAIRRRNIEAPAFQIGRRTPPALAHRSGLLASAFDPVFRFAMRGDPQRRNGIITGFLKNSTVLIRSYAGNTA

SEQ ID 5405

SEQ ID 5405

TTGAACATACATTATCGCCTTTTCAAACCCGGCTGAAACCCGACTTTTCAAACCGGCATTCAAATAAAACCTGCCAAACACGGACACACCATGACCAGACTACGCCCCCGCAGCGTATTCCGG  
AAATTCCTTACAACATATACTTCTTATACCCAGCGGAAATCGTCATCGCCTCGTGGGACACGAGCGGTGGCACATTCTCGCAGGACTTGGCGGGACAGCGCAAAACCGGGCGTTTCGGCGGG  
GATGTTGTTTGAAGTGTTCGGCGGATATTGGGTGGTCGTGCGCAATCCGTATCTGGTCGATGATTTCGTGGAGCATCCGAAACCGCGCGCGCGTTTGATACCGGAAATGCGCCACAGGTG  
ACGAAATTCGACAAACCGCGCGCAGATAATCAGCAAGCGGATGTGTTGATTGCGCGCGCGGAAAGGCGAGTGGAGCGTTTTCGACGGCAGCTTTGACGAAACCGCGCCAAAAGCGGGCGGAGA  
TTTTGGAGCGTTTTCGACAAATTACCAAGCCGACAAATATTATGTTTTCGACGGGCTGGCGCGGGTAAACACAGCTTACCGATTCGACCGACTGCGCGCTCGAATATCGTTTGTCTGCTCAA  
TCCCAGACACGGAGCGGAAAGTCGCGCTTTGGTTCGCGCCTTAATCGAATTGGACTTGGTTATTATCCCGCGCGCGCGGTACGGGTATACCGGCGCGCGAGTACCTTTTGAGCGCAAC  
AGCGCAGTCATCAATACGGAAGCTGGGACACAGCATTCGCGCGGTGAATACGTTGAGCTGCGAGCTGTACCGAGCATCGTCGATATTCGCGCGACGCGTCTCGTGGCGGCAATTGGCGATGAATGCGGGCGTAAAAAGCCGATTTGTGGGG  
TCGAAGAAACCGCGCATCAGCGGGCTTGGGTTCGCGCTCGATTCGACTTCGCGCGACGCGTCTCGTGGCGGCAATTGGCGATGAATGCGGGCGTAAAAAGCCGATTTGTGGGG  
TACTGCTTTCGACAACTCGCTTACGGAATCGTTAACCTCAAGGCGAATGGCTGCGTATCGAACGCGTGGCGCAAAATTCGCGCAAAATCCAGCAGGAAGAACTCGCGTGTTCGAC  
GTGCACGCTTGGATTTCAGACGGCATCAACATCGTTAAACCGAACGCTTGGAAATCCCGGACACAAATTCGCGCAAGTTCGTTGGGCAAGAGCATTCACGCAAAATTTTCGACGAC  
TGCCTGCGTGCAGAAAGAGGTACGACGCGCATCATTACCGGCTTGCCTTCGTATTTCGCAAAATGCCGAANTACACGCGCACCGTGTGTATGAGATTTCGCGACGCGCGCCACCG  
CACGCTTCTATTCGTGAAATTCGCGGATTTTCTGCTCGCACACGACAGCGTGGCGGCTTTGGAGCATTTTGACATGGCGCTATGCTTCGCGCGCTTCGCGTACGCCACCAAGCGGG  
GGCAAGGACGACCGAAATGTCTTCTGCTGCGGACGTGGTTTCAGACGACGAGGCTGGCGGCTGAGAGCGCGCGGCAACACATCTCGAACTTTCGCGCGCGCGTGCACGGCAGAGCTTTA  
TGCCTGATTCGCGCGGCGGCAAAACCTTTTGGCTCGACGCGCGCGCACCGCGCGCCATCGCAACACACCAACGCTTTTAAATCAACGAGACGTGTGATTCGCTTGCAGAGGCT  
GCGCGATATTCGACGCGCATCGAACGATCAACATCGAGCTTTTCCATCCAAACAAACTCAAATCTGTGCGCTTTTGGAGCAATATCTTTCGCGCAACTCCCATCGCAAAATGGGC  
ACCGACTTCGCGACCGCGAATCTTTGGCGAAGCGCGCAACACGCGCTTCGCGCACGTTGCGCGCGTCAAGAGCGGTTGGGACTTGCTGCTCGCCATTTGGATTCGCGCTTCGCGACT

ACAAATCAGCGTACGGTACAGCGGTCACGCGCGCCGAGGCCAAGACGATGAAAGTGCTTACCGGCTTCGCGGATTTCGCGCTGTCGTCAAAGCAGACGTAATGAAGCC  
GCTTGGCGAAATCTTCAGCGGCAAAACCGATACCAAAATATCAAGGCTTGGGCAAAATCCACACCAAAACCGTACGACGCGCGTCTTTGTCGCGCTGCATATGCATCGCGCGACGGT  
AAGCTCCACACCAATATTCGGTCACTCAGACGATGCCGAAATGCTTCAGACGGCTTACCGTCTTGGGAACGCAATTATGAAANTCGCCGCTTCGCTCGCGCGCGGTATTTCGCGCGAAC  
ACGGCATCGGCATCACCAAGCTCGAATTCCTCACGATGAAGATTTCGCAACGCTTTTGGAACTACAAAAACCAAGTCGACCCCAAGCACACCTTCAACCGCCACAACTGATGAAGGTTTC  
GGACTTACGCAACGCTACACGCGCTCTTCGAGCTGTGGCGCGGAATCGCTGATTATGAAAAATCAGACCTCGGCACGATTGCCGATTCCGTCGAAAGCTGCTGCGCTCGCGCAAA  
TGTAAACCGCTGCTCCACCCACGTTCCGCGCGCAACCTGCTGTACGCGCGCAACAAATCTCGCGTGGGTTTGTGACCGGAGGCTTCTTATACGAAGAACAACCCGCGCG  
GCTTTTCGCTCAACATTTTGAAGAACTGATGGACATCGCGCACTGACCGGTGTGCCACCGCTCGCTCAAAACCTGCGCGTCAACATCGACTTCGCGGACGTTACCGTAGCCGTCG  
CACTTCTGCGGATTTCGCGCACTTCGCGCAACAAACGCTTTGCGCTGCGGCTTCAATGGGTATGCGGCTTTTGAACGCCACCGCTCCGAAACCATCAAGGCGCGCGGATGATACAGACC  
GGCTTCCCGCGCAGAACTTTGCTACAAATCGGCAAGCTTCTTCGATCGGCACGAAAAAGCAAAAGCCGAACCCAGGCAACCGTCGCGAAAGCCCGGATTAAAGAACAGGTTATCC  
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AGCGGTGTTTACTTCCCGCGCTCGGTTGCGAGCGTTTGTTCAGCCAAATCGGACTCGCGCTTCAAGGCCATGCTCTGCGACGTCGCGGTACAAACCGTCTCGCGCGCGCTATATGTGT  
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TCGTGATTGCGGCACTTGTTCAGACGAGCTTGAATAATCCGCTTCGAGGAAATCTTCCCGGCTGCGCATCATCGACATCCACGAATACCTGCTCGAAAAAGCGGTGAACCTCGACGG  
CGTGAAGAGTCAGCAATACCTCTACCAAGACCGCTTCCACACCGCGGATTAAACCATGAACGCCACCCAAATGCGCAGCAGCGCTGATGGGCGAGAAAGTCGTTTAAAGCGACCGCTGCTCG  
GGCAATCCGCTATGTTCCGCGTCAACGCGCGGACATCGGCACAGGTCAAGTTCGCAACAGAGGAAATCGAGAAAACTCAAGAGCTGCGCGAGGCGAACCGCTCAAAATGC  
TGACCTCTCGCGCGCTGCTGCAAGGACTGAGCGCTATTCGACGACAACATATGCTCGCGGACTACATGCTCATTTGAAATGGCGAAACACATCTCGCGGAAACCTGCTGATGA  
GTTTGTAAAAAAGCCACCAACGCGCGCTAGAGAAAGTGTGCTA

## SEQ ID 5406

LNYYIAPSNPAETDFSNIGIQTAKHGHMTTTPAPQRIRIEIPYNTSYTDREIVIRLLGDEAHILQLDRGQRKTGRSARMLFEVLGDIWVVRNPFYVDDLLHEPKRRAALVREMRHL  
NEIRKRRDDNQADVLAAAEKAVERFDGSDFTDTRKRRQILERLSKITPHENIMFDGLARVTHVDFATDWRVEYFFVVPVNDTEAEVAPLVRALIELDLVIIFRGGGTGYTGGAFLDAN  
SAVINTEKLKHGVEYVELAGLYGRHPIIRCGAGVVRVEETAHQAGLVFADPTSDASCVGNNVAMNAGGKAVLWGTALDNLAYWNNVNPQGEHLRIERVHRNFGKIHDEETAVID  
VHTLSDGINIVKTERLEIPGHKPRKVLGKDVTDKPLSLPGVQKSGTDGIIITGVAVLHKPKYTRTCMEFFCTAATATPSIVEIRDPLLAHDSVRLAGLEHLHWRVYRAGVYATKAA  
GKGRPKMVLADVVSDDEAAVEAAAEHICELARARDGEGFLAVSPEARFTFWLDRSTAAIAKHNAFKNEDVVIPLERLGEYSIDGIERINIELSIQNKLLCAALEQYLSGLPIIDKHG  
TDLPTAELLGERGKHALAHVAAVKARNDWLLAHLADPLADYKSYRTAVHAAPBAKDDDESCPTAFRDFLRVSVKADVMKPLAEIPSGKTDTKIIGQLGKIHTKTRSVRFVLEHMHAGDG  
NVHTNIPVNSDDAEMLTATYRSVERIMKIARSLGGVISEGHGIGITKLEFLTDEDLFPWNNYQVDPKHFTFNRHKLKMGSDLRNATPSPPELLGAESLIMEKSDLGTIADSVKDCIRCGK  
CKPVCSTHVRANLLYSPRNKILGVLLTFAFLYEQTRRGVSVKHFEELMDIGDHCTVCHRCVKPCFVNIDPGDVTAVVRNVLADSGHHRFPAPASMGMAFLNATAGGCPKTIKALRAAMIQT  
GFPANFAYKIGKLLPIGTGKQAEPRATVKGAPIKBQVIHFINRPLPKSVPAKTPRSLGIEDGKSIPIIHNPAAPEDAFAVFPFGCGSERLFSQIGLAVQAMLWHVGVTQVLPFGYSC  
CGYPODAGNKAKEEMSTNNRVAFHRMANTLWYLDIKTVVSCGTCYDQLEKYRFEIIPGCRITIDTHEYLLEKGVKLDGVKQYLYLHDPCHTPIKTHNATQMASSSLMGQKVVLSDRCC  
GESGMFAVRPDIATQVKFRKQEEIEKNLKLPGSEFVKMLTSCPAQLQLSRYSDNNMPADYIVIEARHILGENWLEDFVKANNGGVEKVL

## SEQ ID 5407

TTGAATCAAAATPACTACCGAATCATGATTGACGGCAAAACACCGAACCACCAAAAAACCAAAATCATACACAGCCCATCGGGGGCTGTAGACGATGTGATGCGCGACCTGCTGA  
CAGTATCGCGCGCTACGACGAATGCGTCAGCGAATTTGTACGCATACCCATACCGTGCAATTCAGATCCATATGGTTAAAAATGTCCCGGAAATCGCCAAACGAAACAAACGTTTTC  
CGGCACGCGCTGCAACGCTCCAATCTTCTGAAAGAGCGGAACTGATATTCACATCGTCAAAACGCTGCGCGGACGTTTGCCTGCACATATTCGCTGACGGGAAAAATGCGGC  
ACCGTCAACAAACCAAAAGCGCGCGCAATCTTCTGAAAGAGCGGAACTGATATTCACATCGTCAAAACGCTGCGCGGACGTTTGCCTGCACATATTCGCTGACGGGAAAAATGCGGC  
TAGGCTATGAAGACAAAGCCCTGCTTTGGAATGCGCGCTGCGGATTCGCGAAGGGGCGCGTGGGACTGACCGTGACCGCGCACCAAGCGGAGGGCTACGAACCCCGCGCGCATTC  
GGAATGATAAGGAAAAATCCAGATACCGTCAATATTCGCGTACCGCAACGCGGACGTTTTCAGCTCGAGGACTATATCGGCATCAAAACATCAGCGCTGCAACAGCGTATGCTC  
GGTCGCGGTGCGGCTCATCGCGCGCAATTCAGCAATACGAGAACCGCGGACCGGTCAAGAGACACGGAATTTTGCAGGATTTCCACATGGATAGGGCAGTTTTCGAGC  
TGTGCTGACAAAGAGGCAAAACAAATACCCGATCGCGCGCTTAAAGCAATGGCTGGGCAATGATGAAAAACGTTGACCGCGCGCAACGCTGTGACCGCGCTCGAACGTTAA  
AGATGCGGATGAAGTGGCGCAATCTGAACGCATTTGACATGAGATGATGTT

## SEQ ID 5408

LNQIPTRIMIDGQTFEPKQKRIIPAFMRGLVDVMDRLLTRIGGYDECVSEFVRITHTVHSRISWLYVPELANGNKTFSGTPTVQLLGSADANMAANALEAVRFGADKIDLNFQCPAP  
TVNRKGGAILLKEPELIPHIKTLRGLPAHILPTGKRLGYEDKSPALECACALAEAGGACGLTHARTKAEGYEPFAHWEIRKIHDTVNIPTVANGDVSLQDYITGKPTISGCNSVML  
GRGAVIRPDLARQIKQYENGFPVKDITFAEVSTWIGQFFELCLTKBANNKYPIARLKLWLMKKTFFDPAQTLFDRVTRVKDADEVRRILNFAHEHMD

## SEQ ID 5409

ATGTTTGTGATATTAATCGGCTTTTTCGCGCTTTGTCGTCGCGCTGCTGTCGCTGCGGTCAATGCCGCGCGCTTCGGTATGCAGGAAGCAGATACCCCGCAATCGGATTATGAAAAACGTT  
TGGGTTTGGGGGCGAAATGAAAAACAAATACACCGAAGCAGGGGAAAAACGGCAA

## SEQ ID 5410

MFYVIGFCFVVALLSLVNAGAFGMQEDDTPQSDYKRLGLGAKLNKNTPKAGEKRQ

## SEQ ID 5411

TTGTATCTTTATTGCGCTTTTCCCTGCTTTTCGGTGTATTTTGTGTTTTCAGTTTCGCCCCCAAAACCAACGTTTTCATATCCGATTGCGGGGTATGCTCTTCTGCATACCGAAC  
CGCGCGGCAATTGACCCACAGCGACAGCAGCGCAGCAAAAGCGCAAAAGCGGATTTACATACCAAAACATTCGCCCTCCAAATTTGTAAAAATCATATCAATACAGTCCGAAATTTATC  
ACAAGCGCAGGACAAATAATCTTTCGACCGCAGTATTTTCATTATTTACCTTGAAACAAAAAGGGCACC

## SEQ ID 5412

LLSLPPFFCFRCIFVFPQRPQTQTFPIIRLRGIVFLHTERAGIDPQRQDRDRAKADYIPKHCFSKFVKIISNTVFNLSQAHEQINLLTAVFHSFTLTKTKGT

## SEQ ID 5413

CCGAGCGCTTCCCGCGAAGCGGCTTTCCCTTTCCGCGCACTGATAAAACAGGGCGAACAGCGGTACATCCCAACCCCTTACTTTTGAATCCGTTTCGTTTTCAGACGGCATCCTG  
CTTGAATGCCGTCTGAAAAACCGATAGGCAATACACACATGACCCACAT

## SEQ ID 5414

PEPLPREAAPPPTVKTGRTGVQSQPTTFESVSFFRRHPAMNAV\*KTDRQYTHDPH

## SEQ ID 5415

TTGGTTGTACCTAAGTCGATACCGATTACTTTTGCCATGTGGATACCTATTGTGATTTGCTTATTTTGAAGAAATGTTGGAACATTTTGTCCGATGGGCTG

## SEQ ID 5416

LWPKSIPITFAMWILLDFAYFEKYVGTFCPDGL

## SEQ ID 5417

TTGATGGAGCAAGGTTGTACGAAGGTTGAAGGCCAACCTGTGGGTGTTGGTATGTCGCGCTTGAAAAACGTTGTTTAAAGGACAAATGCCCTCTGAAAAATGTTTAAAGCGGCAT  
TTTCCGTTTGTGTAACAA

## SEQ ID 5418

LMQRLYEGWKATCGCLWWSRLKKRVLRDKRLKIGFTAFSVCRQ



## SEQ ID 5419

ATGAGCGAAACCGCGAAATCAAACTCAACGACCGGTCCGAAATGCAGAAAAACCAACGAAAAAGTCGAACGCCCATGTCGATAACGACAAAAAGCGGACACGGCGAAGCGCGT  
GCTGCGGC

## SEQ ID 5420

MSETAKIKLNDRENAEKPNEKVELPIVDNDKKGGHGGCGG

## SEQ ID 5421

TTGCCGAAAAACGATACGCGCGAGCAACCGCCTTCGCGGTGTCGCGCTTTTGTGCTTATCGACATGGCAGTTCGACTTTTTCGTTTGGTTTCTGCATTTCGGACCGGTGCTG  
AGTTTGAATTTTCGCGGTTCGCTCACTTCTTACCTCATTTGGAACCGGTTGAAAGATTCAAAATATAGCATGTTAATCCGAATC

## SEQ ID 5422

LPKNVSAATAPAVSAFFVVIDNGQDFVFWFPCIFGPFVVEFDFRGAHFLTSFGKRFERFINIACILIRI

## SEQ ID 5423

ATGTTTAATCCGAATCTGAAAAGGGAAGCGGTATGCGAAATCCCGTCTGAAGCCCAATCAGGGCTTCAGACGGGATTGCTATCTTTATTGCGCGTTTCTTCGTTATCCGGATTTTGT  
TGGGGCTGAAGCAGATTGGCAGTCAGATTGCAATCGAAGAA

## SEQ ID 5424

MFNPNLKRBAVCEIPSEAQSGLQTGFAIFIAFLFYPDFCLGLKQIGSQIAIEE

## SEQ ID 5425

TTGGCAGCGGAATTCGGCAGCGCGCTCGCGGTTCGGAATCCGTTTGGCGATGCCAGCAAGCCATTGATCCTTGGGACAGCAATAAATGTGGCTTCGCAATTGGGTATTTTCA  
AACGCCACGACGCTATGCCGTTTCCGTCGTTACGATTTCCCGGATTTTCGGTTTCAGCGCGCAGCATTCATTTGTTCCGAGTCAAAAACGCAAGTCCGCTATACGCTGCTACTTT  
CACGCTGGAAGTAATCAGATGAAACAGTTCGCGGTGTTGTCGCGAAGCGGGGTCCGATGTGATTATGCCGCTGTAATACAAAAATGCGCGCTTTTCGGAATATGCCCTTAA  
TATGCGAAACACGCGCAATGAGGGGATGATGCTTTCTTTTGTCTTGTCTGCGCAGACGCGAGTATACCATTCATTGAAAACCATCAGGTACACCGCTGACGGGGCGCTATGGGGA  
GCGGCTGAATCTCGCTTGGCGGCTCAGTTGGATTGTTCTGAAAATGCCGACAAAACCAAAACAGTACGACCGCAATTCGCGCCACTGCTTCTTACCGCTTCGCTAATACAGCTCCGCG  
CATCAGCTATGCCCATGTTTCGACTTTGTGCAACGCGAGTCAGAAACGCAACATACCGCTATGATCAATCATCGCGGTGTCGATTACGATTTTCCAAAGCGCACTTCGCCCATCATG  
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## SEQ ID 5426

LAGEFGTLAGRVANPFGDASKAIDFMDNMNVASQLGIFKRHDMPVSVRYDSPGSGFSQIOPVQSNKSAYTPATTTLESNQMKPVPAVVKGPSDVVYAGLNYKNGGFFPNYALK  
YAKHANEHDAFFLFLGRASDTDFLNHGVHRLTGGYEGGLNLALAAQLDLSEWADTKNSTTELAATASVRFNTPRISYAHGDFDVERSQRKHTSYDQIAGVDYDFSKRTSAIM  
SAANLKRNTGIGNYTIQINAAVGLRHKF

## SEQ ID 5427

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CACGGAACCGGCATACCGTCTGGCGCTTTGAAATACCCAATTCGGAAGCCACATTAATTTGCTGTCCTCAAGGATCAATGGCTTTGCTGGCATCGCCAAACGGGATTCGCAACGCGACCG  
CGAGCGCGCTGCGCAATTCGCTTCCGCAAGCGGTAAGAGATTCCCTGTTTACCCCAACGGGTGCGCGCGCGCGGCAACGGATACGCTTGTCTGAGCTGCCAAACAGCGCTTACGCGCG  
CGCCCAATCCCAACCCCTTAAAGCGGTAACACGAGCGGAAATCACTGACTTTCGCTCTGATGCGGCTTTTGGCTTAGTAATGTTATGCGCGT

## SEQ ID 5428

LQSKNEKPKSKTKLSAPPRYLEFVAQTNGGGINLSVADAGISFPQSGRHDGGSALGKIVITDGDLLIAGMFAFLTAFDKVETMGIADARDCITEAVGSSGGNFGRTVFGVIFRQIQ  
LSRQGEIQAAFPFAARQAVLVMVFWIGITRSABEQKESIMPLIGVFRIFKGIISERAAIFVITGTIHLIRPLADNSRNWPHLITPQRESSRRIGLAVLNRKLNAAATGKSGGIVT  
HGNRHTVFAFETQLRSHIILAVPRINGFAGIAKIRINATGERRAEFACQADKGFVPTTGRAAGNGVLLLELPNSLPAAQIPTPLKPLINEPKSLFTVLMRLIALVTLVLPV

## SEQ ID 5429

ATGTTCTGCTTCCACACAGCTTTGACTTCGCGCTACAGGCTGACATCGGCAACTGCCGCAACCGGAGTTCGCGACAATACGAGGGCGGTAAGTTTTCGCTATTCGCTTCTCTTT  
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TATTTCAATA

## SEQ ID 5430

MFLPSTPALTSPLYRLTSATAANGSADNTRAVSFRRISASPKFAKNIGQTPNQSPITPRKKKTIIPRNKFEVNFPIFKNNLSI

## SEQ ID 5431

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CGCAACACGGCGACGATGGGTAAAGCACAAGGCAAGAGCTGTCTCTCTCTCAAAATTTCCGAGAAAGTCTGCGTAAATGAAAGAGCGCCGAAGCTTACTTGGCGGAAAAAGTAAC  
GAAGCGGTGATTACCGTCCCTGCTTCAACGACAGCCCAAGCTCAAGCCACAAAGACGCGAGCGGTATCGCGGTTTGGACGTAAACCGCATCATCAACGAGCGGACCGCAGCGCTT  
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TGAAGTATGGCTACCAACGGCGATCTTCTTGGCGGTGAAGACTTCGACCAACGCTTGTATGACTACATCATTGACGAGTTTAAAAAGAACAGGCAATGATTGAAACAAGACGTA  
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CCGAGCGCTGATCTCTCGTGAAGAAATCTTTGGCGGACTACGGCGCAACCTGACGCTGCGGAGAAAGAAATTCGAAGCGCGCTGAAAGAGCGCAAGAGCGGTGAAAGCGCA  
CGACAAACCGCATCGATGCCAAGCGGAGCACTGGGTACAGCGACGCAAAACCTGGCGGAAATGTTTACGCGCAAGCGCAAGCGGCAAGCGGCGGCGGCGCAACCGCAAT  
GCTTCTGCAAGAAAGACGATGATGCTGATGCGGACTTTGAAGAGTAAAGACGCAAAAA

## SEQ ID 5432

LAISENGQTKVIEAEGARTTSPSIIAYLDGGEILVGAAPKQAVTNKNTIYAAKRLIGHKFPEDKEVQRDIESMPFEIKNADNGDAWKAQKELSPQISAEVLKMKKEAABAYLKEKVT  
EAVITVPAYFNDQRQATKADGRIAGLDVKRIINEPTAALAFGMDKDNDRKIAVYDLGGTTFDIIIEIANLDGDKQFEVLTATNGDTFLGDEDFDRLIDYIIDEFKKQGGIDLKQDV  
MALQRLKEAEKAKIELSSGQTEINLPYITMDATGPKHLAMKITRAKFPESIVEDLIARSIEPRCTALKDAGLSTGIDDDVILVGGQSRMPKVQBAVKDFFGKEPRKDVNPDEAVAGAAI

QGRVLSGGRSDVLLDVTPLSLGIETHGGVMTKLIQKMTTIPKASQVSTAEONQSAVTHVLQGERERASANKSLGQFNLDIAPAPRGMPIEVTFDIDANGILHVSADKGTGKAAN  
ITIQSSSLSEETIERMVKDAEANAEDKRLTELVASRQAEALIHVSVKSLADYGDKLDAAEKEKIEAALKEAPEAVKGDOKTADAKAELGTASQKLGEMVYAQAQAEQAGEGAQAN  
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## SEQ ID 5433

ATGTTTGATGGAGCAAGGTTGTACGAAGGTTGAAGGCAACCTGTGGGTGTTGGTATGGTCGCGCTTGAAAAACGTGTTTAAGGGACAAATGCCCTCTGAAAAATTGGTTT

## SEQ ID 5434

MFDGAKVVRVVEGNLWVFGMVALEKTCFKQMPSENMF

## SEQ ID 5435

ATGTTGCGGGAAGCAACATTTTCAAAAAAGTTAATTTATTTGTTTATATTGAATAATTATTTTCAAAATAAAAAATCCAAATTTACCCGAAATTTGTTCCGAAAAATGGTTTTTTTTT  
TTCGGGGGTAATTGGAGAC

## SEQ ID 5436

MLRESNIFPKVNLFFYLILFFKIKIPKTRNLPRKVVFFRGVIGD

## SEQ ID 5437

ATGCTTGCCCGCCAAACCGGTGTCCGGAATATGGAGAAAAAGACCGATGCAAAAAATCCCCCTGACCGTACCGCGTCCGGAATTGCTGAAACAGGAATTCAGCAGCTCAAAAGCGTGG  
CGCGTCCCGAAGTGTATCGAAGCGATTGCGGAGCCAGATCGCACGCGGATTGTGCGAAAAACGCCGAATACGAAGCGCCAAAGAACGCCAAGGTTTTATCGAGGGCCGCAATTCGAGSTT  
GGAACACAAATTTCCGTGCCCACATCATCAATCCGCGCGAAATCCACGCCAAGGCAAAATCGTGTTCGGTACGACGGTTACGCTGGAAGATTGGAAACGGAAGAACAGTTACCTAT  
CAAAATGTCGGCGAAGACGAGCCGACATCAACAGGCAAAATCTATGTCGGCTCTCCGATTGCGCGCCCTGATCGGCAAGGAAGAGGGGATACGCGCGAAGTTACGCGCACCGGGCG  
GCGTACCGCAATACGATATTATCGAAGTCCGATATAFT

## SEQ ID 5438

MLAAANRCAGTWRKRPQKIPFVRGAELKQELQKLSVARPEVIAIAEARSHGDLSENAEYEAERQCFIEGRISLEHKLVAHILINPAKHABEKIVFGTTTLEDLETEHVITY  
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## SEQ ID 5439

GTGTGTGAGTGTATCGAAATCAAGCCGANTCAAAATATACCGGACTTCGATAATATCGTATTCGCGTACGCCGCCCGGTGCCTGAACCTCCGCGTATCCCTTCCTCCTTCGCGATCAGG  
GCGCGGCAATCGGAGAGCCGAGATTTGCTGATGTCGGCTTCGCTTCGCGCAATTTGATAGGTAAGTGTCTTCGCTTCCAAATCTTCCAGCGTAACCGTGTAC  
CGAACACGATTTGCTTCGCGGTGGATTTCGCGCGGATTGATGATGCGGCAACGGAAGATTGTGTTCCAACTCGGAAATCGCGCCCTCGATAAACTTGGCGTCTTTGCGCGCTC  
GTATTCGCGGTTTTGCGCAAAATCGCGTGCATTCGCTTCGCGCAATCGCTTCGATCACTTCGCGGACGCGCACGCTTTTGAGCTGCTGCAATTCCTGTTTCAGCAATTCGCCACCGCGT  
ACGGTCAGGGGATTTTTGCATCGGTCTTTTCTCCATATTCGCGCACACCGGTTGCGCGCGCAAGCATACCGGTACCGTCTGTTTTGTCGCTCCGATATTAATA

## SEQ ID 5440

VCRVYRNQAESNIPDFDNI VFAYARCLNFRRI PFLADQAGNRRADIDFALDVG FVFADNLIGNVFRFQIFQNRRTEDHDFAGVDFGRIDVGNKGFVFLGNAALDKTLAFFGGF  
VFGVFGQLAVRSFGNRFDFHFGTRHAFELLQFLFQQFRATAYGQDPLHRSFSPYSGTFCVGKHTAYRLVLCVRLIK

## SEQ ID 5441

GTGTGCCGAATATGGAGAAAAAGACCGATGCAAAAAATCCCCCTGACCGTACCGGTGCGGAATTGCTGAAACAGGAATTCAGCAGCTCAAAAGCGTGGCGCGTCCCGAAGTATCGAA  
GCGATTGCGGAGCCAGATTCGCGCGGATTTCGCGAAAAACGCCGAATACGAAGCCGCCAAAGAACGCCAAGGTTTTATCGAGGGCCGCAATTTCCGAGTTGGAACACAACTTTCCGTG  
CCCACATCATCAATCCGCGCGAAATCCACGCCAAGGCAAAATCGTGTTCGGTACGACGGTTACGCTGGAAGATTGGAAACGGAAGAACACGTTACCTATCAAAATGTGCGCGAAGACGA  
AGCCGACATCAAAACAGGCAAAATCTATGTGCGCTCTCCGATTGCGCGCCCTGATCGGCAAGGAAGGGGATACGCGGAAGTTACGAGCACCGGCGCGGTACGCGAATACGATATT  
ATCGAAGTCCGGTATATTGATTGCGGTTGATTTCGATACACTCGACACACGAGGAATTAAGCACCGCGTGTGTTTTTTATGCTGTTTT

## SEQ ID 5442

VCRMEKKTDAKNFPDRTRCGIAETGLAAAQKRGASRSRSDCRSLARRFVRKRRIRSRQRTPRFYRGPHFRVGTQTFRCPHHQSGRNPRRRQNRVYDGYAGRFNGRTRYLSNCRRR  
SRHQTQNLRLSDCPRPDRQRRGYGSSGTGRRTIRIYRSPVYLIRLDPDLTRRLKLRVCFPHVF

## SEQ ID 5443

TTGCGCGCGCAAGCATACCGCGTACCGTCTGTTTTGTCGCTCCGATATTAATAAAAAATACAAGCCGCCGGAATAATCGCGGCTGTCTGTGTTGAACAGCGCTATTCTACCAAA  
TTCTA

## SEQ ID 5444

LRRQAYRVPSCFVRPDIKIKIQAARKIGLSVVEQRLFYQIL

## SEQ ID 5445

TGAACACCGGCTATTCTACCAAAATCTATGAAATTGGCAATCGTCCGTCGCGCGCAACCGGCTATGTCGCAACAAAAGCCGAAAAATATGCGCGCAAAAAATTTAGAAACAAA  
AATTTAAAAAAATCAATTTTCGCGCA

## SEQ ID 5446

LNSGYSTKFEIGNRAVPPANALCPQQPKICRQKNFRNKKPKKNQPSA

## SEQ ID 5447

GTGGAAGGTTTGGCGAGGCGCGGGGAGCGGACGGATTCCGTCATGCGCAAAACGTAAATATAAGATAAAAAACAGCCTGCATTATATGTTGCAATGCCGTCTGGAATACTCAGGTT  
TGGCAATTTTCGTTTTAAAGTACGTGAATTTGGTTTTTTATGCCGAAAAAT

## SEQ ID 5448

VEGLGEAAGRTDSVMKRYKDKNSLHYTGNAVWKISGLAFSVLKYVNLVFAEN

## SEQ ID 5449

ATGCTCGAAGCACTCGATAAACTCGGCGTTCAATCGAACATCTGCGGAAGCGCTCTGAAAGTACAGGCAAGCGCGGACGCTTCCCCAACCGCTCTGCGGATTTGTTTTGGGCAAGG  
CGGGCAGCGCGTTCGCTCGCGTGACCGCGCGCGTGGCGGTTTTGGGCGGGGATTATCATCTGCACGCGCGTCTGATGCAAGACGCCATCGCGGATTTGGTCGATGCGGTTGCGGAF  
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ACCGCGCTTTGATGCGGTTGCGCGTACCGGCGAGCGGTTGAAATCCGTATGTTGCGGCAATGATTTCGAAGCCCTATATGACATTACTTTGAACTGATGCGCAATTCGCGGTAC  
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## SEQ ID 5450

MLEALDKLGVQIEHLAEGRLKVHGTGGRFPNRSADLFLGNAGTAFRPLTAALAVLGGDYHLHGVPRMHERPIGDLVDALRIAGADVEYLGNEHYPPHLHGKQDCGERVPIKGNVSSQFL  
TALLMALPLTGQAFIEHMGVGLISKPYDITLKLMAQFGVQVANEGYRVFKIPADAHYHAPEHLHVEGDASGASYFLAAGLIAATPVRVTGIGANSIQGDVAFARELEKIGADVVGGENPV  
EVSFPKGRAVQAFDLDAHNPDAANTLAIVLATRQCTCL

**SEQ ID 5451**

SEQ ID 5451  
ATGACCACCATGATTATACCCAAAAAACCACGATGTCTATCGTCGTCGGCGCGGCACACGCGGCACGGAAGCCGCGCTTGGCGCCGCCGATATGGGCGCGCAGACGCTTTTGCTCACACACA  
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GACCTTTTCCAACAGCCGTCGAAGACGTAACACTCGAGGGCGAAACGCATCAGCGCGTGATCACCGCGATGGCGCTGGAGTTTAAAGCACGCGCGCTGGTGCTGACCGCAGGCACGTTCT  
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**SEQ ID 5452**

SEQ ID 5452

MTHTMYPKTYDVTIVVCGGHAGTEAALAAARMGAQTLTLLTHNIEFTLGQMSCNPISIGGKKGHLVRELDAIGGAMALATDKSGIQPRLNASKGAAVRATRAQADRIILYKASTREHLENQENL  
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VSCWHTHTNTQIHDIRSGFDRSPMTFGKIEGVPRYCPSEIDKINRFADKDSHQIFLEPGLITHEYYPNGISTSLFPDIQIALVRSMKGLENAHILRPGYATEYDTPDPNKLKASLET  
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**SEQ ID 5453**

**SEQ ID 5453**  
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 TAACCGCAGGCAGCACCGGTTTGCGGGGCGCTTTGGTGGCGGGCGCGCGCAGCGGAAGCTCTGGTCTTCAGCTTCGCGCAGCACCGCGGACCGATGCCCTTCACCTTGATCAAACTGTCAC  
 AGACTTTGAAACGCGCGCTTTTGCGCGCGGTATTCGCAATGGCCTTCGCGGGGCTATGCCCGCGCAGCGCTCCAGCTTCTGGTGGGAAACCGGATTTGAATGTTAACCGCGCGAAGGAGAA  
 GCGCGCAGGAGAACAGCATACAGAACAATACAAACATTTTTTCATGGTTTTCTTTTAAAGGTTGCAACAACAACCCGATCTTTCGCGAGATATGCGCGAT

**SEQ ID 5454**

SEQ ID 5454  
LHRFIPRYSAGLSLPAISLFPNKEQKSAGGSRCPFLYRFPYFLTAGSTGLAGPFGAGAPTEAWSFSFASTAGMPFTLLIKSSTDLNAPPCARYSAMAFAGMPGSASSFWWETRLNVNRKGB  
GAGEOHTEQYKHPFHFGFSFKGCKQQTASCDMDAD

**SEQ ID 5455**

SEQ ID 5455  
ATGCCGAACGAGTGTGGCAAACTCGGTGCAAAAGTCGTCGAAGAAGCCGAAGCGATTACATTACCCGCGCCGAAACGCGACACCCGATGCCGTCATGCACCTTACGAGGACCACCGCA  
TGGCGATGTGTTTCTCGCTGATTTCGCTGTGGGAGTACCCGTCGTCATCAACGACCCGAAATGCACCCATAAAACCTTCCCGACTTATTTTGAAGTGTTCTCATCACTGACCGAAACAGC  
GGAA

**SEQ ID 5456**

MANELRLKGAKVVEEAIAIHITPPETPTPDAVIDTYDDHRMAMCFSLISLLGVPVVINDPKCTHKTPTTYFEVFPSSLTETAE

**SEQ ID 5457**

SEQ ID 5457  
ATGAGCCGCCGCCGCCGGAATCGCGGCAAAATGCCGTCGAAGCCCTGTTTTCGGGTTTCAGAGGCCATTTTCCGCCCTAATCCGCTGTTTCGGTCAG

SEQ ID 5458

MSRPPRRNRGKMPSEALFSGFRRHFSALFRCFGQ

**SEQ ID 5459**

SEQ ID 5458  
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CGCCAAAAATCTACCTTGGAGGACATCAGTCTTTTACAGAA

SEQ ID 5460

SEQ ID 5460  
LETHRRKNPIAAHRRFIIEMPSETPSDGISEPAKEKTFMPSDKTLFLCLGALLLASCOTSGKHRRPKPKQTQVRQIQAVRISHIGRTGQSQELMLHSLGLIGTPYKGGSSSTATGFDSCG  
MTGCVKNAI.NVKI.PPTARMMAAASRKIPDSRIKAGDLVFPFMGGAHRYSHVGLYIGNGEFIHAPGSGKTIKTEKLSPTPYAKNYLGAAHTFFTE

SEQ ID 5461

SEQ ID 5461

ATGTCATACAGACCCCAAAATACAGGAATGCGCTCTGAAACTATATCCCGCATGAAAAACAGCAGCCTCATTTCCCTTTTATGCTCTCTCTCTGTTCATGTCTTCATGGTTGCCCCAC  
TGGGAAGACCGGACGGAAAGCCGTCATTTTAATACTTTCAAAACCTGTCCTCTGGACAACATCTCTGCAAAATCCGGACACCCCTCATAAACAGGGGTATCCGACATCTACCTGCTCGACGA  
CCGCCACGAAGCGTTTGGCCGCCCGCGCCGCTTATCGAATTCGCCGAACACAGCCTCGATTGGCAATACTACATTTGGCGCAACGACATTTCGGGACAGCGTGTGTTCAACCTCATGTAC  
CTTGGCCGAGAACCGCGCGTGGCGGTACGCTGCTGTGGACGACAAACAACGCGCGGCTGGACGATCTCTGCTGCGCCCTCGACAGCGCATCCAATATCGAAGTGGCGGCTGTTTCAAC  
CCTTCGCTCTACGCAAAATGGCGCGCACTCGGCTACCTGACCGCTCTCCCCGCTCAACCGCCCATGCAACAAATCTGCTTTACCGCGGACAGCGCGGCACCACTACTCGCCGCGGACGA  
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CGGGAGGCTGCAAGACGCGCTCAAAACAGCCGAAAAAGCGGTCTATCTGGTTTCAACCTTATTGCTCCCTACAAAAATCCGGCACAGACGACATGGCAAACTTGGTCAGGAAGGCATATGC  
GTTCACCGTCTGACCACTCTCGCTACAGGCGACGACGCTGGCGCGCTTCATCTCGGCTACGCTCAATATCCGAAACCTGCGCTCAAAAGCGGCATCAAACTCTGAGGCTGCACACCAAC  
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TTCCGATCGGCTCAATACCAAGTGGGCTGCTCATCGAAAGCCCCAAATCGCAGAACAGATGGAGCGCACCTCTGCGGATACACACCGGAATACGCTACCGGTTTACCTCTGCACAA  
CACACCCTGCAATGGCAGCATCCCGCCACCGGAAAAACCTACCGGAACGAACCGAAGCCAACTTTGGAAACGCATCGCCGCAAAAAATCTTATCCCTGCTGCCCATCGAAGGTTAT

SEQ ID 5462

MHTDPKIQAMPSETISPMKTRSLISLCLLSCSSWLPPEERTESRHFNTSKPVLDDNLIQTRHPTHNNGLSDTYLLDDPEAFAPARAALTESAEHSLDQYIWRNDISGRLLFNLEY  
LAAERGVRVRLLLDDNNTRGLDDLLALLDSDHPNIEVRLPNFPVFLRKWRALGYLTDPPRLNRRMMANKSFADNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDPRYNASH  
SAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVQSPLYQIKQTRGRIIMQSVQYTRLISDSFAGLDRDRRKPPITAGRLQDALKQPEKSVLVSPYFVPTKSGTDAIAKLQVQDII  
VTVLWLSNLAQDVAABHVSQYKVRKPLLKAGIKILQYEPNHAVPATKDKGLTSSSVTSLHARTFIVDGKRIPIGFSNLDPR SARLWTEMGVVIESPKIAEQMERTLADTPPEYAYRVTLDK  
HNSLOHWDPATKTKYTPNEPEAKIKWRIALAKISLLEPGL

SEQ ID 5463

ATGATTTCGATAAATAATTATCAATTACAATGCAATGCCGATTCGTTTGCTGTGTAACATTCAGGATGCCGACTCGCGCGCATTCAGACAGCATCTGAAAACAATAACGGCACAAGGATGG  
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ACTGCCCGAAATTTGCCCGGACCTGGAACGAATCCGCTCCGGATATGCAACAGGCAAGCTGTGGCTCATCGTACGACGTTGCCCTGCTGATTCCTTTGAGCAGTTATTTTGGCGGACAAGTTC  
GGAACGAAAAAAGTCTTTTTCGGTGTGATTCGGCTTTTATGCTCGGATGGCAATTTGGGCGCGCATACGCGTGTGCGTGTGAATGACGCTTCCCGTGTGCTTTACAGGGATCGGCGGTT  
CGATGCTGGTTCCGATACCCGCTGTGACCATCTTTCGCTGTATATGAAAAATCGAAGCTGCTCAACGCCATCAATTTATGCGGTCATGCGCTGCATGTCATGCGCTGCGCTTGGGACATCTTGC  
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GCTCTGGATTTCAAAGGCTATTCTGACCTTTTCCGCTGGCCGCTGCCCTGCTGCTGCTTGGCGCAGAAAGCCCTGTCGACACGGCTGCTCCGCTATTTGACATGCTGTTACCGCTGTGCGCGGAC  
TGCTGTTTGGCAGCGGTTATTTCCGACATATGAAAACCGCGCTCAACCCGATTTTATTCGGCGGACCTGTTTCTGATACGCACTTCCGTTTGGGACGTGGCGGGCACTGTTTTCAGCCGCTC  
CGGCATCAGCTCGATTCCTTTTCTGATGCCCCGTATGTTTCAAGTGTCTTCCGCTTTCGCGCGAAGCTGCTGCGGCTAGCTGGTGTGCGACCCGTCGCCCTGTCTTCTGCTGGTCAAAACG  
CTGATTGCAACCGCTCATGAAACGTTTCGGCTACCGCACGGTACTGCTTTGGAAACACCAAGCTGCTTGGCCGCTTCATCATGCTGCTGCCCTGCCCTGACGGAAACTCGCCGCTGTGGATT  
GGATTTTCCCTCTCGCTGGGCACTGGCGGCATGCAACTCCCTACGATTTTCTGCCATGAACACATGACCTCTGCCGATTTTTCGCCGCGCAACAGACCGGCACGCGCAACAGCTGTATGCGCGT  
CAACCAACAGCTTGGCCATCAGCGTGGGCAATGTTCGCGGCGCATTAATCTTAAAAACTGGAACATCTTGATACACGGGCTTCTTCAGCGCTGCATTTTCGCCCTTCGGTATGACCTGCTCAGT  
ATCGGGGCACTCACCTTTCGCTCTGCTGTGGTTTAAAGGCTCAGTCAAGCTTACAGCGCTGCAACCTCTGACAAAGGACAGCGGGCT

SEQ ID 5464

MIPDNVHYHNAPIRLLVNTIQDADSAGIQASENNNGTRMGVYHPEKNTLSARAPSPWLP LLLAIAIFQMQLDATILNTALPELAADLNESPFDMQAVVAYTLTVALLIPLSSYLADK  
 GTRKVPFGSIAVFMLSGALGAASGSLFELTLSEVVQGTGGSMVLVPIRLTLIRVYEKSKLLNAINYAVHPALIGPALGPGLAGGYLVEYASWHTFLLNLPIGLIGPVLGNIMPVKNDF  
 ALDPKGYLTFVSAACLLLALESLSHALPYFFALPLCCGLLFPARYFRHKMTASPKYISADFLIRTKPLGLAGNLPSTRLGTSISPIPLMPLNQVAFGFGASISGWLVAVALSSSLVFP  
 LILAPLMKRFPGYRTVLLNWKLLAAPIMLLADPGNSPLINWIFLSLAIGACNSLQFSAMNTLTADLRSPQGTGSCNSLMAYVEQQLAISVGIVAGALILKNWTFLI PASSGLHFAPRMTLS  
 IGGITFLASLVKRLHVSDDGNM/TEGTRP

SEQ ID 5465

ATGAGCGCAACCACTTCCCCAAAAATCATCCGATACGACAGCAATCCGACAGATGTCTATTTTTCGGCAGCTTCGCTCCTTGATCTTTTATGCCCGAAGCAGGCAATGGATGCCATTGCC  
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TTTCCCAGAAAACATGGCCGATTTGCTGATACCTCCGGCTCATGCGGGCGGATGATGAACAATCACTGGCCCTACCCCTGTTTAAAAATACAGAAATACGAATCCAAAGCGGTTGATTGTGCCAAC  
CGTATCATTTAGTPTIACCTATTCTCTGTCTGCCATCGGCTACAAAGCTGAAGACAAAGGCGAGCCAGTCAAAGTCGCCGTTCACTCTCTGTGCCGCCGCCGCGGAGAAATGAATTCCTCATC  
TTTCAGGCTGGCAGTTGATTGACGGTATGAAAAACGTGCAAGCGCATCTCCACGACCACGAAGCGAGTGTTCGGGCTTCGGCGGCACATTCTCCGTCAAAACAGCCGATATTTCCTGGCGC  
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CGTCCGAAGCAATTCGCACTCTCTCTGTGTGGAAGCAGCCGCGAACAAGAAATA

SEQ ID 5466

MSATIPPKILIRYDSNPTDYVFFPGTCVLDLFMPEAGMDALALIEQQGIRVHFPMQSCCGPAYSSGHPTAEDVAKVQLDLFPENWPIVVPSCGCGMKHHWPTLFKNTYEYSKAVDCAN  
RIIEFTHFLAIGYKPEDKGEPVKVAVHTSCAARREMNVLHSGWQLIDGMENVERIVHDHESECCGFGGTFSVKQADISGAMVTDKVAALKETGATEIISADCGCMNITGGKIAKDEPDME  
RPKHIASEFLLETTGGKV

SEQ ID 5467

ATGAAACTAAATACTCTTCACATGGGCTTTGATGACGGCTTTTTCCGTTGCGCCATCTTGGGCGAACAACCGGCAAACTGAAGAAATACAACCCGTCAAAGCTTCTCCCGGCCAAAC  
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CAGCAGTTTTCACGGCAAAAGCTTTTACACATCCGTTACCGCGCAAGCACTCGGGCGAAGGTATACGGCGTAGCCAACCTCAATCGCAACCAAGGCAAAACGGGTACAAGATGGCGTGGG  
CGCGACACTGATTGGAATACAGCCCGTTCAATCAGGCTTTGGTACTCGGTTTCGTGCGCTCTGAAATACAAGTAACCGCGTCACTTATCTGACGACGACATCAACAACGACCGCCAGC  
CGAGGTGTCAGGACGCAATGTGACACCGAAGCCGACATCTCAAACTCAACGTGCGTTGGGCGAATGCGGATTGTGAGCAATGCGTACGCGCGGAAGCAGCGGCTCACTCAAACTCAACCG  
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TTTCCCTTCGCGCTCATCAACAATACTGGAAACCCATTACGGCTACGACTTCAACGGCAAGTGCGCCGTCTATGCTTTGTGAGGCGAATCAAATACGATTTTACGCGCTCTGAAAC  
CAAAATACAGCTTTTCCCTCGCGCAATTTGAAACCGCATCGCGGACAACACCGAAGCGTTCAACTCGCTTGCTGCCATGCGTGAACAAACCGTATGAGCGGCATGCTGATGAACCAAAATCCAG  
CGCGGCAATTGCAAGCAATCGCCCTGTGTAAGAAC

SEQ ID 5468

MKLNLTLTALMLVFPVSAPSNABQPAANTEELQPVKTFSPPKPIAPTAAGQYFPENQFDRSDRSDYFVTEINIDQAFRPLKANSSFYKSPFYNSVTAQALGAKYVGVANLNRKTKANGYKDGGO  
 RDTDWKYSRFNQALVLGFPVSPSENQYRLTYLHDDINNDRQPOVVNDALDTERHISKLVNRWGNADLSNVTSAEAGVILKKRHADNYSLRPNMTQQQVVELDRKVDYDFSLKHDADPGKFE  
 TAAVSRYRDSQNGERNHTHTAMCDFLNGRYPADVHIDRWCIADTLSYKFFDRHKLGLGLSYELNEADIRKNTAQPENPIKPGFPFPASSQQIWKTHYGYDFNGKVRHRLSGELKYDFTPTSE  
 OKYSVSLAHLERIGDTERFNTSLAATVONRMSGLMLNPNPAAAIAGNPPAKN

SEQ ID 5469

ATGAGCGCGCGCGAAATATTTTGGCAAACGTGAAAAAGCGGGCGCATTTGCCGATGGAAGAGCTCGCGTTTGTGATTATACCGCGAAAAGGGCGTTTCTTGGGACAGCGAAGCGGAGTCTGAAACATTTGGGCTGCCGCATGCGCGCGGTCAAACCGAAATCTATTGGGTGACGAAAAGCAATTTGGATGCAGGTTTTCGCGGAAGCGGCAGAGGCAAGGTTTAAAAACATCTCTGCTGCCCTTGGCAACCGAACCGGACAAATFGCCCGTCCGCATATTGGCGGGCAGCAATATCGACCCGATTTGCCCTCGAGCGCGAAATCGATACTTGGAAAAACCGAGTTTTCACGAACATGATGACGGCTCTCAGCGCGCGCAATCGCGCATCGCCGACCGGCACGCTGATGCTGTTTCCAGCCCTGAAGAACCCGCGTACTTTAGAGCTCTGTTCCGCCCGGTGCATTTCTGCTGTGCTATACGCTCAAGATGTACACAGAGTTTCTACACCGCGTCCGAAGCGCAAACCTGTGGAAAAACGGTATGCGCGACCAATGTATCTTGATTTCCGCCCGTCCGAAACCGCAGACATCCAGTTGACGCTCGCTTACCGTGCACCGGTCCCGCTGATTTTGGTCATCTCCGCCCATTTCCCGGACCAATTTCCCGTCCGATTTGGAGGAAAAACGCA

SEQ ID 5470

MSARENIIAKLKAGALPMEEPVDFDYIRKGVSDSEARLKHWAAMRAVKTETVYVTKSNMMPVREAAEGKGLKNILLPLATEHQIARAALAGSNIDPIAFEREIDTWKTEFFTN  
DAGFSGAOCGIARTGTGLFSSPEEPRTLSLVPPVHFLDFTSKMNEFHNVAVRGKLLVNGMPTNVFLISGSPKTIADIOILTAYGAHGPRDLVILAILPDHISPADLEENA

**SEQ ID 5471**

ATGACTACGCAAAACATCAAGTTCCACATGAAGCGGAAACCTTCAACAACAAACGCGCCAAATTCCCTTCAAGACAAGCCCTTGCGTAAAAAGCCTGCGTACCGCGATGGATATGCTGATGA  
CCAAGCGCAAAAGCCGTTTTCACCGACGAAGAAGATTGCAAGGCCGTGCGGATTGTGTGGAACACATCCCTCAGCGTTCCCTCTCCAAATTACCGCGCTGCTGGAGCAGTTGGAAGAAAA



CCTGACTAAGTTGGGCGTGAAAGTACACTGGGCGGAAACCCCTGCCGAAGCCTGCCAAATTTATCCACGACATCATCACGCCAAAAACGGCAAGCTGATGGTCAAAGGCAATCCATGGTC  
AGCGAAGAAATCGAGCTGAACCATTTATCTTGAAGCAAAAGGCATTAAGGCGGTGGAAAGCGACTTGGGCGAGTTTATCGTCCAAATGGCAGGCGAAACCGACCCATATCGTGATGGCCG  
CAATCCATAAACAAGAACAGGTTCAGCGAACTGTTCACCAAAACCTCGGCACACCGCTTACAGACGACGTGGACCAACTGACCGGATTTCGCGCGCAAGGCCCTGGCGGATATTTACAG  
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GCCGAGTGAAGAAATTAGACGCTCCGCGAGAAATGCATTTGGTTTGTCTGCAACAGCGCGCAGCGCAAGCTTATGCCGAAGACCAATGCGCGCACCCCTGCAATGTATCCGTTGGCGCG  
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CGACCCCATTCGAGGGCAAGGCGCATCGCATACCTTCGCGCAACAAATGGCGTGGCGCACATTCACCGGTATTTTACGCGGTAGCAAAACCTTACCGCGCTTCGGTGGCGAGCCACCA  
GTTCCGCAATTCGACCCCGCGCAACAGTTGGGTGGAGCAAAACCGCTACCGATGAACACCGCGGAAGAAACCTTCACGAACTGATGGCGAAAAATGCGCGAAAAAGAACAGGCA

## SEQ ID 5472

MTTQTIKPHMKPFTFKQNAALSLQDKPLRSLRTAMDMIMTKRKAVIDEELQSLRDLCEHTRQSLSKLPALLEBQLEENLTKLGKVVHWAETPAEQIIRDIITAKNGKLMVKKSMV  
SEETLNLHYLEAKGKAVESDLGEPVIVMAGEKPTIIVPAIHKTKBQVSELFHQNLGTPLTDDVDQITGFARKALRDIYSTADVLSGVNFVAETGFLCIVENBENGLSTTVPVPHV  
ITGIEKVVARLSDVPLIYSLIPRSALGQNTITYFNMITGPRRSEELDGPQEMHVLILLNGRSQAYAEQMRRTLCIRGACMNHCFVYTRIGGAAYGTYTTPGPIGBIISPHLLGLDNRD  
LPTACTMCGACVEVCPVRIPIETEQMQLRVEAQRSPTEVPHPIRQGASHTFGEQMAHRTFNIGPSKTYRAFQWAAATKFRNLTPRKQLGWQNRVPMKPAKKTILHELMKMRQKBEA

## SEQ ID 5473

GTGATGATTTCCTGGACAGAAATGTGATTTCCGAACCTTTGCGGCCACACCCCAATGAACGTGTGGTGGCATGGTTGGATAGTTTGATATTTGGAAGATGTGATTTGTCTGCCATTACTG  
TTGAGAAATTCGCTTTGGGTGGCGGTGTGTCTCAATGGCAAGAAAGAAATGTCTGTCACGAACTTTGGAACAAATCCATTTTGCCTTTATTTGCGGGCGGATTCCTGCTTTTGATGA  
ACCGGTTCGCGCAATCTATGCGCAAAATTCCTTCTATGCCAAACACATGCGCAAGAGATTCCTGCGCGAGACGGCTATATTCGCGCGCTGCAAAACAGCACAGTTTGACAGTTGCTAGC  
CGTATACCGGCTATTTTTCGCGCGGATGTGCGGCTTCAATCCGTGGCAGAT

## SEQ ID 5474

VMLLDNTNVEISPLRPQNERVVAVLWLSLIEDVYLSAITVAELRLGVALLLNGKKNVLHERLEQSLFLFAGRIILPFDEPVAATYAIQIRSYAKTHGKEIAADGYIAATKQHSILTVAT  
RDTGSFFAADVAVPNFWD

## SEQ ID 5475

ATGGATTGTTCCAAACGTTCTGTCAGCACATCTTTTCTTGTCCATTGAGCAACAACGCCACACCCAAACGCAATTCGCAACAGTAATGGCAGACAAATACACATCTTCCAATATCAAAAC  
TATCCAACCATGCGCACACATCTTATGGGTGTGGGCGCAAGGTTCCGAAATACATCTGCTGTCAGCAAAATCATCAAAAGAAACCTCGTTATCAGTATTACGACCGGTACGTCT  
TCCAGCTCAACACTCCGATTTCCTGCGCTATGATGCCAACATGACCCCAACGTTACAGTTTGTGTGCTTTGGCGATGTTATCCAAATTAAGCGGATTTCTGCTTCGCTACTGCGCC  
CTGCGGCTCGCGCAGCAAAAT

## SEQ ID 5476

MDCSKRSCSTFFFLPLSNATPKRNSATVMADKYTSSNIKLSNHATTSGLCGRGKSEITFVSSKIITKKPRYQYDRVRLPAQHLPFALLMPTLTPNVQFVVLWRCYFKLSGFLRLRYCA  
LRLAHGI

## SEQ ID 5477

TTGTTCCAAACGTTCTGTCAGCACATCTTTTCTTGTCCATTGAGCAACAACGCCACACCCAAACGCAATTCGCAACAGTAATGGCAGACAAATACACATCTTCCAATATCAAACTAC  
AACCATGCCACACATCTTATGGGTGTGGGCGCAAGGTTCCGAAATACATCTGCTGTCAGCAAAATCATCAAAAGAAACCTCGTTATCAGTATTACGACCGGTACGTCTTCCAG  
CTCAACACTCCGATTTCCTGCGCTATGATGCCAACATGACCCCAACGTTACAGTTTGTGTGCTTTGGCGATGTTATCCAAATTAAGCGGATTTCTGCTTCGCTACTGCGCCCTCGC  
GCTCGCGCAGGAATTTGATTGCGTGTGCTGCGCTCGGATAAATTTCTAATCAACAGAACGCAATTCGCTTCTCTTC

## SEQ ID 5478

LFQTFVQHLLFLAIEQQRHTQTQPCNSNGRIHIHQYQTIQPCHTTIFGLWAQRGMHVRVQNMHKEITSLVLRPRTSSSTPPISCPIDANIDPKRTVCCALANLSKIKRISASVLRPA  
ARARNLIALCVASDKFLITTEALAFPS

## SEQ ID 5479

TTGAAAAACTTTTTCAGGAAGGAAAGGCAATGGCTTCTGTTGTGATTAGAAATTTATCCGAGGCCACGCACACGCAATCAAAATCCGTCGCGGAGCGCAGGGCGCAGTACCGAAGCAG  
AAATCCGCTTAATTTGGATAACATCGCCAAAGCACAACAACTGTACGTTTGGGTCAATGTTGCGATCAATAGGCGAGGAATCGGAGGTGTTGAGCTGGAAGACGTACCGCGTCTGTA  
TACTGATAACGAGGTTTCTTTG

## SEQ ID 5480

LKNPFQBGKAMASVVRNLSEATHNAIKPRARAAGRSTAEIRLILDNIAKAQTVRLGSMLASIGKEIGGVELEDVGRNVDNEVSL

## SEQ ID 5481

TTGATTAACCTGTCGACTTTTGGGGTGCAGTTCAAGAGCGACTGTTTTTATTTATCAGAAAGAGGGAGGGAGAGCTTTTTTTAGATGTAAGAAAAAGCCTGGGCCACCTGAATTTT  
CAGGCATCCGAGCGT

## SEQ ID 5482

LILSDFLGSSRAATVYFLSERGRGVFLDVKKRLRPPEPSGIRRR

## SEQ ID 5483

ATGAGAAATGGGTAAACGAGCTTACCAAGTTCGATGTAGGCGGAGAAAGATATACCTTTCTCCGATTATGGATTGTTTAAACGGGAAATCGTCAGTTACCGTAATTAACCCGCCGGA  
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GAAAGGCAACGGTCTGTTTCAAGTCTGTCCCGCAAGGAACTGCTTGGCAATCGCGCAATGGAAGTTTCTTCGGAACGTTGAAATCGGAATGTTTCCATACGTGCAAAATATGATTC  
GTTACCGAATCGAAGCGGCACTGCACGAATATATCCGTACTACAACACGATAGAAATCAAGTTGAAATTAAGGAGTACGACCTGTTTCAAGTACAGAAATTCAGTCCCTGAAAGCGCT

## SEQ ID 5484

MRKVVTDVTKFDVGGKITYLSPINDLFNGEIVSYRIQTRPTFDLAGEILKGAPEKPGPSEKPMHSDQWQYQMPFYQKQLKGNLQVLSLRKGNCLDNAMESFPFTLKSECFHTCKYDS  
VTESEAAHXYIRVYNNDRILKILKGLSPVQYRIQSLKAA

## SEQ ID 5485

ATGCCGCTGAAACCAATTTTCAGACGGCATCGTACCATCCCGACAGGAAACATCATGCACATACTGACCGCCGCGGTGGACGAGGCGAGCGGACCTTTGGTTCGCGAGCGTGTTCGCG  
CGCGCGTATCTTCCGAAACATTCGACCTGCCCGGACTGACCGACTCCAAAAACCTCAGCGAGAAAAACCGGACCGCTTCCGAAATGATTAAAGAACAGCGCGGTTCGCGTGGCAGGT  
CGCGCGCTCCACGCGCAAGAAATCGCAAGCTCAACATCTGCACGCCACCATGCTCGCATGAAACGTCGCGTTACGGTTTACGGTTTGGCTGCGCGTCCCGAAAAATATTCATCGACGCGAAC  
CGCATTTCCGAACATTTAGGCATCCCTGCGCAAGCAGTGTCTCAAAGGCGACAGCAAAATCATCGAAATTCGCCCGCATCGGTTTGGCAAGACCGCAGCGATCGGAAATGTACGCAC  
TGGCGCAACGCGGTCCCAATACCGTTTCGCAACACAAAGGTTACGCGCAAAAGCAGCATCTGGAAGCCCTCAACAATACGCGGTGCTGCCGCAACCGCGCGGACTTCGCGCCCGCT  
CAGAAACCTGCTCGCGCAGCAGGCTTGT

## SEQ ID 5486

NPSETTIFRHHRTITPTGNIMHILTAGVDEAGRGPLVGSVFAAVILPETFDLPGLTDSKLSSEKKRDALAEINKEQAVAWHVAASTPEETIASLNLHATMLANKRAVYGLAARPEKIFIDGN  
RIPHEIGIPAEAVVKGDSKIETISAAVSLAKTARDAEMYALAQRRPQYQFDKNGYGTQHLBALQYGVLPHEIRDFAPVRNLLAQDALF



## SEQ ID 5487

ATGCCATCCGTTGAATGCTGTGGGGATTGTCGGACTGOCACGCAGCACTTCTATTACCAATTGGCCGTCOAATCGGCAGAGGCAAAATATGCCGATTGAAACGACATATCCATGATA  
TTTATCAACGATATTAAGGGAAGATACGGCTACCGGAGGATTGCGGCAGCCATCCGTACCGCAGGAATACCGGTCAATCACAAGAAAGTCAGCCGCTGTATGGCGAAGACGGGGCTGAAGGC  
AGTGATACGGCGCGCAAAATACCGCTCCTGTTCAAGGAGAAGTCGGCAAGATTGCGCCGAACATCTCGCAACGCTGTTTCCATTACAGAAAGCCGGAA

## SEQ ID 5488

MPSVELLIGIVLPRSTFYQLAVQSAEGKYADLRHIDIVQRYGRVYRRLAAAIRHAGIPVNHKKVSRMLMARTGLKAVIRRRKYSFKGBGVKVPNLQRCPHSEKPE

## SEQ ID 5489

ATGGAAACAGCGTTCAGGATGTTGGCGCACTTTGCCGACTTCTCTTTGAACGAGCGGTATTGCGCGCGCGTATCACTGCTTCAGCCCGCTTCGCCATCAGACGGCTGACTTTC  
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CTGCCGATTGGACGGCAATTTGTTAATFAGAAGTCTGCTGCGGAGTCCGCAATCCCAACAGCAGTTTCAACGGATGGCATTTCTTAAACCTGCGACGAGTTGCGTCTTCTTCTGCGCA  
CTTCTTTCAAGGATCGAGCTTTTATAGGACAGCGCTTCCGCTT

## SEQ ID 5490

METALQDVRNFDPSFERAVFPYPHCLQPLRHQTFADFLVIDRYSCVTDGCRNPFVAVSSLSLINIMDSFQIGIFAFCLDGLVIEGAAGQSDNPOQOQFNGHFLNPATSCVLSAA  
LLSRHRAFLGQPLPL

## SEQ ID 5491

ATGTCCCAAAAGCTGCGCGAGACCACTGAATCTGCCCGAATGCTCCGTTTTGCCGCAATGGTTGCGCTCTACCGTTTGAATGGTATTACCGTTTAAAGCCCAAAACCAAGGAAGAA  
AGCCCGTGAAAAACAGTATCCGCCGCAACGAAAAAGCGACTATCTGAAACCAAGGAAGAACTGTTTGGGAATGGCTTACCTTAAAGCGGAAGCGGCTGTCTAAAAAGCTCGA  
TGCTTTGAAAGAACTGCGCGAGAAAGCAACCTCTGCGAGGT

## SEQ ID 5492

MSQKAAADQNLNLFPCSVLPQWLLRLYLRLNGINGLKPKPKGRKPVKKYPPQTKKADYLKTKBELFAELAYLKAEAAVLKKLDALKEVRQKERNSSQG

## SEQ ID 5493

ATGCCGCTTTACCGTGTATCTGTATCTTGCCACCCATTTGCGTACCAATGAATCGGAAATGGAAAAATATAGTGAATTAACAAAAATCAGGACAGGCGCGGACCGCAGCGCTACAA  
ATGTTACGGAACCGGTTGCGCCGCTGCTTCAATACCTTAGGGAATCGTTCCCTTTGAGCGGGGCGGGGCAACGCCGTACCGGTTTTTGTATTAATCTACTATATA

## SEQ ID 5494

MPLSPCNLYLATHLRNEMSEKYSLETKIRTRRTAGSTNGTEPVRPVLHYLRESFPLSRGGATPYRFLIHYI

## SEQ ID 5495

ATGGCAGCTATTACAAAATGTCTGCATCAGGTTACGAAACGCAAGTCGAAAGCGTCAAAACACTGATTGCCCGTTTTGACCGGCTGATTGACGAATCGGACAAACAAATCGACACCCACA  
CCCCCAGCATTTTGACGGCAAGCCCAAGTGGCGGAGCAAAATCAAGGCATCGGTTCCGATACGACGCTACGCTGATGGCGATGCTGCCCGAATTTGGGGCGGCTGTCCACAAACCGGAT  
AGCGGGTTTGGTCCGCTTGCCTCCGACCCGAGGAGAGCGGGAAACAAATCAAAAGCCGCTGCTTCCGCGGAAGGTTGCGGCTGCGTAAGCGGCTGTATATGCTGCCCGCGCAGCG  
ACACGTTTGAAGCGCTTATTCGGGATTTCCACCAACGCTGCTGTATAGCGAATTAACAAAAACCGGTACGGCGTTGCCCGCCCCGGCTCAAAGGAACGATTCOC

## SEQ ID 5496

MAAITKCLHQVHEQVESVQKLIARFDRLIDESDKQIDNHTRTFDGKAQVAEQIKGIGSITTTATLHAMLPELGRLSHKRIAGLVGIAPHPRESGETKPKSRCPGGRSAVRKALYMAAAAA  
TRPEPLIRDFHQRLLYSELTTGTALPRPGSKGTIP

## SEQ ID 5497

TTGTTTTTAATCCACTATATTCTGACTGCCTCAAAGGCAAAAAATATGTGAATGTTGAGGCTGCCTCTTTTGAATGACAAACAAATGCCGCTGAAACCCGATTTCCGGTTTCAG  
ACGGCAAT

## SEQ ID 5498

LFLIHYILTASGKNNVSMRLPLFEMTNKMPSETRFPVSDGI

## SEQ ID 5499

TTGAACATCAATGCCGCTGAAACCGGAATCGGCTTCAGACGGCATTTTGTGTGCTATTCAAAAAGAGGCAGCCTCAACATCTACATTTATTTTGCCTTTGAGGCAGTCAGAA  
ATAGTGGATTAAAAACAAA

## SEQ ID 5500

LNKCRCLKPEIGPQAFCLSFQKEAASYSHYFCPLRQSEYSGLRK

## SEQ ID 5501

ATGAGCGTATTGATTAATAAGACACCAAGTATTGGTTCAAGGTTTTACCGGTAAAAACCGTACTTTCCACTCCGAACAGCTCTGGCTTACGGCACTAAAGTTGTGCGCGCGGTTACCC  
CAGGCAAGGCGGTCAAACCCACTAGACTGCCTGATTCAACACCATGAAGAAGCGGTAAAGAAACCGGCTGACGCATCCGTGATTACGTTCCCGCTCCGTTTGTGTTGGATTG  
TATCGTTGAAGCGGTGATTGACGGCTAGGCTTGGTCTGTGATTACCGAAGCGGTCCAACCTCTGACATGCTCAAAGCAACCGTACTTGGAAACCAAGCGTACCGCTACCGCTTG  
GTCGCCCTAATCGCGCGGCGTATTACTCGCGGCAAGTGCAAAATCGGCATTATCGCGGCGCACATCCCACTCCGGGCGCATCGGTATTATTCCGTTCCGGTACATTGACTTACG  
AAGCGTGGCACAACCAACCACTGGGCTTGGGTGAGTCACTGATCGGTATCGCGCGGACCGGATTCCTGGTATGAACAAATCGACGCACTGAACTCTTCCAAGAAGACCCAGA  
TACCGATGCCATCATGATTGGTGAAATCGGTGACTGCGGAAGAAGAGCAGCGGAATACATCCAATCCAACGTAACCAACCTGTTGTGCGGTACATCGCGGTGTACCGCTCCT  
AAAGGCAACGCTATGGGCCAGCGGCTGCGATTATCTCCGCGGTAAAGGTACTGCGGAAGAAAAATTCGCCGCGTTTGAAGAAGCGGTATCGCTACACCCGAGCCCTGCCGAGTTGG  
GCACGACGATGCTGAAGTGTGAAAGCAAAAGGTTTGGCA

## SEQ ID 5502

MSVLINKDITKVLVQGTGKNGTFHSEBQALAYGTVKVGVTGKGGQTHLDLPVFMNKEAVKETGADASVIVPAPFVLDSIVEAVDSVGLVWVITEGVPTLDMKAKRYLETNGNTRL  
VGPNCVPIVTPGCKIGIMPCHIHTPGRIGIISRSGLTYEVAQTTNLGLGQSTCIGIGGDPIDPMNQIDALKLPQEDPDYDAIINIGRIGGTAEKEAEYIQSNVTKPVVGYLAGVTAP  
KGRMRHAGAIISGKGTAEEKPAFEKAGIAYTRSPAELGTTMLVLKAKGLA

## SEQ ID 5503

ATGGGATTGGCGCAGGCGGATTCTTAAACCCACTACCTTAAGGAGAAATCCATGAATTTACACGAGTATCAGGCTAAAGAACTGCTGGCTAGCTACGTTTGGCCGTACAAGCGGTA  
TTTTGGCGCAACAGCGGGAAGAGCGGCTGCAGCTTACGACAAATTTGGCGGCAAAATTCGCTGTTGTCAAAGCACAGGTACACCGCGCGCGCGGTAAGCGGCGGCGTAAAGTCTGT  
TAAAGCGCGGCAAAAGCCAAAGAGTGGCTGAAAGCCTGATTGGCACCAACTTGGTAACCTTACCAACCGCATGCCAACGGCCAACTGTCAACAGCGTTTGGTTTGGCAAGATATGTAT  
CCTGTTCAAACCGAGCTGTACTTGGCGCAGTGGTTGACCGTTCTACCCGCGCGTTACATTCATGCTTCTACCGAAGCGCGGTGGAATCGAAAAAGTTGCTGCTGAAACTCCAGAAA  
AAATCTTCAAAGTAACCGTTGATCCGCTGTCGGCTGCAACCTTGCCAGCTCGGAAGTTCGCTTCCAACCTGGGCTTGAAGACAAACAAATCAACGAGTTCCGCAACCTGATGACCGG  
CGGCTACAAAGCGTTTGTGCAAAACGACTTCCGCTGTTTGAAGTCAACCGCTGCGCAGTTTCGCGAAACCGCGCACTGGCTTGCCTGGACGCGCAAAATCGGCATCGACAGCAACCGGCTC  
TACCGCTTGCACAAATCGCTGAATTTGCGGACAAATCTCAAGAAAACGAAGCTGAAGTGAAGCTTCTGAATTCGACCTGAATATGTTGCCCTGGAAGGCAAAATCGGCTGTATGGTTA  
ACGGTGCCTGGTTTGGCATGGCCACCATGGACATCATCAACTCAAGGCGGCAACCTTGCCAACTTCTTGGACGTTGGCGCGCGCGCAACCAAGACCGCGGTGTTGAAGCGTTCAAAC  
GATTTTGGAGACAAATCCGTTAAAGGCGTATGATCAACATCTTCCGCGGTATCGTACGTTGCGACATGATTCGGAAGCCATCGTGGCAGCGGTTAAAGAAATCAACGTCACCGTTCT  
GTGCTTGTGTTGGTGGAGGCAACACCGCGGAATCTGACGAATCAGGTCTGAACTGACTTCTGCAGACGCTGTAATGACGCGCGGAAAAATTTGTTGACGCG  
TAAACGCC

**SEQ ID 5504**

**SEQ ID 5504**  
 MGLAAGRFLKPTHLKEKSMNLHEYQAKELLASYGLPVQGGILAHNGEEAAAAAYDKLGKGFVAVKAQVHAGGRKGAGGVKVSREKAKEVAESLIGTNLVITYQTDANGQPVNSVLVCEDMY  
 PVQTELYLGAVVDRSTRVVTFMASTEGGVEIEKVAETPEKIFKVTVDPLVLGLQPCQAREVAPQLGLKDKQINEFAKLMTGAYKAFVENDFALFEVNPVLAVRENGALACVDGKGIGIDSNAL  
 YRLFKEIAELRDKSQENERELKASEFDLNVYALEGKIGCMVINGAGLAMATMDIILKGGQPANFLDVGGGATKDRVVEAFKLILEDKSVKGVLINIFGGGIVRCMDIAEAIVAAVKEINVNVP  
 VVRLLEGNNARLGAKILNESGLKLTADGLNDAAEKIVAAVNA

**SEQ ID 5505**

SEQ ID 5505  
ATGATAGTGTGGTCTTCATCGCAAGATAGGTCACTGCCAAACACCCCTTCAGAAAACCCCGGATATCCGGGGTTTTTCGCTTTCGCCGAAAAAATGTCCGGGATGGCGGGACGGCAT  
CTGTACGGTGTCCGGTCGGTTTTCGGGAGCAACGGCTTGAAACTTTGGGATATTCAATT

**SEQ ID 5506**

MIVWFFHAKVGHCCQTPFQKTPGYPGVFPALPGKNVGDGGTASVRCFVGFAEERLETLGYSP

SEQ ID 5507

SEQ ID 5507

ATGAGTAAACACAACCTCGTAGAACAAATTTCGCCGCGAGCTGAAACGCGCCGCTCGAAGACCTGTGAAACAGTGTGAAAGAAGCCGCGCTCAGCAAAAAACAGCGCAGCGATTCCCTGACGCTGG  
ACGACAACACAGCTTCTGAAACGCTTACTGACCAAGAAAAACGGCAGCAACCGCGGCACCATCAGCATTCGCGCGCACCAAAAAACCGAAGTCAGCACCGGTGACGGCGCTAAAAGTCTGAAACACG  
CAAAACGAGCAGCAGCATGTCAACATTCTCTTCCGCAAGAATTGGCAGCACAAGTAAAAGCCGCCAAACCAAGCCGACCTGTTACGCGGGAGCAGACCGCAGAAAGACCGGGTAAAGCC  
CGAGCCGAAGCTGCCGACGCGCAGAAAGCCGTGCCAAGCGAGAAAGCGGAAGCGGCAAAACTGAAAGCGCAAAAGCAGGCAACAAAGCAAACTCTGCCGCGCAGAAACCTACCGAAGCAA  
AAGCCGAAACCGGCACCCGTGCGCGCGGAAACCAAAACCGCGCAGCCAAAGAAAAGCCGTCAAGCCGAAACACGAGCGAAACGGCAAGAGTGCCAAAACACCGCGCAAACTCG  
CGACCTTCCGTGCCGCAACCCGTGGTCAGCGCGGAAGAACAGGCGCAACCGCAGGAAGAGCGCGCGCTCGCGCATTCGCGCGCCACCGAGGAGCCCTGTTGAAAGAGAAACAGGAA  
CGCCAGGCAGCTCCGGAAGCTGTGAAACACGCGCAGCAACACGAGCAGCAGGAGCGCGCGCGCTCGCGCATTCGCGCGCCACCGAGGAGCCCTGTTGAAAGAGAAACAGGAA  
CGCGCTCGTAAACACCTGTCATCTCCGCAAAAGCAAAAAAGAAAGACCGCGCAACCGCGATGACGAAGGTCAAGGCCGCAACGCCAAAGCGCAAAAGGTGCAAAAAGCGCGCGTGACCG  
CAACAATGCCCGCAACGCGCGCGACGAGCGCTACGCGCGCGCAAGAAAGCAAAAACTCAAATCTGAGCCGAACCAACACGCTTCCAAGCACCGACCGAACCCGCTGTCACACGAGTT  
TTGGTTCCCGAAACCATTACCGTTGCCGATTGGCGCAAAAAATGGCGGTCAAGGCGTGGAATGGTCAAGCCCTGATGAAAGAGGCGATGTTGTTACCATCAACCACTCATCGACG  
AAGACACCGCCCTGATTGTCGTCAAAAAATCTGGACACATCGGCAAAACCGCGCGCGCAGCATCCGCAAGCTCTCTTGGCGAGGCGCGGGAAGCGGAGCGCAAGCATTTGCCGCG  
TCCGCGCGTCTGTTACCGCTAGGGCCATCGCTGCACACCGCAAAACCTCGCTGACTGATCATCCGCGCGCAAACTGATGTTGATGTTGACAGGCGTGTACAGGCGGAAGCGCGCGCATACGCGAGC  
TACCACGCTCAAAACCCCGCGCGGTGATTACTCTTCTGGAACACCCCGGCGCACGAAGCTTTTACCGCTATGCGCGCGCGCGCGCGCAAGCAACCGGATATCTGTGATTCTTGTGTCGCG  
CGACGACGCGCTGATGCGCGCAAAACCATCGAGGCATTGCCACCGCTAAAGCGCGCAGCGCTTCGATTTGTGTTGCCGTCAATAAATCGATAAAGACTGCCAACCCCGAACGCATCCG  
TCAGGAATCTGACCAACACGAGTCAATCCCGGAGCATTTGGGGCGGCACGGTTCAATTCATCGACGTTTCCGCGAAAAAGGAACGAACATCGACGCGCTGCTCGAAGCCGTATTGCTCGAA  
GCGCAAGTATTGGAACCTGACCGCATCTGTGATGCAACCCGCCAACAGGCATCATCTGTCAGGAGGCGCGCGCGCGCGCAAGCTGTGCGCTGCTGCTGTTCAAAACGCTACGCTGA  
AAAAAGGCGACATGCTGCTGGCCGGTCAAGCATTTGCGCAAAATCCGCGCATGTGTCGAGGCAACCGCAAAATCCATCAAGCAAGCGCGCGCGTCCATCCCCGTGCAAAATCTCTCGCTTGT  
CGACCTTCCGAATTCGCGGTGAAGACGCGATGTTATTCGCGGACGAGAAAGAGCGCGGAAATCGCCCTTTTCCGCCAAGGCAATATCCCGCAGCTGCGCTTGCACCAACGACGCGCGG  
AAGCTGGAATAATGTTTCAACAAATATGGCGAAACCCAGGCCCAATCTTTGTGCGTCTATCATCAAGCGCAGCGTTTCAGGCTCTTACGAGGCTTTGGCGGGCAGCTGAAAAAATCTGCTC  
CCGACGAGGTGAAAGTGAACTGTGTCACAGCGCGCTGGCGGCATTACCGAAATCGATGTCACCTTTCGCATCGCTTCGGCGCGCTTACCTCGGCTTTACGCTGCGTGCAGATGCTC  
TTGCGCGCAACCTTGCAGAAATGAAACGCTGGAAATCCGTACTACAAACATCATCTACGATGCCATCGACGACGCTGAAGCGCGCATTCGCGGATGCTTACCGGATGCTGCGGATGCTC  
GTTACCGGTACGCTCGAAATCCGTACGCTCATCTCCGTTTCAAGGCTCGCAACATCTACGATGCGTATGTCGACGAGCGCGGTGTCGCAACGCGGATTCCTATCCGCTCATCCGCAAC  
ACGTGGTCACTCCACCGGCGCACTGGCTTTCGTTGAAACGCTATAAAGACGACGTAAGAAAGAGTCCGATGGCTTCGATGTCGCGCTGATGCTCAAAGCTCAACGAAATCATGGAAG  
CGACCAACTGGAAATGCTTCGACATCTGTCGAAGTTGCCCGCACCTTG

**SEQ ID 5508**

SEQ ID 5508

MSNTTVEQPAELKRPFVEDLLKQLKEAGVSKNSGSDSLTLDLDDKQLLNAYLTKKNGSNGGTISRTRTKEVSTVDGVKVKTRKRGRTVNI PSAEELAAQVKAQQAAPVQPEQTAEDAVKA  
RAEAAARAEARAKAEAEAAKLAAGAKNGAKPAAPQPTAEAKAEPVAAEATPAEPPEKAVPKPHERNGKGDAKKPAKPAAPVQPVVSAEEQAQRDEBARRAAALRAEQEALKEKQE  
QARRREBMQQAEEQAQAQAEAKTGRQRPAPKPAEKPAQAAPAVENKPVNPAKAKKEDRRNRDDEGQGNKAGKGAKGGRDRNWARNGDEKVRGGKKGKLLKLEPMQHAFQAPTEPVVHEV  
LVPEITTVADLAHKNVKGVMVKALMKKGMVMTINQSIDQDTALIVVVKLGHIKGPAAADDEPAFLGEGAEAEBAALPRPPVVTVMGHVHDGKTSLLDYIRRAKVGQGEAGGITHQIGA  
YHVKTFRGVITFLDTPGHEAFTAMRARGAKAFDILVLLVAADDGVMPTTIEALAHAKAAGVPIVVAUNKIDKDTANPERIRQELTQHEVIDPDWGGTQFVIDSAKVTGNTIDALLBAVLE  
AEVLELTPVDAPAKGIIVEARLDKRGAVATLVNGTLLKKGDMMLLAGTAFGKIRAMVDENKSGITFAGSP1PVEILGLSDVPNAGEDAMVLDAEKKAREIALFRQGGKYRDRVRLAKQQA  
KLENNFNNMGETOQAQSLSVITKADVQASGYTALAGSLKGLSADEVKVNVLHSGVGGGITESDVNLAIASGAF1IGFNVRADASSRKLAEVENVEIRYNYIYDAIDDVKAAMSGMLSPERKEQ  
VTGTVEIRIOY1SVSKYNNIAGCMVTDGVVKRDSHRLIRNNVVIHTGELASLKRYKDQVKEVRNGFEGCLMLKGYNEIMESDQLECFD1IVEVARTL

**SEQ ID 5509**

[illegible]

TGAGTTTATTATCTTCTTCTTGGTACGGTATTTTCTTGGAAACAAAACCGCGCGCACTGCAACGCGCGTGGCAGGAACACGACCAGCCATCCAAAGCCTTGC GCGCAAAOCTTGCTTGC GCG  
 CAGACGAGTTCGCCCTGATTGGCGACAACGAAACGACGCGCATTTGTTTCCGACGTGAAGTTTCGACGTGAACGAAGACATCGCGCGCGCGTTTATCAACAGTGGCGGAAACCTAAATCG  
 CCATCTCGCGCAACAGGGGCTAAACGGGCAAAATCGAAATGGCCGCCGCCCTTACCCGCGCGGATTTCGATGCCCTACGACGTGCATATGTGCGACCTGATGGCTGGCGCGCTTCGCGCTTGC  
 CGACTTCAAATGCTGGCGCGCTGGCGCGCTTCAGCTACGGCGACGTACTTCGGCGCGGTTGAAGGCTGGGCGAAATCCATCTGTTCCACCTTGCTTGC GCGACCAATTCGCCGCCCTTC  
 TTTGCCGATCCGAACACGCTGCACATTTGGCGGTGTCGAACCGCTGCCAAATGGTCAGCAACCTTGCCGAAATTCACCGCGGCGCAGAAATATGGCCGAAGTTCAAACGCAACTGAGCGAGC  
 AGTTTGAAGCGCGCTGAATATGTTTACAGTCCCCAAATCAGCGTCGCTGATTTTGAACGAATTCAGACATTCACCGCTGCCCTGTGCTGTGTCAGCAACGCGCGAAGCGCGCGGACCTTCGC  
 GCTTCACGGCGGCAATATTTCCGCGGATTTGGGTCATCGCGCTGCATATTTGAGACGCTCAAACAGGTTACCCAAACCTATTCGCTCAACCCCAACGGCTCGCCGAGGGCATCGCGCGG  
 APTACCAACGCGCGACGCGCGCTTACCAATATGATGCCCCACCCCGAACCGGTGTACCGTGCCGCACAAATGAGCCGGAACCGGAAGCTGGACGGAATGTCCGGCTGTATCCGCTCT  
 TTGCGCGCGCAGCTAAAGCCTTGCGC

**SEQ ID 5510**

LLAQSDVEQTPPEAREGHLPLVTPLRGTISPWASKATNIAENCLAGIERIERGMVAVLEAGLTDBEQQQWAAALLHDMRTESVLPDFQATSKLPHHLKSTPSTVDVLGGKEALVKANTE  
 TGLALSADIEDIVLENVQALQRNPDSVLELMMFAQANSEHCRHKIPNADFILNGEKPKSLPGMTRDTHNAHPEGTVVAYKNSSVTKGAKIERFYPAANENQGYRPHBEDTHIIMKVETHN  
 HPTALAPFAGAATGAGGERTDBGATGKGRSPKAGLTGFTVSNLNPDLKQPWQDYGKPEHISPLDIMEGPIGGAAPNFGRPNLLGYPTPTPEKPGDQVGRGYHYPHIAAGGLSGIQA  
 QQTHKDEIPEGALLIQLGGPGMLIGLGGGAASSHTGTNDASLDPNVSQRGNPEIERRAQEVIDRWCWQLGQNPPIISIHVDGAGGLSNAPFELVNDAGRGAVFELREVPLEEHGLTPLQIN  
 CNESQERYVLSILEKDLDTFPAICERERCPPAVVGTATYDGHKLVKRDLDLFSNNFVDFLPLNVLGKPKPTKTRTKTVPSTPKKPFHAGDIDITEAAYVRLRLPFAVAANKFLITIGDRSVGGRT  
 HRDQHVGYKQTPVADCAVTMMGFNTYRGEAMSGEKPVALFDAPASGRMCVGEATNTAAVNIIGDIGNIKLSANWMAACNGNEGEDEKLRYTVEAVSKACQALDLSIPVGKDSLHKTVPQ  
 DGEKKSVSVSPLSLIISAFAPVKDVRKTVTPELKNVEGSVLLPIDLGFGKARWGSGSAGQVYNNMSGDAPDLDDAGRLKAPFYSVIQQLVAEKLLAYHNRSDGGLFPALEMAAPARCSG  
 ADIDICLMDKFLPIHLPDFQGDPAEDLSDELYNHAAKILFNEELGAVIYIQKRDQYVDAAPFAGTAYDVSRLGSDPFINFEISFFKGYGYFLEQNRADLQRAWQETSHAIQRLRDNFACA  
 DSEFALIGDNERSAIPADVKFDVNEIDAAPPINSGKPKJALIKQFGVNGQIEMAAAPTRAGFATDVHSMRDMAGRFRLLADFKMLAACCGFSYGDVWLGAGEGHAWSILFHPALRDQFAAF  
 PADPNTITLGVNCNGQMVSNLAEIPGAETPWPKKNSLSEQFEARLNMVHVPSKASLILNEMQDSSLPLVVVSHGEGRADPALHGGNISADLGIALQYVDGQNVQTYTPIINPGSPQGIAG  
 ITNADGRVTTIMPHPERVYRAAQMSRKPEGWTELSGWYRLFAGARKALG

SEQ ID 5511

SEQ ID 5511  
TACAGGCAGAACCCCTATCTTTGCACCTGCAAAACCAACAAATTTTGTGTTTGATTAAATGCAAATATGCACAGATGTTTTTGAAAAAAGATGGAAATATGTCAT

**SEQ ID 5512**

YRONPIFAPAKPTNFVLINAMHRCF\*KKMEICH

**SEQ ID 5513**

SEQ ID 5513

ATGTTCCGAGAGCTTCGTTTCTGATTATATAATTCCTGCAGACAAACAGCATTACATTCATTATGAACAAAGAAATAGTCGGTATTTTCTTTATACCGATGGGCATCATCAGCATGTGTA  
TGCCGCCATTTGTGCAGAGTATGTGATGATGACCGAACTTATACGCTCAACCGTTTCAAAGATAAAGAAATGGTTTGGCGCGTGGCATTGTGTATTATCAGTTTCAGCCTTGCCGTTTA  
TCTGCTCTGTCGGAATTCGCGTAAAAAAGGCATCGTCTTTTTATTCTCGGGGAGCGGTGCAGTCATGTATCTGTGGCGCGGAGTGGTTGCCCTTCAGTAA

SEQ ID 5514

SEQ ID 5514  
MFRELRLPLIYNSVRQTAFITLMNKEIVGIPFIPMGIISMCAALNQMYVMMTETVTLNRFKDKELVWRVALLFISFSLAVYLLCPNSRKKGIVVFFILGGGGAVMYILLARMWLPFSK

**SEQ ID 5515**

SEQ ID 5515

ATGCTCCAAATGATGTAGTAGTAGTATGGTGCAGGTCGGGGCGGATACGTTGCCGCCATTCGTCGCCGCACAACTGGGTTTCAAACTGCCTGTGTGCGATGACGGCGTTAAACAAAGCAGGCA  
ATGCCCTGCATATGGGGCGGTACTTGCCTTGAACGTAGGCTGTATCCTCTCTAAAGCCCTGTTGCAATCCAGCGAACATTTCCACGCTGCGCAACACGATTTTGGCGAACACGGTATCACTGT  
CGGCGACGTAAAATTTCGACGCGGCCAAAATGATTGAGCGCAAGATGCCATCGTGACCAAACTGACCGCGCGCGTGAAATTCCTGTTCGCAAAAAACAAAGTAAACGACCGCTGTTCCGTACT  
GCTTCTCTTTGCGCGGTAAAAATGGCGATGCTTACCAAAATGGAAGTCGATTAACAAGGCGAGAAAAACCGTTATCGAAGCCCAACACGTCATCGGTGACCGAGGTTCCGTCACCGCTCCGTTACT  
CGCAAGTCGCTATCGACAACTGGAACGCTATTGGACAACAAGGCGCAACTTGAACCTTGTGCTGAAGTATGCTGCCAAACTCGCGGTAATTCGCTTCGGTGATGTTGGTGTGAAATGGGTTCCGT  
ATGCAACCGCGCTGGTGGCGGAAGTTACCACTTCTTGAAGCGCGCGCACTTCTTGCTGCGCGCGACCAACAAATTCGCCAAAGAAAGCCTTCAAATATCTTCAACAAAGAGCAAGGCTCTGAGC  
TTGCAATGGGTTGTGAAATTCGGCGACATCAAGTCTGAAGGCAAAAGGTGTTTCCGTTGCTTACGAAATCTGCTGCGCGCGAAGCCAAAACCGAAGTATTCGACAACTGATGCTTGCCATCG  
GCCGTATTCAAAACACCAAAGGCTTGAACGCTGAAGCCGTAGGCTTGGAAAAAGACGAGCGCGGCTTTATCAAAGTGGATGCGCGAATGCGGTACCAACCTGCCTAACGTAATGGGCAATCGG  
CGAGCTGGTTTCGGCGCCGATGTTGGCACACAAGCCAGCGAGCAAGGCGTTTCCGTTGCCGAGCGCATTCGCCGTCAAAACCCGCATATCGACTTCAACACAGTACCGCTTTGTGGATTAC  
ACCGACCGCTGAAATCGCTTGGGTGGGTAAAACCGAAGACGAGCTCAAAGCCGAGGCGTGAGTACAAAAAGGTTACTTCAGGTTTCGGTGCAAGCGCGGTGCAATTCGATTTGGCAAAAG  
CCAAAGGTACCGTTAAAGTTGTGGCAGATGCCAAACCGACCGCTATCTTTGGGCGTACAGATGATCGGCCCGGTGTCTCAGCGAATTGGTTACCGAAGGCGTACTGCGCTCGAATCTCTCGC  
CAGCAGGCAAGACATCGCCGCTGATATCCATGTGCCACCCCAACCTTGTCCGAAGTGGTTACGAAGCTGCAATTGGCGCGCCGACAAACCGCGCTTTGCACGGT

**SEQ ID 5516**

SEQ ID 5516

MSQYDQVVVIGAGPGGYVAAIRAAQGLGFKTACVDAGNVKAGNAPALGGTCLNVGCI PSKALIQSSEHFAAQHDFAEHGITVGDVKF DAAKMIERKDAIVTKLTGGVKFLFQKNKVTSLPGF  
ASFAGKNGDAYQIEVDNKGKFTVIEAKHVTI VATGSSVPRPLPQVAIDWNVLDNEGALNLTSPVAKLGVIGSGVIGLEMGSWNVNRVGAEVTTLEAAPTFLAAADQQIAKEAFKYFTKEQGLS  
IELGWKIGDIKSEGGKSVAYETAAGEARTEVFVDKLTVAIGRIPTNKGLENAEAVGLEKDERGFIKVDGECRTNLPFNVAIGDVRGPHLAHKASDEGVAAERLAGQKPHIDFNPNVFTY  
TDPETIANVVGKTEBQKAEGVVEYKGTSGFGANGRALAGKAGTKVVKVLADAKTRDRLGVHMGIPVVS ELVTEBGVTAL EFPASSED IARI THAHTPLSEVVHEAALAADKRALHG

**SEQ ID 5517**

SEQ ID 5517  
TTGAAATGACTGCGTTTGTGATGGTGTTTAAGAAAAGAGCCGCTGAAAGTCCATATCTGCCGATTCATTCCGAATCAAATGTTTCAGACGGGCTCAATCGTTCGTTGAGCCTATTGTAGCAGCAT  
ACTACATTCAGCTACATCTAAATAAAAAATTCAGACGGGCTTTTCATTAAACAAA

SEQ ID 5518

INDCVLMVLKRSRLKVHICRFIRIKCFRRPOSFVEPIVARYYITLHLNKNSDGLFINK

SEQ ID 5519

SEQ ID 5519

ATGATTATTGATGTAAAGTACCTATGCTGTCTGTAAGCGTATCTGAAGGCACACTCTTGAATGGAAGAAAAAGTTGGCGAAGCAGTTGCCCGTGACAGAAATCCTGATCGATATCGAAACGGACAAGTGGTTTGAAGTACCTTCTCCACAAGCGCGGTATTTGGTTGAAATCGTAGCGCAAGACGGTGAAACCGTTGTGTTGCCGACCAAGTTTGGCCCGATATCGATACAGCTGCTAC TGTGCGTCTGAAGCACCTGCAGCCGCTCTGCGCAAGCTGCCCGGCTGCGGTTCTCTGCTGTCTGCACAAACAAACGCCGCATGCTTGCCTGTCCAAACTGGTTCGCCGAGACCGGTGTT GACGTGAACGTATTTCAAGGTTCCGGCCGTGACGGTGCCTATTGAAAGAACGCTACAAAATGCGCTGCCAAACTCTGCCGACGCGGTGGGCCCTGCCCTTGCACTTCTTGCCTGCCGCGCAC GTCTTGAAGAACGCTACCAATGAGCCGCTTGGCTGCCGTTGTCAGAACGCTCTTGGCTTCTCAACAAGAAAAAGCCACTTCTGACTACATTCACGAAGTCAACATGAAACCGATCAT GGACTTGGCGTGGCAAGTACAAAGAAAAATTCGAGAAAGAACATGGCGTAAACTGGGCTTTATGTCTTCTTCGTTAAAGCCGCTGTACACCCCTTACCGAAAAATACCGGTTGTGAATGCT TCTGTGACGGCAAGACATTGTGTACCAACGGCTACTTCGCATTCGTAATGTCACATGCGACGCCGCGGTTGGTTTGAAGCTGTCACCAATCTCGCGGATGCCCAACAAATGAGCATTTGCCGACA TCGAACAGCAATTGTTGATTACGCAAAAAAGAACGCGCAAAATTCGTAATCGAAGACCTTACCGCGGCTGACCTTCAGTATTTACCAACGGCGGCTACTTTCGGTCTTATGATGTCAC CCGCATCATCAACCCCGCTTCAATCTCGGAATTTGGGTATGCATGCCACTAAAGAGCGCGCTGTGGTTGAAAACGGCCAAGTTGTTGTCCGTCCAATGATGTAICTGGCTCTGTCTTACGAC CACCGTATCATTGACGGCCGGAAGCTGTATTGACCTTGGTAGCCATTAAAGAGCGGTGGAAGACCGGTCGCCCTGTGTTGGATCTG

SEQ ID 5520

SEQ ID 5520

MI IDVKVPSSESVESGTLLLEKKVKGEAVARDEILIDIEFDKVVLEVPSPQAGVLVEIVAQDGETFVADQVLARIDTAATVAEEAPAAAAAEAAAPAAVPAQAQNNNAAMPAAAKLAETGV  
DVNVLOGSGRDGRVLKEDVNAAKPAAAVAPALPAGARPEERVPMRSLRVARERLLASQOENAILTFPVENWKPINDLRKYKEKFEKEHGVILGFMSPFVKAAVIALKYPVWNA

SVDGKDIVYHGYPDIGIAIGSPRGLVVPILRDADQMSIADIEQAIVDYAKKAKDGKIAIEDLTGGTFSITNGGTGSGMSTPIINPQSAILGMHATKERAUVENGQVVVRPMMYLALSTD  
HRIIDGREAVLTLVAIKDALEDVRLILDL

**SEQ ID 5521**

SEQ ID 5521

GTGGTCGTAAAGACAGAGCCAGATACATCATTTGGACGGACAAACAATTGGCCGTTTTCACACACAGCGCGCTCTTTAGTGGCATGCATACCCAAATCGCAGATTGAGGCGGGTGTGATGATC  
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CGATGTCGCGAATCCTCAATTGGTCGGCATCGCGAGGATTGGTACAACCAAAACCGCGTGGGCTGCCAAFTTGGGATACCGATGTGCAAGTAGCCGCGGTACACAATGTCTTTGGCGCTCAAC  
AGAAGCATTCAACAACCGGGTATTTTTTCAGGGCTGTAAACAGCGGCTTTAACGAAGAAGACATAAAGGCCAGTTTACGCCATGTCTTTCTCGAATTTTTCTTTGACTTCGCACGCAAG  
TCCATGATCGGTTTCATGTGTGACTTCGTGTAATGTAGTCAGAATGGCGCTTTCTTGTGTGAGAAGCCAAGAGGCGTCTGCAACACCGGCGCGCAGGCGGCTCATGGTACGCGTTCCTTCAG  
GACGTGCGCCGCGAGGAAGTGCACCGCAGGGGCCACGGCTCGCGCAGGTTTGGCAGCGGCATTTTGTACGTCTTCTTTCAATACCGGACCGCTCAACCGCGGAAGTCAATAAAGTTCAC  
GTCAACACCGGTCTCGGACGCCAGTTTTTTCAGCGCGCGGATCGGCAGCTGTGTTTGTGTGACAGCAGCAACCGCAGCGCGGGGACGCTTCGGCAGGAGCGGCTGCAGGTGCTTTCAGCAGCG  
ACAGTACGACGCTGTATCGATACGCGGCAAAATCTTGTGCGGCAACACCGGTTTACCGCTCTTGCCTACGATTTCAACCATAACGCCGGCTTGTGGAGAAGGTACTTCCAAAACCACTTTGT  
CCGTTTCGATATGATCATCAGGATTCGTACGGGCAACTGCTTCGCCAACTTTTTTCTTCCATTCCAAGAGTGTGCCCTTCAGATACGCTTTTCAGACAGCATAGGTACTTTTACATCAATAAT  
CATTTGTGTCTCCAAATGGCCCTTTTCAGACGGCTGTGTGTGTGTTTTTAATCTGCATATAGGGCAFTTCGCCC

**SEQ ID 5522**

SEQ ID 5522

VVVRQSQIHHWTDNNLAVFPHNSALFSGMHTQNRRLRRVDDRGGHHRTTESTAVGMTCTAGQVFDSDFAVFGFFCVINNCLFDVGNHLVGIADQWYNQTAWAANCDDVEYAVVHNVFAVN  
RSIHNRRVVFQGCNSGFGNEEGHKAQYAMFLEFFVLRTQVHDDRPHVDVFECSQNGVFLLRSQEAFCTNTQAAHWYAFFRTCAGRKCNGRGHGCCGRFGSGILYVFPQYATVTAGTLQIVH  
VNTGLGSGQFCSGRHGGVLLCSRNRSGRSFGRSGCRCFSSDSSCIDTQNLVGNNGFTVLRYDFNQYAGLNRRTYQNHFVRPDIIDQDFVTGNCFANFFLFPQBCAFRYAFRQHEHYFYIN  
HPVSPMALSDGLLCVFNISAYGESA

**SEQ ID 5523**

SEQ ID 5523

ATGTCCTTTTCAGACGGCATCAGTTTCAGCCGTCAGGACGCGGACTTCTACCCCTTTGTTTATATTTTAAAGAAAGAGCGCACGCCATGATGGACGAAAACTCAATTTTCTCTATCTGTTGCG  
GTTCCGAACGCCACCCCTACATCTTGATTTGAGGAATTTGTCAGAGGCTTTTTTGGAAAAACCCGATGCGGTTGATGAAAAATGGAAGCAGTATTTTCCACCGMTTTGAGCAAAACAGCCGGGGACGGTTGCTGT  
CGATGTTGCGACACACACCGAATTCGCGAATCATTGTTTACTTTTGGCGAAAAAGAAANTGCACTCTGCGGTTGCGGGCGGTGCGGATGAGGCAATGCTGAAAAAGACAAGTCAGCGTTTTCACGG  
CTGATTTCTGCTATCGTATCCAAGGCGTGGGTGCGGCCCACTTGATTCGCTCAACGATATCCCTCGCGCGATATTGAAGCCCTTCGATCCGAAATTCACCGGTCTGTCAAGTCCGCGATA  
TGGCGCTTCGATTCAATATGGCGGAGGGTGATTTTGCCAAATCGCGGCAAACTGCTCTTGTCCTCCAAATCATCAGCAACCTCAAAACAACTTACTGTCGCCACATCGCATTTGGAATATATCTTA  
TATTTCCCAATACCGAAGAGCGCGCTTGGGTACGCAACTATTTTGAAGCGGTATTTGTCACACGCCAATTAACATGCCGATCAAAAACCGCGGTATCTTGAAGAGATGACCCGCTCCCGAGAGCT  
TTGGAACGTTATCTGTCATACCAAAATATGTCGGTCAAGAAAGCTTTTCGGTGTGAAGCGCGCAAGCGCGAATTTGCCGTTTGAACCTACTCTGATTCAAACGCGCGTAAGGACGCGGTGGAAG  
AAGTCATCATCTGCTATGTCGCGCAACCTGCGCGCTCTGAATTTTGTGGTGAACATTTTGGGCAAAAACCCGGCGAATTTGTTTGGCGAATTTGAAGCGCGTCCGGAATCAAATGCTCTAGTGG  
CGACGTGAAATACCATATGGGCTTCAGCTCCGATATTGCCACCCCTCACGGCCCGATGCACGTTTCTTTGGCGTTCAACCCGTCACACTTGTGAAATCGTCAATCCGCTAGTGGAGGTTCT  
GCACGCGCAAAACAAAACGTTTGGGCGAAAAACGGCGCGATAAAGTCTTGCCGGTATGATTACGCGGATTCGCGCATTTATCCGTTTGGSGTGTCAACCAAGCAACATTTCAACCTGTCTA  
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TACCGTTAAATCGGTTCAACAAGGCGCGATGATCCGATTTGACCCACCGATGATGTACAAAAAGTATCGCAACATCCGGGTGCGCGTGTCTTGTACACCGAGCAACTGATTTGCCGAAG  
GCTGTGTAATCTGAGTTTGAAGCCGACGTTTACATCCAAGCTTACCGTGATGCTTTTGGACAAGGCGCAACATGTTGAGCAACAACGTTGAGCAACTTCCAACGCAACACAATCGACTGGAG  
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CACGCGTAGAACGTTGGTTGCAACTGTGTTCTTGAGAACAAATATGCAAGTCATCATGCGCGTCTGAAGCGTCGCAAAATGTTTCATCTTTGCAACGCCAAGTCTTGGGTTTCATACCGCAAAAC  
GCTGGTGATTTTCATGTCCAACACGCTGTTTGGCGCTTCAAGGTGCAATGAGCCCGCTGGAAGAACTTCAACGAAAGTCTGCAATTTCCGTCGGTTATTTGGTGATACCGCGCAACGCAAG  
AACGACACCGGTGAAACGCGTGGTATTGTGTGCGCGTCAGGTTTACTATGACTTGAAGAGCCCGTCGAGCCGCAAGCTTAAAGTGAAGAGATGATGTCTGTTCTGTGTCGCGGTTGAGCAGCTGTATC  
CGTTCCTCATACGACGAGGTTAAAGCCCAACTGGCGAAATATCCGACACCAAAATCTGTGTTTGGCGCAAGAGAGCCGAAAAACCAAGGCGGTTTACCAAAATCCGCCACCGCATCGA  
AGACGTTATACCGCAAGAGCAAAAATGTCTTATCGCGCGCTTCAACGACGCGCATCGCTGCAAGTGGCTACTCAAGCAACACATTTGCTCAATTGAAACCAATTGGTTGAAGACGCTTTG  
GGCTTA

**SEQ ID 5524**

**SEQ ID 5524**  
 MSPQTASVQSGRGLLPVYTIKKRAHAMDEKLNFSYLPGSNAPYIEELYEAFLENPDVADEKWKQYPTDLSKQPGTVAVDVABTPIRESFVTLAKKKIASAVAGGADEAMLKKQVSVLR  
 LLSAYRIQGVGAQQLDPLKRIPPRIDEALDPKPHGLSDADMALRFNMGEGDFANRKGKLLLSQIISNLKQTYTCGHIALEYITYIPNTEERRNVRNYPFESVLSVTPHYNADQKRRIILKEMTAET  
 LRYLHTYQYVQKRPFGVEGGESATAGLNLYILINAGKDGVEEVIIGMAHRGLNLVNLIGKKPGDLPAEFEGEABIKLPSGDVYKHGPFSSDIATPHGPMHVSALFNPShLETVNPVVEGS  
 ARAKQKRLGENGRDKVLPVLINGDSAFIGLVGNQATFNLKTRGTYTGGTVHVLVNNQIGFTTSDIRDTSTVHCTDIAMKVSAPVITHVNGDDPERVCFIAIQAALDRKKPHKDIVIDVVC  
 YRWGHNEDGDDPTLPQPMYKVKVSQHPGARALYTTQLIABGVVTVQVEADGYIQAYRDALDKGEHVBTTLTNFQRTQIDWSKYQCKDWREKLETGLPAADIERLFEKTAVPEGFALHPTA  
 KRVTIARKAMASGGQAIDWGMATFLAYASLLTKGHGVRISGEDSGRGTFSHRHVAIHDQKREKWDGFTVPLRNNGBGLGEPLVIDSLINNEEAVMAFVEYFACASAPDKLITWEAQPGDFAN  
 GAQVITIDQLSSGETWKWRLCGLTITLPHGYDGGQPEHSSARVERWLQKSENNMVQIMPEASQPMHLLQRQVLGSYRKPLVIFMSKRLRLRFKGMSPLENFTEGSTFRPVPVIGDTAERAS  
 NDSVKRVVLCAGQYYIDLEAGRAERKLEDVAIVRVEQDLYPPFYDEVKAEALAKYPNAKSVVWAQEBPKNQAGFYQIRHRIEDVISEEQKLSYAGRPPSSAPVGYSSKHIAQLKQLVEDAL  
 AL

**SEQ ID 5525**

SEQ ID 5525

GTGGGTTATFAACTTGCAAAGGAGCGGATAATATGTGCTCAAAATCAATCAAACCTCAACGTCACGGGTCGGGCAGGTTTGGAGCTGCCGGTATTGGAAGCCAGCATCGGGCATGATGTGGTTGACA  
TTCGGGGCTGACAAAAATACAGGTTTGTTGGCTTCGACCCCGGATTGTGTTCAACCGCAAGCTGTGAGTCTAAAATTACTTACATCGACGGCGATCAAGGCTTGCTTTTATATCGCGG  
ATACCCCAATCGACAGCTGGCGGAAAGTCCGATTATTTTGGAAGTCTGCTACCTGTTGATTACGCGCAACTGCCGACTCCGAGCAAAAGCCAGATTTGACAATACAGTCCGCCGCCAC  
ACGATGGTGATGAACAGCTGACTTGGTCTCTCCGGGGTTCCGCCCGCAGCGCGATCCGATGCGGATGATGGTCGCGGTGGTCGGCGCGCTGTCTCGCTTCTACCAAGACAGCTTGGACA  
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TTCCTATTGAAAAACTTCTCTCATATGATGTTTGCCACACCGGTGGAAGACTACAAACCTAAATCCCGCTTTTGGCAGCGCGCTCGACCGGCTCTTTATTTCGATATCGCGACCAAGACAA  
AACGGCTCAACTTCAACCGCTCGCTTGGCAGGCTCTTCGGGTGCGAACCCGCTTTCGCTGTATTGCTGCGCGTATCGCTGCTGCTGGGGTGCTTCGACAGCGGGTGCGAACGAAGCCGTGT  
TGAAAAATGCTGGATGAAATCGGCGATGTGCCAATTGCGCGCATACATGGAAGGGCTGAAACAGCGTACGATCAACCGCTGATGGGGCTTCGGACACCGGGTATACCGCAATATGGATCCGG  
TGCCAGCAATTATGCGCAAAACCTCGATGAGAGTTTGAAGGATTTGGGCTTGGGAAGACAGTCCGAAATCAAACCTGGCGATGGAATTGGAACAGATTGCGCTGAAAGACCCGCTCTTTATC  
GAACGCGCAATGATGCCAATGTGCGATTCTTATTCGCGCATCGTCTGTCCGCGCTGGGCATCCGACCGAAATGTTTACCGTCACTTCGCGCTGTCGCGCAGCTGGGCTGGATTTCGC  
ACTGGCAGGAGATGATTAGCGATCCTTCGCTGAAAAATCGGCCGCCCGCGCCAGCTTTATACCGGTTTCGGAACGCCCGGATTTATGTGCGCGCAGGCGAGAGG



## SEQ ID 5526

VGYNLQRSDNMSKILNVPGRAGLELPVLEASIGHDVDIRGLTKNTGLFAPDPGFVSTASCESKITVIDGDQGLLYRGYPIEQLAEKSDYLEVCYLLIYGELEPTPEQKAEFDNIVRRH  
TMVHEQLTWFFRFRDRAHPMAMVGVVGLSAFYQDSLDITNPEHRKIAIYRLISKIPTIAAMCYRYSNGLPFPNPKNNLSYSENFLHMPFATPCEDYKPNFVLARALDRIFILHADHEQ  
NASTSVRLAGSSGANPFACIAAGIACLWGAHGGANRAVLKMLDEIGDVSNVAAVMGVRKQYRILMGFGRVYRNMDFRASHRSTCYEVLKELGLEDSPKFKLAMELEQIALKDPPTFI  
ERKLYPNVDYFVSGIVLSALGIPTEMTFVIFALSRSVGMISHHHEMISDPSLKI GRPRQLYTGSERRDYVPAGER

## SEQ ID 5527

TTGCAAGTTATAACCCACGTTACTGCATCCGCAGCACGTTCTTGCTTTACAGCGGCTTTGCATTTTGAAATCTGCCCTCAGACAAATTTAGATGCCCTCATGCCGCTCTGATTTTTTCA  
AGCATCGCGATAGGTGCCCTTTGTCGCTTCCGAATGCCGTGAATCAAGGCAAGCAATTTCTGATCTTGAAATCAAGGATTTCCGAAAATCGGACAGCTTTTATCGCTCAATGCT  
CGAATCTTTTTTCCATAAACCTGCCGAGAT

## SEQ ID 5528

LQVITHVTASAARSLSDGLCILKSLARQISDASCPSPDFKHRDVPFVRFPMPVNGKQFLILKPKDFGKLGQLPIAQMLEFFPHKPAED

## SEQ ID 5529

TTGCAGGCAATCCCTGCTGAAACTGAAAAACACAACCGCATCAGGCTCACCGCGACAGCGCAACGACTACTACAACGGCTACATGAATCGCTCGCAGGCGCGGGCTGGAAAGCTGG  
GCGGCACGCTTGTCGGCGGACAAAGTCAAAGACCTGATTTTTCACCGCGCACAGGACAAAGCGGCACAGCTTCCAAAGACGGCGGCATCATCACAGCAACGTGGACGACGATTTT  
TACCGCGCAGGCTTACGCGCTTACAACTTCAATCCGATTCGGCGCGCAGGCAATCAAGCGCGCTTACAACCTACGACACAAACGACGCGCAGGCGCGCTTATCAAAATCCGTCGCTT  
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GCATAGACAAACGCAAGCGCCAAAGGCTTTACCGTTGCCGACGTGTACGAGCGCTAAACATCAAGACAAATACGCTTGCGCTTGGCGGTGAACACGTATTCACAAAAAATACGT  
CGAATACATCAGCGCGCAGCAGTCTCGCCCTATCCCCAGCGTAGTGATGACCGCGGAGGACATATTGGTTGAGTTTGCATCGCGCATTT

## SEQ ID 5530

LQAIPLLKTEKHNIRLTPADSRNDYNGYMSLAGAGWVGGTLVADKVDLIIFDRAHGSGTASDKGGIITRNVDARLFTAQAYARYNFPNPHAAIKAAANYNHGNETDGRPPYQIRFP  
EAAVQADYKNYFAHGSYNIGATRFVAKQTRGDFDNASGLGIDKREAAKGFTVADVYAGVNIKDKYGLRIGVMNVFNKKVVEYISGLEVLALSPSVVYAPGRFYWLSLHAAP

## SEQ ID 5531

ATGCTTTCAGCGCTTATCTCTCCGAACCTAGTACACCGCTATGCAACTGGCGTTTACAACGCTACACAGAGGTTGCTCCACTCGGCTCCTCTGCTACTAGGAGCAGCCCGCTCAAAC  
TTCCAACCGCCACTGCAGATAGGACCAAACTGTCTCAGCAGCTTTTAAACCCAGCTCACGTAACCACTTTAAATGGCGAACAGCCATACCTTGGGACCGACTACAGCCCGCAGGATGTGAT  
GAGCGGACATCGAGTGGCAAACTCCCGCGTGCATGAACTCTTGGCGGGAATCAGCTTGTATCCCGGAGTACCTTTTATCCGTTGAGCGATGGCCCTTCCATACAGAACCCAGGAT  
CACTATGCTCTGCTTTTCGACCTGCGGACTTTCGCTCTCGCAGTTAAGCTTACTTTTCCCATTTGCACTATCAGTCCGATTTCCGACCGGACCTAGGTAACTTCCGAATCTCTCGCTTAC  
GCTTTGGGAGGAGACGCGCCAGTCAAACCTGCTTACCATGCACGGTCCCGACCGGATGACGGGTCTGGGTAGAACTCAAAGACACAGGCTGATTTCAAGGACGACTCCACAGAG  
ACTGGCGCTCTGCTTCCAAGCTCCACCTATCTACACAAG

## SEQ ID 5532

MLSALISSELSYPANQLALQPVHQRVHSGPLVLGAAPVKLPPTPADRDQTVSRFPKPSRTTLNGEQPYPDRLQPDVMSRHRGAKLRRRYELIGGISLISPEYLLSVERWPFHTPEPD  
HYVLLSHLPDLVSQSLSYLLPLHYQSDFRPDLGNLRTPLPRGRRPPQSNCLPCTVPDPDGSGLPEQRHGGISRTTTPQLASLLPSLPLILHK

## SEQ ID 5533

ATGATGGTTTTTGACGACATTGCCAAACGGAATAATCCGTTTTCAAACCCCGCGGGATTTGTTGGAATAGATTAAATCTTCGCGAGTTTATGGAAGAAAGATTCGAGCATTTGAGCGATA  
AAGAGCTGTCCGAGTTTCCGAAATCTTGAAATTCAGATCAAGAAATGCTTGCCTTGATTCAGGGCATTCGGAACGGAACAAAGGACCTTATCCCGATGCTTGAAGAAATCAGACG  
GCA

## SEQ ID 5534

MMVFDIAKRIRFQTRGLLELDLIFGRFMEKEFEHLSKELSEFSEILEPQDQELALIHGHESETDKGHLIPHEKIRRA

## SEQ ID 5535

GTGTTTAGGACATACGTTACGCGATTCAATAGTGTGGCAGCGGAACAAACGGTACGGATCGTTCAAATATCCAAACGCTCATAGTGTATCTCGGCTGTCCGCAATGAAGCGG  
TAGGCGTTACGCAAGCGGACGACCGACGAATTTGTGCGGATTCACAGAA

## SEQ ID 5536

VFRITYVAHVNGVABQTVRIVQIIQTLISDGISAVRNEAVGVQAGRTDEFVGIPPE

## SEQ ID 5537

TTGATGAGAAAGGAACACTTCTCATGGAATAAATGAGTTTTGAAATTTACCGTTACAACCGCGAGCTTGATGCCAAGCCTTATATGCAGCGTTACGAGTTGGAATTTGGAACCGACCGAG  
TGAACTTTTGACGCTTTTGGTACGCTGAAAGCACAAGACGATACCTTGTCTTTCCCGCGCTCTGCCCGGAAGGATTTGCGGATCGGACGTTGGAATCAACCGCAAAACCGGCTT  
GGCGTGTGACCGGATTTACGCGCTTGAACAGCTGTCAAATCCCGCGCTGCCCGGTGTGCCCGCTCATCCGCGACCTGATTTGGATATGACCGAGTTCTTCAAACATACCATTC  
GTCAAACCTTATGTTGTAACGACAAATCCGATTGATCGGACAAAGAGCGTGTCAAACCTCAGGAAGAGCGCAAGAGTTGGATGTTGTACGAATGATTTTGTGCGCTGTCTGCA  
CCGCTGTCCGCTATCTTGGTGAATCCCGACAAATTCGTGCGTCCGTCCGCTGTGTAACCGCTACCGCTTCAATGCGGACGCGGAGATACCATCAATGAGCGTTTGGATAATTT  
GACGATCCGTACCGTTGTTTCCGCTCCACACCATTTATGAATGCTAGACGTATGTCTTAAACCTTGAATCCGACCGGACCATCGGTAAAGATTAAGAGATTTATGTTGAACCGGTT  
GTT

## SEQ ID 5538

LMRGTFLMEKMSFEIYRNPVDKAPYMQRYELELEPTDVKLLDALVRLKAQDDTLFRRSRCSBGICSGDGMNINKNGLACLFDLRLKQPVKIRPLPGLPVIRDLIVDRITQFFKQYHS  
VKPYVNDNPIDADKERLQTEERKELDGLYECILCACCTACPSFWNPNDFKVPGLSLNAYRPIADSRDITNERNLNDPYRLFRCHTINMNVDCPKHLNPTAIGKIKEIHLKRV  
V

## SEQ ID 5539

TTGAATTTGGCGTTTGTCTAAAGTGTCCGACCGCGCTCGCATACGTAGCGCGCAGGCGGTTATTTCCGCTCTCTGGGTAATGTGCAGGAGGACGTTGGGACTGGCACATGTACG  
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CGGCAAAATTTATCAGCGCTTCTTCGGCGGACATCTGCCGAACATGGTAAACGTGCGGTAGAACGTGATGCGGTTGCCGACCGTACCGGTCATGCGATGTTGCATATCTTTGTACCAA  
CAAAACGTCGTCATAACACAAATCTTTGTGGAATGGACGGCGCAAGATTTGATTCGTGATGAAACCGCGGATGTCTGCGGTAACCGCCATGGAAATGGAACCGGCGAGTTTATA  
TTTTCCAGCCAAAGCGGTGATGTTGCTACCGGTGGCGCGGCTGATTTATGCTTCTTCAACATGCTTATATGAATACCGGTGACGTTTGGGCAATTTGCGCCGCTGCGGCAATTC  
GTTGGAAGATATGGAATTTCTGGCAATTCACCCGACCGCGTGGCGGCTGCGGCGGTGATTATACCGAAGGCGTACCGCGCGAGGCGGTATTTCTGTGAACCGCGACCGCAACGCTT  
ATGGAACGCTATGCGCGGACCGTAAAGACTTGGCTTCTGCGACGCGTTTCAACGCGGATGGCGATGGAATCTATGAAGTGGCGGCTGTTGTAAGAACCAAGACCGCTTACTGA  
AAATCGACCATATCGGTGACAGAAAAATTTGGAAGAACTGCCGGCATCCCGGAGATTTCCATTACGTTTGGCGGTATCGATCCGATTAAGACCGGATTCGGTTGTGCCGACTACCA  
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CACGTTGCCAAGCGTTTGGGTACCACTCCCTGTGAGCTTGTGTTGTTCCGCAAGCTGCCGCTGACGACATGATTAATTCATCAAGAGCAAGCGATTTGGAACCTCTGCGCTGCTA  
ATGCGCGGTGAGTTGACCGGCAACGTATCGAGCGTTTGGACAGTCAAAACGATGTTGAAACGTTGATGCAATTCGCTGCGAAGTCAACGCTCCGTACCACTGCACGCGCGGCTGTTCG  
TACCGATGAGATTTCTGACCAAGCGCTTCAAGAAATCATGGCGATTGCCGAGCTGTGAAACGTTACCGAAATCAAAGACAGACAAAGTGTGGAATACCGCGGTATCGAAGCTTTGGA





AGGTTGCCAATTCCTGCGCAAGTCAAACAGCTTTCGCAAGCAAGGTTTGTCTACGAAGAAATCGTATTGGGCAAGATGCAACCGTTACTTCCGTCGCGCTATTACCGGCAAGATG  
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## SEQ ID 5556

LHGVECAAIHNYTSNQSISIKELMALQDRTGQKVPVSVFTRVGDVTKDVSDDLFGKVVVPSLPGAFPTPCSSSHLPRYNELFGAPKENGVDIAICVSVNDTFVMAAABEESDNLYH  
IPDNGEFTFEGHMLVKGEDLFGKRSWYSMLVNDGVVEKMFIEPEEPDGPFPKVSADTMLKFPVAPDKAQESVALPTKPGCQCAKVKQALQDKGLSYREIVLGDATVTSVRATITGKH  
TAPQVFIGGKYIGSSELEAYLAKN

## SEQ ID 5557

TTGCCGAAAACTTTTCATTGCGAGCTGTGTTTCTCTAATTCGGCTTTATATGTGGGAAACAGGCAAAATCGGAGTTGTATTGATAGTTTTAAATAATTATATTATTTAACTATAAAT  
TATACAAATCATTTTGCATGGGG

## SEQ ID 5558

LPENLFIAACFSLIRLYMWTGKSELYLIVLNNLYLYNLYKLYSFCMG

## SEQ ID 5559

ATGAACAAATGCGCTCTGAAAGCCTTTTCAGACGGCATTTGCTCTGAGTTGCGGCGCAGGGGAGCAGTTGCCGGAATATCTTTTCATTGCGAGCTGTGTTTCTCTAATTCGGCTTTATATG  
TGGGAAACAGGCAATCGGAGTTGTATTGATAGTTTTAA

## SEQ ID 5560

MNKRLKAPQTAFCPELRRRGAVAGKSFHCSLFFSNSALYVGNRQIGVVPDSFK

## SEQ ID 5561

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GAAATGACCAAAATGTTTCGACCAACATACCACTACCTGCTGCTGATTCATTCGCGATACCGAATTCAAAGCCAACGCCAAACACTACGTTCAACAACTGCAAGAAGCCCAAACTTTGG  
GCTTGAAAGCCAAACCGACCGTTGTCGCTCCTTTGACTTTCTGTGGTGGGTAAGAAAAAGGCTCGTTGAATTCGACCGCTGAGCCTGTGCTTAACTGTGCTGTTTACGTTGA  
AATCTGACTGCTTTGTTGTTGAAGCCCGTGGATTCAAATGACGAGCGCTGCTTTGCTGTGCTGCTGCTTAAAGATGGGTAGAGCATAGCAAGAGCTTTACGCTACTTTTGAAC  
AAATGACGCCAAATCCTGTGGGCATTTACTTGGTCTGTTGCGCAACCGCGCATTTGAATCCCTGCTGTTGACGCGCTGCACATGAGTTGGTACGCGCACCGCGAGCAAC  
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CGAGCGTTTGTGATTTCCAGCTCTGCTGCTGCTGCACTCCGTTGACTTGTGCTGCTGAGAAAACTGAAAGCCAAACAAACCGACCTTACTCTTGGTTGGCATTCACTCTGCAA  
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TATGTTGACCGGCTCTGTAACCAATCTTCAATGCTTTCGCTCGCAACGATATTCGCGCGCTTACCGGTGCAACAAATCGCACTGGCTCTGAACGACGAAGTATTGGATCTGGA  
GCGCGCATTAAGTCATCAAAATGACGAACCTGCCATCCGCGAAGCTCTCTTTGAACGTCGCGATTGGGATGCTTACCTGAACTGGGCGGCGCAATCTTCCGCTATCTCTGCGAG  
GTTGCGAAGCAGCAGCTCAATCCACACTATATGCTGCTGAGTTCAACGACATCTGCTGCGATTGCTGCAATGGATGCGGACGTGATCACCATTGAGACTTCACGTTCCGACAT  
GGAATCTTGGCTGCGTTGCGGCAATTCAAATACCGCAAGCAGCATCGGCGCGGCTTTACGACATCCACAGCCCGCGCTACCGACAGAAGCGGAAGTGAACACTGTTGCGCAAGCC  
ATTGAGGTTGTTCCGTTGAGCGCTGTGCGGTTAACCGGACTGCGGCTGAAACACCGCGCTGGAAGAACTCTGGAACAGCTTCAAGTAATGATGAAGCTAACCCGCAACTGCGTG  
CCGAATTGGCGAAA

## SEQ ID 5562

LNRLQNPTGFPNMTLHPSGPRVGAFLKFAQEKYWRKEISEQELLIDVAKDLREKNKHAQAAANADYVAVGDTFFYDHLIDLVATGAIIPARFGDSQNLPLEQFPQLARGNKDQFAI  
EMTKWFDNTNHYLVPEFHADFEKANAKHYVQQLQEAQTLGLKAKPTVVVGLPLFLWVGKKGVSVEFDRLSLLPKLLPVYVEILTALVEAGAEWIQIDEPALAVDLPKBNVEAYKDYATLN  
KVSAILLGLTYPGSAEHAALLKSLPVDGLHIDLVRAPBQLDAFAGYDKVLSAGVIDGRNTRANLKNVLETVGPIQAKLGERLWISSCSLLHPTDLSVEKILKANKPDLYSLNLAFTIQ  
KTQELRVLKAALNEGRDSVAELAASQAADSRANSSEIHRADVAKRLADLPVNAQRKSPFADRIKAQAWLNLPLLPITNIGSPQTTEIRQARAAPFKGELSADSYEAAKKKEIALVY  
EEQKELDLIDLVLVHGRAERNDMEVYFCELLSGFAFTQYGVWQSYGSRVCPPIIFGIDVSRPEAMTVAWSTYAQNLTKRPMKMLTGPVTLLQWSFVRNDIPRATVCKQIALALNDEVLDLEK  
AGIKVIQIDEPAREGLPLKRWADAYLANWAGESFRLSSAGCEDSTQIHTMCYSEFNILPAIAAMDADVITTIETSRSDMELLAAPGEFKYPNDIGPGVYDIHSPRVPTEAEVEHLRKA  
IEVVPVERLWVNDGCLKTRGWKETLEQLQVMNVTRKLRAELAK

## SEQ ID 5563

ATGAATTATGCAAAAGAAATCAATCGGTTAAACAAACAGCCTTTCCGATTTGAAAGGCAACATCAACGTTTCGTTGAATTTTCCCGCGAAAAACGAACAAATGGAACGATGCTGTGGG  
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GGAAGCAGCTTCCGACCTGACCGCATCGATGATCCACGACGAATTCGCGCAAAATCGCGAAAGACTATTGGGACAGCGGATTCGCGCGCATCGTTGCCCTGCTGCGGACGAGCGGCG  
GTTATGAGAAAAACCGTTTACGCGGAAGACTTGGTTAAGCTATTACGCTCCGTCGCGCATTCGACATCTCTGTAGCAGCATACCCGAAGTACATCCGAAGCGAAATCCGCACAAG  
CGGCAATGATTAATCTGAAGCGCAAAATCGATGCGGGCGCGAACCAGCTATCAACCAATCTCTCTGATGTGGAACGCTACCTGCGCTTCCGCGACCGCTGCGTATGTTGGGCAATCGA  
CGTCAAAATCGTTCCGCGCATCTGCTGTTACCACTTCAAGCAACTCGGCAAAATGGCTCAAGTAACCAACGTCAAAATCCGAAATGGCTGTGCAAAATGATGAAGGCTTGGACGAC  
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CCATCTGCCATATTTTAGCGCGCGCCCT

## SEQ ID 5564

MYNAKEDNALNLSLDKGNINVSFEFFPPKNEQMETLWDSIHLQTLHPKFVSVTYGANSGERDRTHIGVKRIKETGLEAASHLTGIDASHDELQIAKDYWDSGIRRIVALRGDEPA  
GYEKFPFYAEDLVKLLRSVADFDLSVAAYPEVHPKASQADLILKRLKIDAGANHVITQFFDIVERYLRFDRVCMLGIDVEIVPGILPVNTNFKQLGKRAQVTNPKIPKWLQMYEGLDD  
DQGTRLVAASIALDMVKLSREGVDFHFFYTLNRSSELYTAICHILGARP

## SEQ ID 5565

ATGAACCGAATATTATCTGACAAATATCGAACCGTCTTTTTCGACAGCAGTGCCAAATGAAGGCTGGCTGATTCTGCTTTCGCGCGGAAACGCAAGCAAGGATTTGGACAG  
ACGGCAAGAAATATCTGCTCTTTCTTATAGATATCTCTCTCCACATCCCGCTATACCGGCAACAGCGTAAACGTAATACCGAAGGCGGTCAGCAAGTTCAACCAACGTTTCCA  
ATCCGCTATGTCATCGTTTAGAAGGACAAA

## SEQ ID 5566

MKPNLHPDNYRTVLFFDSSANEGHLIRSCAGTHGKTMVWDGKEYLLFSLDTSSSHSPVYTGQRNVNTEGRASKFNQRPQSVMSFPRDK

## SEQ ID 5567

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CGGCACGGCTGACGGTAAGCAAAGGCAGCGAAGTGAACACGAGATTTTGAAGTTTACGAAATCTGATGCAGTTTCAACCCGGAACCTTTTGGGCGGCAAGCTGCCGATACCGGCTCTT  
CTGGCT

**SEQ ID 5568**

MDMKRRDFLRMTAALAAAGVSPSLAAGKEQFTVYGAPAMPSTIIVAAALQGLAKQADVSLKIWRSPDQLRAGVASGQFKVMHSPSNVGVNLRNQGQKVMVNIITNGITQLVCKGSAIA  
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**SEQ ID 5569**

TTGCTTAAGTCTTCCACCTACCGGCTTAAACAAGCTATTCCAACAGCTTGCCAACTAACCTTCTCCGTCGCCACATCGCATTTGAATCAAGTACAGGAATATTAACCTGTTTCCCATCGA  
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TCGCACCTTCGTACTCTCAGCACACTTTACAATGCACCTTCATCAGCTACAGAACCGCTCCCTACCATGCCGTTAAACCGGCATCCGCGAGCTTCGGTTATAGATTTGAGCCCGTTACA  
TCTTCCCGCGAGGACGACTCGACAGTGAGCTATTACGCTTCTT

**SEQ ID 5570**

LPKSTYRLKQAITPACQPNLLRPHIAFESSTGILTCFPTTHFCLALGADSPYADERCVGNLGLSASGLTRFPIATHVNIRTSSTLYNAPSSAYRTLPHYHAGKPASAASVIDLSPVT  
SSAQDDSTSELRLFL

**SEQ ID 5571**

AAAATGACTGAAACTCAAAAAACCGGATTCGCCGAAAAACAGGAATCCGGAGTCTCAGGGTTGGAAAAACCGTTTTCGCCGATAAGTTTCGTCACGACAGACCTAGATTCCCGCTGCG  
CGGGAATGACGATATTTCAGTTTTCGTTTTCGATTTCGTTTTCGCGGGAATGACGATATAGCGGATTAAACA

**SEQ ID 5572**

KMTETQKNRIPAKTGIRSLRVGKTVFPDKFPYRQT\*IPACAGHTIFQFSVDFFCFCGNDIAD\*Q

**SEQ ID 5573**

ATGCAGGTTCTGCTTTCGCTCAAAACCGCCAAACAACGCCACCGGACTGCCAAATCTGCAGACGAGGGCAAGGTACGTCTCTGCAAAAGCAATCCGCGTTTAAATCGCGCCAAC  
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**SEQ ID 5574**

MQVLSLKTAKQRHRDCQIVRRRGKYVICKSNPRFKSRQR

**SEQ ID 5575**

TTGAAAGGGCTTCGGTAGGAGGGCTTTACAACCGAACCGAAGGGCAGGGGTCAGCGTTGGCGCGATTAAACCGCGATTTCGTTTGCAGATGACGTACACTTTGCCCTCGCTC  
TGACGATTTCGCGATCGCGGTGGCGTTGTTGGCGGTTTTCGCGAAGACAGAACCTGCATTAATTGCTCCTTC

**SEQ ID 5576**

LKRACGRGRFTTEPRAGGQWRDLKRGILLQMTYTLPLRL/TINQSEWRCLAVLSEDTCLICPF

**SEQ ID 5577**

ATGATAGGCAGACTTTTCGCTATTTCCTTTTCGCACTTGCCGCGCTGATTATCAACCGCTCTTTAGCCGAGGCAGAAACGTTCTCTGCGGAAGTCCGCGAAATCAGCGCATGG  
TACTGCTCGGTGACGCGCGCGGCTGCTTTTGGTATCTGTTTATGCTGTATTTCAACAACATTCGCGATTCTGATCGACGGAATAATGCCCTC

**SEQ ID 5578**

MIGRLFRIFFFALAAALINRLFSRRQKRVLEVAEISANVLLGAAATLFWYLFMLYFKHIPDSYRRKNV

**SEQ ID 5579**

GTGTTTGAAATACAGCATAAACAGATACCAAAACAGCGTCGCGCGGCTGCACCGAGCAGTACCCATCGCGTGATTTCGCGGACTTCGCGCAGGACAGCTTTCGCTCGCGCTAAAGAGG  
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TCAGGCTGCTTTCGCGACCGGTGCAAAAAGTATGCCGTTTGCAGATATAATTAACGCTTTTCGCCGCGATTGTTGGAACAGGATATGAGTCAAAATACCTCGGTGGGCATTGTACGCCCA  
AAAAATCCGCT

**SEQ ID 5580**

VFEIQHKQIPKQRRGGCTEQYPCADGDFADDTFLPAKEAVDNQRGKCEKEKNTEKSAHYVGRKRVWFGRGGMGKDVSAARQAACPTVSKSHAVCDIITLFAAFVGTGYESKYLGGHCNAP  
KNSV

**SEQ ID 5581**

GTGGCGATTGTAAACGCCCAAAAAATCCGTTTGAATGCGGCTGGTTTGGAAAAACGGTAAAACTTTGCCGCGTTTCGATCTGATGATTGAAACCTACGGCGAGCTGAATGCTGAAAAA  
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ATGAACAATGTTGACAAGGATTGCCGATTA

**SEQ ID 5582**

VGIIVPQKIPPEMPLVLNKGKTLPRFLMIETYELNAEKNNVLIHALSGNHVHAGRHSADKYTGWWDNMGVPGKPIDTERFFVVGLANLGGCDGSSGPLSINPETGREYGADFPMT  
VKDWKSQLAALDYLGIQWAAVVGSLGGMQALQWASYPVPRVHALVIAAPKLSAQNLAFNDVARQAILTDPDFNEGHYRSHNTVPARGLILARMNGHITYLAEDGLGKRGFRDIASN  
GYQYGSYVEFEVSYLRQGDKFVGRPDANTYLLMTKALDYFDPADFGNSLTRAVQDVQAKFPVASPSTDWRFAPERSHBLVKALAAQKSVQYIEVKSAGHHDAPLMEDEAYNRAVTAY  
HNNVDKCRLL

**SEQ ID 5583**

TTGGCGGAACCAAAAAATGACGCGCTACGGCATCGAAATCGACACCGACAACGTGATTGCTGCGATGTCGCGCGCGCTAAATGTTATCCAAGCCGATTGGAAGAAGGTTGACCGCAT  
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## SEQ ID 5584

LAEHKCSGYGTEIDTNDVIAAMSRGVNVIOADLEGLTAFNDQSFVIVLSQTIQAMQNTXILRLCLMLAKQAIVSFPNPGYWRNRVQIALGGHPVSEMPYHWYDTPNINHCTLKDF  
DLCAKNINIRVLERAAMTGNRQVXHPNLLGSLAFYRVG

## SEQ ID 5585

ATGAAAAACAAACGTCATCACTTCCCTTATGGCTTCCGCAATCATGCTGGCGCGCGTTCCTCCGAGCAAAAGATAAAACGAAAGAAACGGCGCATCCGCGCTTCGTCTTCCGCGT  
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## SEQ ID 5586

MKNKTSSEPLWLAIMLAARSPSKEDKTKENGASAASSASSSQDLPAPASAPDNVQKQASAPL

## SEQ ID 5587

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CGCGCTTTCGATCGCGCTGCGGCTGCTGCGATTCGCTGCGGATCCAAATCGACCAACAGCAGCGGTTTCGCGCGGATGCCAGCGAAGCGCGCAAAATTCACGCTGCTGCTGTTTTGCG  
CACACGCGCTTCTGATTGGCGATGGCAAGGATGTCGCACTCAT

## SEQ ID 5588

FFRHPRQFVRQKIRLGLTCLRVVSHRHFTVARRFRKADIARDGGFKQIPENAAQLFADFQNPAAAVVHRTHDARDVQIGIDRLTDFAHGRNQIGNPFQVRVIAQHRHNHAARRHQAV  
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## SEQ ID 5589

TTGTATCCGACAGCCCGCTTTAGCCGAAATGTCGGATTCAAGATCCGACCCACGCGCTGACAATGCTTAATAGCGGCTGAAAAATGATAAATCAGGTATTCACAACCAACCTACCC  
TTTTAGACGCGCTCTTCCCTT

## SEQ ID 5590

LYPTAPFSRNVGKPNTHAADNALIGRLKNDKSGIHNHPTLFRPLSL

## SEQ ID 5591

TTGTATCGACTTAATCTGAAACACAAAAGGCGAGGATTAAGACACAAAGCAGTAAGCTTTATCAAGTAGGGATTTCAGATTTCCTTACT

## SEQ ID 5592

LYRLNPETQKAGLRHNKAVSFIVGSSLLT

## SEQ ID 5593

TTGCGCAATCATGCTGGCGCGCTTCCCGAGCAAGAAGATAAAACGAAAGAAACGGCGCATCGCGGCTTCGCTCTCCGCGTCATCGGCTTCTCCCAACCGATTTCGAACCGGC  
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GACTGCTGTTTTCCTTCTCCATAACGAATGGAACCGCTTCGCTTACCGCGCGCGGCTATGACAACATACAGCGGCTGCTGTTCCCGACATCCGCGCTGAAGATCCCGACTACC  
ATCAGAAATCATGCTGGCAATCAGAGACTTCGCTTACGGAAGCGGCAACATCAGCGCGGAGGACAAAGATGCCA

## SEQ ID 5594

LPQSCWPRVPRAKIKRKTAPHLRLFRHLLPKPICNRPHPLITSSRQKARHCETAPCTPPPALAISYSKSPNTSTRVCLPFIITNWKPVSAIPAAATTTYSGCCPTTSALKIPTT  
IRKSCWQSKTCVTERAPSAGRHKMP

## SEQ ID 5595

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CCGTGAACGCAATCCGACAAACCGTTTATAGACATCCATTTTACGAAATGCGAAATCAGCGGATTTGCTTTACGAAAAAATATCTATAGTGGATTAAATTTAAATCAGGACAAG  
CGGACGAAGCGAAGACAGTACAGATAGTACGGCAAGCGGCAACGCTGTACTGTTTAAATTTAATCCACTATACTTCAATCCAAACACGGGCGGAATA

## SEQ ID 5596

MEQERRLREATLMLTQGSQKTRGQGEPRKARYFEVSATSAYLNRHNNGLGNFQYIGQLPGYLKMHGEMLENQSLFRLSNRERNPKPFLDIHFDENGKIRIVVYEKNIYSGNLNNDK  
ATKPKTVQIVRQGEATLYWPKFNPLYPNPTGRI

## SEQ ID 5597

ATGAAACAGCACAAAGAACTGGCGCGCGCAATGTATTTATGGTCGCAACGATCTATGGTCGTTCAAAAAACCGAATACATCAAGGCGCGCGCTTCCGCCAAAGTCAGCATGAAC  
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## SEQ ID 5598

MKTAQELRAGNVPMVNDPMVQKTEYIKGGRSSAKVSMKLNLLTGAASETIYKADKPDVILLSRKNCTYSYFADPMYVPMDEEFNQYEIADNIGDALKFIVDGMEDQCEVTFYEGNP  
ISVELPTIIVREVEYTEPAVKGDTSGKVMKTLARLVGGTEIQVMSYIENGDKVEIDTRTGEPKRA

## SEQ ID 5599

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ATTGATGATTTCCTAATCAATCGGTGCTGTAACCGGCTATTCAGCGATTTCCTGATGCTT

## SEQ ID 5600

LDFGAADQTRGFPHFAGSIAFDGLGVLDFAHDGGQFDRNGIAFIEGNFALVFHTVNDQFQVADVVGPDFVLVEFFVHKDVHRVGKIAVRTVFAGQDDHVEFVVGVFVSGSAGQGVF  
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## SEQ ID 5601

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**SEQ ID 5602**

MNTYAFFVCWTFCKVIDNFGDIGVSWRLARVLHRELGWVHLWTDVVSALRALCPDLPVFPVHQDIHVTHWSDAADIDTAPVFDVITFACDLPEVNLNIRRHKPLWLNWYLSAEE  
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VRLVKIPFVPQDFDKLLHLADCAVIRGEDSVFTQLAGKPFVWHIYPQDENVHLDKLHAFWDKAYGYTTPETASVHRLSDDLNGGEALSATQRLBCTWQTLQHQHNGWRQGEDWSRYLF  
GQPSASEKLAAPVSKHQKIR

**SEQ ID 5603**

ATGGCGTTTTCGCTTTTTCGAAAGCCTTGCAATGTCCGAAACCTGCTTGTGCGCTGGCTGCGCGCTGCTGCTCATCCCTTGGCGAOGCTTGGCGTTTTCGCGCCAATCGCGCGAAGACA  
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CATGTTCTGTTTATTCGATGTTTTCGCTGCTGCTATTTGTTCCACTATTTCGCGCGCTT

**SEQ ID 5604**

MAFCFFESLMSRNLIVRLAVCLIPLATLAVFAANPPEDKPKQHLINGIILACEATFLFKFVLFETIKHHLKQGFDLKRTMFLFIPITVLLVVYLFHYPGAF

**SEQ ID 5605**

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GCCGACCAACGAACTT

**SEQ ID 5606**

VEQIHQNNRRNKQKHGLTFQIKPLFKMLDGFKEDEFKQRRFAGKDDAVDQMLGFVFRIGGKRRRQGEADGEPADKQVSGHCKAFKAKRHYRLKNAFCLTDAPEMPSEALPPEN  
AAPFNL

**SEQ ID 5607**

ATGAATGAAGATAAATATAGGGAATATGACATGGGATGAAATGAAATGTAGTAGGAACCTTAGTTTCTGAAGAAAGAAATGCTTAAATCCAATAGCTTTTAAAGTATTAAAAATAGTA  
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**SEQ ID 5608**

MNEDKYRENMTWDEIENVVGTLVSEERMLKSNSFLSIKNSKNRLA

**SEQ ID 5609**

TTGTGCTTAAATCTGCTTTTGTGTTTTCAGGATTAAGTCGATACAACTCATCACCAAACTACTATGTTTGTGTTTCTTTCTCTTTCGAGAGGTTTATCTCTTTCGAAAGATAAAAAATC  
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**SEQ ID 5610**

LCLNPAFCVSLSRYNHHPNMFVPSLARGFYPLQRIKNQNLIVPVC

**SEQ ID 5611**

ACGCTTGCTCAGGATGACGATATGGCGTCCGATCCAGCCCGGACGTCGAGCCTTTGGACTTTTTCGACGCACACATCTGCGCGCAGGCGCGGATTTCCCTTCGCGATATACGCC  
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CGCAGGCGGTGATGATTTGTTCCACTTTTCAACAAATCCATAGGCCAAAGCGCTGCTGCGCGCTTTCGAAATATCGCGCCCATCGCGGCAATGCTGCACGCAGGC  
GTTCTTTACGTTCCAT

**SEQ ID 5612**

TLAQDDEMAFRIOARHVEPLDFFDAHLRQAADFPLRIYALHRRFVAAVFQVRRFRHKIRQFRKRTAGNHVGTHTVRNLHAPRHHAIHVQPLDSRLPQKSRFLRIRIQGYLHIRTARR  
RRNAGLAAARTDIOHRLCAFDIGQQRQAVQKMDNHFFLVAQGGQIVGVPLPQIHIGKPVLRFRNRIRPHRGNACTQAFPTFH

**SEQ ID 5613**

ATGCGTCGGGCTTCAATATGCCGCGCGCGATGCGCGCTTGTGCGCAGGCATCGCGCGCAGCGTCCGATTCTCGGGGAACGCCGTCGCGGTATTTAAAGGTTGCGTGGTGGCGG  
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**SEQ ID 5614**

MRRAPNMPAPDAALSAGIGGSVRFLGERPSRVYLKVRWCVFRQGFRRHLRRVR

**SEQ ID 5615**

ATGTTTCAGGTTTGAAAAATCGGATATAGCGGAAAGCGCGCGCTTATATTTTTCGTTTTCGGAAGCACGCGAGCGCAAGGGCGGGTTTCCGATACGCTTTTAAATTCGCTTC  
AAACGATGCGTTCGGCTTTCAATATGCCGCGCGCGATGCGCGCTTGTGCGCAGGCATCGCGCGCAGCGTCCGATTCTCGGGGAACGCCGTCGCGGTATATTTAAAGGTTGCGTGGT  
GCGCGGTTTTCCGCGCGCAAGGCTTCAGACGGCATCTCCGCGCGTCCGTTAGACAAGGTGCGTCT

**SEQ ID 5616**

MPQVKNADYSGKRAALIFCFEARRRQAGLFPYAFIKCVQFDASGPQYARARCLVRRHRRQRPISRGTVPVPGIFKGSVVRFPARLQTPASPARPLDKVRS

**SEQ ID 5617**

GTGCGGACAAAGCGCGCTTCGAGCGGACGCTTTCGCGTGCCGATGTCATACCGGATAGAGCAGTGCAGATCGAGCGTATGATTTCGACCGGAAGGTTTCGCGCAATTTGAGG  
GCGAGCGCGTTTTCGCGCAGCGGTGCGCCGAGCAGGCTAAAGGCTTTCGCGGTGCGCATATGTTTCAGGTTTGGAAAAATCGGATTA

**SEQ ID 5618**

VRDKGAFGGRRFRADVHTGIEQCRIEADDFDRKGPNFEGSERGPAAGGRPEQKGFGRGHNVSLEKCGL

**SEQ ID 5619**

ATGATGTATTTCCGCGCTTACCCAAAGGTTTGAACGATTTGCCGAAAGCGCGATGCGTGCCTGCGTGGCGACTTGGACGAACAAAAACAGATGTACGCTTGGATTCTCTACCGCACCC  
TGCAAAAGTCGACCTGAAACAGCATGCGCTTGAACCGAAGCAGCAGCGCATCGGACGCGCTTGAAGTCTATTACCTGACCGCGAGCGGATGAGCGCGCACTTGAACGGACA  
GCCCGAATCACACCTGCGCTTGAACCTTACACCGCGCGCTGATTCGCCGAAGCAGCGCGCGGACTGCAAGAAACATCGCGCTTCCACCTGATGCTTGAACAGGCGCTTATCGGC  
GAAGTAGAAAACTGCGCGCGCTATCCGCGCTGACCGCGGACTTCCCGGCATCCGCTGCGTGGCTACCGTCAGGCGTGGGAACCTTGCAGCGTGAACCGACAGACAACTTCA  
TCGAAAAGGCAATGCGCGCACGCGCAACTTGCCTAAACGCCAACTGACTTGGTTACGCAAAACACCTTTAGACTGCGTTGCCGACCGCTTTCAGACGGCACTTCAGGACGCGCTGAT  
TGAGCGCGCAACCGTTTTTCGCGGA



## SEQ ID 5620

MMYFRALTOGLNDLPEADACLRLADLEQKQMYGLDFLYRTLQKVPETACRLKPNDSQIRIGRALEVVYLITGRPMASHLNGQPEHTLPPELYTAALIPEDRARLHENTIALRFHLMLEQGFIG  
EVENLRRRYPGITADSPAIRCVRQANEHLGDATERQTFIEKGIAATRLQAKRQLTWLRKTPDLCVADPPSDGTSGLRIIEAAKRFPGF

## SEQ ID 5621

ATGCTGGCCACGCGCGCTCGCGCCCAAAACGTCGCGCCCTGCACAGCGTCGGTATCCGTACGCTCGAAGAACTCGCGCAAAACGTTTCGGTCAAGCCCTTTCGCTGCTCAAGCAT  
CGGCTTTGACCTCAGCAAAAGCAGCTGTGGCACTCGAGTCGCTGAACGCGACGCGCGCAAGAAATGTCCCAAGCGCAATAAGACTGCTGCTTCCGAGTTGAAAAACCATCC  
GCCGCTCGCGCTTTCGCGCGCAGGAAGAAATGGGATATTCATCGCGCAAGCACTCGCGCAAGCAAAATCGCGCGCAGCGGAAATACCGCTCGGGCAGTCATCGTTTCAGAC  
GGCAAAATCATCAGTCGCGCACAAACCTGCAATGCGGACTGCAATGTGAGCGGACACCGGAAATCAACGCTTGGCACAGGACAGGAGGAAATGCAAAATACCGCTTACGGAT  
GGCAGTCATCATCACCTCGAAACCTGCGCATGTGCGCTCGGCACTGATACAGGACGAATACAGGCGGTGATCTACGCTCGCGGAGAACCAAAACCGCGCGGACGAGCATCGT  
CAAOCTGTTTGCCGACAAACGCTCAATACGACACCGCCATACGCGCGGAATCCTCAAGAGAATCGCGCGGTATTAAGCCGTTTTTCCAAAAAAGAAAGGT

## SEQ ID 5622

MLATPPLAPKTPVAALHRLGIRTLLELRQNSVKAFLLLKASGLTLTKSTLWQLESLLNGTTPQEMSOAHKDCLLAELKNHPVAAFPQEMGYPMREALRQAEQSAADGEIPVGAIVSD  
GKITTSAHNTCIADCNVSRHAEINALAQAGSEHQNIRLDGCDIYITLEPCAMCASALIQARIRRVYGAAPKTAAGSIVNLPADKRLNTHTAIRGILQEBCRAVLSRPFQNRKG

## SEQ ID 5623

ATGACCGCCCTACTCGTCATCTCGCCCTCGCCCTGATAGCGCTCGGCACGCGAGCATCGTCTATCCGCGCTGCGCGCTTGGCATTGATGTTTCCGGAACATGGCTGCTTGCTATG  
CGCGCGGCTATCAAGCTCTACGGCGCAGGCACTCTTGAGCGGTGGGACTCATCAGCTTTGGCGGCACTACTGGCGGACTATATGGCAGCATGTTGGGGTAAATACACTGGGCGAGCAA  
ACTGCGGCTCGGAGTGCAATGGCGCGCAGCATCATCGCATATTTTTCCTCCCTCCGGAATAACTCTCGGCGCTTATCGCGCGCGGCGGAGGAGTATCGGCGCAATATG  
CTTCAGGCGAGTAAAGCGGGCTTGGGTACGCTGTTGGGGCTTTCGTCGCGCAGCGCTTCAAAATCGGCTCGCGCTATCATCTTGTATCTCTGTTGTTGAAATACATCGCATACCTGT  
TT

## SEQ ID 5624

MTALLVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYAGILWTVGLISLGGILADYMGMLGVKYTGAGKLAVRGALAGSIIGIFPSLPLGLLPGFAGAAAGELIDRRNH  
LQAGKAGLGLLGLVVGTAFKIGCAVSLIFILLVKYIAYLF

## SEQ ID 5625

GTGTCGCGCTGATGTTGAAAAAAGAAAAACAGTCGGAATTTACCTTTATCCGCACAAAAAGGTAATTCATGCGCTGTAAGCGCGCTCAAGCTTGTCTAGGATGACGATATGGCGT  
TCCGATTCAGCGCGCGCAGCTCGAGCTTTTGGACTTTTTCGACGACACATCTCGCGCAGGCGCGGATTTCCCGCTGCGGATATACGCGCTTTCATCGCGCGCAGTAGCGCGCTCTT  
TCAACAGGTGCGCGCTCCACGACACAAATCCGCCAGTTCGCGAAACGACGCGTGTAAACGCTCGCGCAGCAGCTCGGAAACCGCTTCCACGCGCGCGGACACACCGCGCATATGTC  
CAACCCCACTCGATAGCGCGCTGCGCAAAAGCGGTTTCTTCGTAATTCGATCCACAAAGGTATTCGTCACATCCGAGCGGACACCGCGCGGAAATGCGCGGCTGCGCGCGCGG  
GAACCGCATTCAGCATCGTCTGTGCGCTTCGATATAGGGCAGCAGCTCAGGCTTCCAAAGATGATGGCAATCATTTTTCCTGCTGCGCGGCGGCTGATGTTAGGTTTGT  
TCCACTTTTTCACAAATCCACATAGGCGAAAGCTGTCTGCGCGCTTTCGAAATATCCGCGCCATCGCGGCAATGCTGACGCGAGGCTTCTTACGTTCCATATCTGCTTCTG  
TCCATATTCAGCGCTAATGTTAGCGGAAACATGCGCTGTAACCGCGTATCGGCTTTCAGACGCAATTTCCGTTCCGCTCTATTTTCTCTGGAACACCAGGCTGACCGCGCG  
GCGGCTCAGCGCTTTCGCGCGCTCAGCA

## SEQ ID 5626

VSRMLKKRTVRNFTPIRTKVKFMPSEARSTLAQDDMAFRIQARHVEPLDFDAHILRQADFPRLIYALHRRPVAAVFPQVRRPRHKIRQFRKRTAGNVHGVTHVRNLHAPRHHATV  
QPQLDSRLPQKSAFTLIRIQGYLHIRTAAHRRNAGLAAARTDIQHRLCAPFDIQQRQAVQKMMNHFFLVAQGGQIVGVPLFPQIHIHQKLEVLRRFRNIRFHRNACTQAFFTFHICFL  
SIFRRNVSGRTCLRKPRIGQTAFFPRPIFSCGTPQAAPARASGVSAASA

## SEQ ID 5627

TTGGTAGAGCACTGCTTTGCAAGCAGGGGTTCATCGGTTTCGATCCGCTTTGCTCCACAAAACCTTTACAAATGAAGCAAGTTTGTCTGTTTATAGCAGCTTATTTGATTTCGGAAGTA  
GAATAACGACGATCGATCTTTAACAATTTGAAAGCGGAAATCAACAAACAAAGACA

## SEQ ID 5628

LVEHLLCKQGVIGSIPFASKTLQMKASLLFLAAYFDLRSRTTHRSITNNKAEINKQKQ

## SEQ ID 5629

TTGACAAACACCATATGGCAAAACCAAGACCATCTACGCGTTCCACGCGCTCAACGCGCGGATTGTGGCAAAACCCAAATCGATTACCGAACTCTATATCCAAAGAGGCAAAATCCGAGC  
CAGCGACGCGGAGTGTGGAAAGGCGGCAACGAAACATCCGCGTATATTTGCGGATCGCGACCGCTCAACGCCATCAGCAAAAGCGCGCGCATCAGGCGGTGTCGGATTAT  
CGATGCTTCAAAAACACGCTCCACTCGAAGACGTAATGGAAACTTGAGCGAACCGCGCTGCTGCTGATCTCGACGGCATCAGCATCCGACAACTCGCGCGTGCCTGCTGTAAC  
GCCGACCAATGGCGGTACACGCGGTACACGCGGCAAGACAAAGCGCGGATGAAGCCACCGTCAGCAAAAGTTCGCTGCGCGCGGAAACCGTCCCTACATCAACGCAACCA  
ACCTCGCGCGACCTTGGCGAATGAAAGAAATACGGCAATTTGGATCATCGGCACGACATGGCGCGGACCGCGACCTTTACCATTTGCAATCTGCGCGACAGCAGCGGTGGTGATGGG  
CAACGAAGGCGAGTATGCGCGCTCACGCGCAACATTCGACATGCTGGTGTCATACCATGTTTCGCGCGGTGAAAGCATGAACGTCCTCGGTGCGCGAGGAATGATTAAGC  
GAAACCGCGCGCAACGCTAATGAAACAAAGAGC

## SEQ ID 5630

LFWTIMANQPIYGFHAVNARLWQNPKSITELYIQEGKSDARTREVLEKAANENIRVYPADADRLNAISKARHQGVVGFIDASKNHVLEDVLENLEPPLLLILDGTTDPHNLGACLR  
ADAMGVHAVIAPKDKSAGLNAFVSKVACGAETVPYITVTNHLARTLRELKEYGIWILGTDGGDADLYHCNLPDSTAWVMGNEGDMRRLTREHCIMLVSIPIMGTVESMNVSVSAGHVLS  
ETRRQVRVKNKA

## SEQ ID 5631

GTGGCAAAACCCCAATCGATTACGAACCTATATCCAAAGAGGCAATTCGACGCGCAGCAGCGCGGAAGTGTGGAAAGGCGGCAACGAAACATCCGCGTATATTTTGGCGATGCC  
GACCGCTCAAGCCATCAGCAAAAGCGCGCGCATCAGGCGGTGTCGGATTATCGATGCTTCCAAACACCGTCCACCTCGAAGACGTATTGGAACCTTGAGCGAACCGCGCTGC  
TGCTGATCTCGAGGCATCACCATCGCACAACTCGCGCGTGCCTGCTACCGCGGACGCAATGGCGGTACACGCGGTATCGCGCGGAAAGCAAAAGCGCGGATGAACGCCAC  
CGTCAGCAAGTTCGCTGCGCGCGCGGAAACCGTCCCTACATCAGCTAACCAACCTCGCGCGCACCTCGCGGAATTGAAAGAAATACCGCATTTGGATCATCGGCACCGCATGGGC  
GGCGAGCGGACCTTTACCATTTGCAATCTGCGCGACAGCAGCGGTGGTGATGGGCAACGAAGCGCAGGTATGCGCGCGCTCAGCGCGGAACATTCGACATGCTGGTGTCATACCCA  
TGTTGCGCAGGTGAAAGCATGAACGTCCTCGTTCGCGAGGAATGATTAAGCGAAACCCCGCGCAACGCTATTGAAAAAAGAAAGCGTAAAGCTCAAAACATGCGCTC

## SEQ ID 5632

VAKPQIDYRTLYPRQIRTHARSAGKGGKRPRIFCRCRPPQHQORRAPSGRGRIYRCLQKPRPPRRRIKLERTAAADTRRHRSAPRRVPAYRRNRGRTRRHRAERQKRGTERH  
RQQLRLRRGNPLHHRNQPRPHPARIERIHLDRHRHRRRRPLPLQSAHQVGDGQRRRYAPPHARTLRHAGVHTVHRHGRKHERLVRNRNGIKRNPATRIEKQKSVSLKNNV

## SEQ ID 5633

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CGCGACGGTAGCGCGGTGGTGTGATGCTCATTTGAGTTTGGTACAGCTCGGTATTCGCGGATTTTCGCGCGCGGCTTCGCGCGGAAAGCGGACGCGACGTTCCGCTCGATGAAAA  
CTTGGCGGTGGTTCGCTGGTACTGCTGATTTGATTTAACTCATGAAAAATCCGCTGCTCGCGGATGAGCGGCAATTCGCGGTGCTGATTTGCCGCTCATATGTCGCGCTGTTT  
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GSTGATTGCGACGGCTTTGGGTTGCTGCGCGTACGACGTTTGGCAAACAACGCGGTGATTACAGATGACCGGAGTGGCTTCGCGCCACGTGGGCAATATATATGCGGTGATTGTTGGTG  
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GCCACGGCATCCGACGGCGGAGGCGGTGATTGCGGCAACGTCGGTGGTGTGGGCTTGGCGGTGGGTTTGGAGCGGAAGTGTAAAAACCTGCGCTCTGTTCACAACTCTATTTC  
CGGCGCGGCATTACGCGAGTCTGCTGAATTTGGTCTTCCCGAAGATAAAACCGAGGCGCGGTCAAGTTTGATACCGACCATTTGGAACAC

**SEQ ID 5634**

MKEGGLSEGANVSTLLGVSFAGAFIVCFSAWLLPYLKKVITPTVSGVVMLIGLSLHVGLADFGGFGAKADGTFGSMENLGLASVLLVLIPLFNMKNPILRMGLIAGVLIAGYIVLAF  
LGKVDPSALQNLFPVTLFPVFKYGFADWHAFLAAGAFLLGVFEAVGDLTATAMVSDQPIBGEYTKRLRGVGLADGLVSVIATAGLSPLTTFAQNGVIMQTVASRHHVGYIAVLI  
LLGLFPVVGRAFTTIPSPVLGGANVLMFGLIAIAGVRLVHGIRREAVLAATSVGLGLGVGFEPFVKNLPLVLFQNSISGGGITAVLLMLVLPBDKTEAVKFTDRLH

**SEQ ID 5635**

ATGGCTGAAACAATGAAAAACAGCGGGATTGCGCTGATTGTTGGTGTACGGTTTGGAGACAGCGCGCGTTCGGTAATGCGCTCTTGAGCGCGGTACCCATCTTTTGGCGGATTTTCGTGC  
CGATGATTACGCCCGCGCTGATTGTGGCGCGCGCTGGAATTCGGGTGGAGATGACGCGGTATCTGCTGTCGATGCGGATGCTTGCCTCGGTGTGCGCACTTATTGCGAGGTCAACCG  
CTTCGGGTGCTGCGCTCGGGATGCTGTCCATCCACGCTTACCGTCATGATTGCGCTCGCGCGCGGATGAAAGAGGGCGGTTTGA

**SEQ ID 5636**

MAETHKKQADSPDLVYGLEDRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMTAYLVSMAMVASGVGTYLQVNRFGSVGSGMLSIQYREDCCARRGDERGRFE

**SEQ ID 5637**

ATGACGGTAACGCTGGATGGACAGCATCCCGAGCGGACCGCCGAGCGGTTGACCTGCAATAAGTCCGACACCCGACCAACCATCGCCATCGACACAGATACCGCGTCACTCC  
ACCGCAATTCAGCGCGCGCCCAATCAGCGCGCGCTAATCATCGGCACGAAATCGCCAAAGATGGTAACCGCGCTCAAGAGCGCATTACCGAACCGCGCGCTGTCTTCCAAAC  
CGTACACCAATCAGCGGAATCCGCTGTCTTTTCATGTTTCAGCATTTGAAGTCTTTCTATCGGTGCCAACCGTTAAAAAATTTTAAAGAACGAATTTGTAACGAATCAAGATTCCTT  
ATCAATTCAAATCTCATGTGCAAAAACACCACCGGTTGTCGAATTCAAATTCCTT

**SEQ ID 5638**

MTVTLGQHFRADRPFAVDLQISADTRNRHRRHQIRRLHRRQFQRAAHNRGRNRHNRQKMGNAQERITERRPVFQTVHQIRRLRLPHCFSHWLSLRQDTLKNFKNEIVNQRL  
INSNPHVQKHRLSEFKFL

**SEQ ID 5639**

ATGTTACAAAGGTAGCTTGGTTGCCCTGATTACCCCGATGAATCAAGACGCGAGCATCCATTACGACCAACTCCGCCAATTAATCGACTGGCACATCGAAAACGGCAGGACGGCATCGTGC  
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CACCGTCGAAGCCATCGCCCTTTCCCAAGCGCGGAAAGCGCGCGGATACACCCCTCCGCTCGTCCCTTATTACAACAAACCTTCCCAAGAGGCAATGTAACCGCATTTCAAGCG  
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AAGCAAGCGGCAACGTCGCGAGCAATCATCAACCGCGCGCGGAGGCTTCGCGCTCTTTCCGCGCAGCAGCACACCGCGCTGCGCTCATGCTCTGCGCGGACACGCGGT  
TATTACCGTAGCGCAACCGCGCGCGGAACTCTTTCGATATGTCGCTGCCGCGCTGCAAGGCGACATTGCCCTTGCACGCGAATCAACGACCGGCTGATTCCGATTACGACAC  
ATGTTCTGCGAACCAAGTCCCGCGCACCGAAATGGCGGTATCCGCTTGGCGAGATGCGGACCGCGCTGCCCTGCCCTCGTTCGCTGACGGAAGGCGGACAGGCAAGTCCGCG  
CCGCCCTGAAGCGCTCAGGACAACCT

**SEQ ID 5640**

MLQGSILVALITPMNQDSIHYDQLRLIDWHIENGTDGIVAAGTTGESATLSVEHLSVIEETVKHVAKRVPVIAGTGANNTVEALIALSQAARKAGADYTLVSVPPYNNKPSQBMRYRHK  
VAEAAAIPTMILYNVPRTVTVSMNNEITILRLAEIPNIVGVKEASGNVSNIELINRAPEGFAVLSGDDHTALPFMLCGHGVITVAANAAPKLFADMCRALQGDIALARELNDRLIPIYDT  
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**SEQ ID 5641**

ATGCCGCTGAACCGTTCCGACGGCATACATGACAAACACTTTAATATCCATCACACAGGATGACACGATGACCCATATCAAAACCGCTCATTCGCCCGCTCGCACTCATCGGCGTTCGCG  
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GCGAGCCAAACGCTGCGCTTTCGCTTTCGCGCAATCCCGCGCGAATCTGGCGCTTCTGAAAGCGCTTTTGGCAGGAAACCGGCTTCGACATCGAATCCGAAGAACCCGCGCATCGGACAA  
TGAAACCGAGTGGCGGAAACCGTGCCAAATCCCGCAAGACAGCTTCGCGCGCTATTTCGACACAGTGGGTTGGCGCGCATCTACTCCACCGCGAGCGGACAAATTCATCGTCCG  
TATCGAACAGGGCAAAACCGCGCTTTCGACATCTTCTTCGCCCAACAGCGATGAAGAAGTGTATGGCGACAAACAAAGACAGACCATGTGCGAGCTTCCGCTTCGACCCCAAC  
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**SEQ ID 5642**

MPSEPPGRHNMWTLISITQDDTWTHIKPVIALALIGLAACSGSKTEQPKLDVQSRSHRLIKLEVPDLNPNQGNLYRLPAGSGAVRASDLKRRTPFAVQPPADAELVLSVKGVRLERD  
GSQRMLVVDGKSPAEIWPLLKAFWQENGFDIESEPAIGMETEWAENRAKIPQDSLRLLFDTVLGGIYSTGERDKFIVRIEQKNGVSDIFFAHKAMKEVYDKNKTPTMWPQASDPN  
LEAFLTRFMQYLVGDGQAEALAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTGLALDRIGLTVVQGNTERHAFLVQKAPNESNAVTEQKPLFLKRLGKGAERPAEQPELIVYAE  
PVADGSRIVLLNKDGSAYAKDASALLGLHSELR

**SEQ ID 5643**

ATGATGTATGAAATAAACAGCCCTTTTCATAGCGGATCTTGCAGGTGTCTGAAATTCATCAAAATTTATTTGGGAAGAGTCCGGCAATCCCGACGGTGTGCCGTGCTTTTTCACAGCGG  
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TACGACTTGGGATTTGGTGGCGGATATTGAAAGTCCGTGAAATGCTGGGTATCGGGAATGGCTGGTGTTCGCGCGTTCGTGGGCGAGCACTTTGTGCTGGCTTATGCCAAACCCAF  
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AACAAATATCGGCAAAATACGGCATATCCGACCGTTATCTGTCAGGGCGGTATGATTGTGTACGCTATGCGAGTGTGCGGAGCTGTGAAAGCCCTTCCGGAAGCGGAATGAGGG  
TGTTCAGGCGGGCATTTGTGCTTCGATCCGCTTTGGCGGATGCGTGGTTCAGGCGGTGAGGATATTTTGCCTGTTGTG

**SEQ ID 5644**

MYTEIKQPFHSGLYQWSEHQIYWEESGNPDGVVIFLHGGPGAGASPECRGFPNPDVFRIVIIDQRCGRSHPYACAEDNTTDLVDADIEKVREMLGIGKWLIVFGSGWSTLSLAYAQTH  
PERVGLVLRGILCRPSETANLNEAGGVSRITYPEQWQKFPVPIAENRRNRLIYAYHGLLFHQDEEVLCSAAKAWADWESYLIRFEPEGVDEADYASLAIARLEHNYFVNGWGLQDKAIL  
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**SEQ ID 5645**

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CGCGTGTGGGATGTTGCGATTGTGAGAACATATGGGAGAAGATGATGTA

## SEQ ID 5646

VLDLRAGACAILNQAALPRRLRGLTVRKQWQSGFLSDIVWVFFSMIYFRLEFMYFFIDGPTDRFSAPAFRGGCLFVRDVAACRDVRIVRSMGEDLV

## SEQ ID 5647

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G

## SEQ ID 5648

MAMVALMANGSAVPEFMLPAPVEVFKSLDLLKHPQENKIGISLWRSVVGISVALIAGLAAGLVAGLVAGSFKTAMALLKPVITILLAMPPIINWVHALFWPFGNPSVLFTIIVLVAPL  
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## SEQ ID 5649

ATGGGCGCAAGCGTATCCAGCATGCGCGGTCTGAGAAGGCGTTCGGGTGTAAAGGACTTTTGTGAGGAAGAAAAGCGCGTTGCCAATATCGCGCGCGATGACGGTACCTGAAG  
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## SEQ ID 5650

MGASLIQPCRVSEGLRVKDFCQGRKRCQYRRPMTVPER

## SEQ ID 5651

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CTACAACCTATAATGCTAATCCACAGACGCAAAACCTTATCACCAGGACGACATCCGCGCGGTGGGCTCGCGCTCATCGCGCGGTGCGGTTTCGACATCACGCCCAACCTGACCT  
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## SEQ ID 5652

VQADLAYAERITHDYPEPTGARKDKKISTVSDYFRNIRTHSVHPRVSVGYDFGSWRIAADYARYRKWNNSYVNIKRKVENNGSGKKLTQDLKTEQNGTFHVVSSGLSAYVDFDTG  
SRFKPYAGRVSYGBVRHSIDSTKKTVDVITAPPTSDGAPPTYNANPQTQNPYHQSISRVRGLVGIAGVGFDTTNNLTLDYGRYHWNWGRLEWRFKTHESLGRYRF

## SEQ ID 5653

ATGACGGGTTTAAAGATTGCGGTGTGTGCGGACGGGTTCGAGATTACGGTATTGTCGGGAATGACGGTTCGGGTATTTTACTGCGCCCCCGCGCGCTGTAAACGGCAGGTGCATCAA  
AATCGCGCTGAAAGGTTTCAGACGGCATCGGTATCGGGGAATCAGAAAGCG

## SEQ ID 5654

MTGFKIAVLSDGRDYIVGNDGSGILLRPPRACKRQVHQKRLKQVTSASVNGQR

## SEQ ID 5655

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ATCGCGACGCGCAAAATCATCAACCGCAATTATCAATTCAATTACGGTTTGTCTTTGAACCGGTATACCAACCTCAATCTGACCGCAGCTTACATTCGCGCGAGGCAAAATATCGAAG  
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CCAATGCAATCAATACCGTTTCGCGCGCAATATACGGCTTATTCGCGTTCGGAACCAATTTAAGCGGCGATTTCGAGAAAACTCGCGGCAATACAGGAACATTCGACCGGAGCTG  
CGGCTTTATGAAACCGCTATTTGAATAAATACGCGCAAAAGCGCGCAACCAATTCGCTGCGGATTTATTCATGCGGCTTTCGCGGCTATTCGCGCATCACAC  
CGTATGCCCAACATCAAGAAATGTTTTCCTCAATCGCGACTTCGCGGTTACACCGCTTAAAACAGAGCGCGCAACACTTGGCAATTTGGCTTCAATACCTATAAAAAAGGAT  
TGTTAAACCAAGATGATATATTAGGATTGAACCTGCTCGGCTACCGCAGCGCAATTGACAACTACATCCACAACGTTTACGGGAAATGGTGGGATTGAACGGGATATTTCGAGCTGGGT  
CGGACGACCGGCTTGCCTACACCATCCGACCGCGCAATTTCAAGACAAGTGACAAACACGTTTTCGAGCTGGAGCTGAATTACGATTATGGGCGTTTTCACCAACCTTCTTAC  
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AACCTTATTTTCGCGCGGAAAGTCAAAACCTGTTGACAGCGGTTATATCGATCCGCTCGATGCGGCAATGATGCGGCAACGAGGCTTATTACAGCTGTTGACCGGAAAGACAAAG  
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GTTT

## SEQ ID 5656

LFIVEENRMRSSRLKPICFYLMGVNLYHHSYAEDAGRAGSEAQIQVLEDVHVAKRVPKDKKVPFDARAVSTRQDVFKSGENLDNIVRSIPGAFTQQDKSSGIVSLNIRGDSGPRVYTHV  
DGITPTFTYSTADGRAGSSQFGASVDSNPLAGLDVVRKSGSAGINSLAGSANRLTVGDVVDVQGNNTYGLLLKGLTGTNSTKGNANAAIGARKWLESGASVGVLYGHSRRGVQNYR  
VGGGQGHIGNFGEYLERRKQYFVQEGGLKFNAGSGKWERDLQRQYWKTKWYKYEDPQELQKYIEHDKSWRENLAPOYDITPIDPSGLKQSGAGNFKLEYDGVFNKYTAQFRDLMT  
IGSRKIINRNYQNYGLSLNPPYTNLALTAAYNSGRQKYPKGAFTGWLKDFETYNNAKILDLANWATFRLPRETELQPTLGFNYFHNEYGNRFPPEELGLFDGPDQDGLNLYSLGRFK  
GDKGLLPQKSTIVPQAGSQYFNTFYDAALKKDIYRLNYSYTHNINRFGGEYTYGYSNEFKRPAFGENSPAYKEHCDPSCGLYEPVLKYGKRRNNHVSISADFGDYFMPFAGYSRTH  
RMPNIQEMYFSQIGDSGVHFAALKPERANTWQFGNTPYKGLLKQDDILGLKLVGRSRTDNYIHNVYKWMDLNGDIPSWVGSTGLAYTIRHRNFKDKVHKHGFELNLYDYGRFTNLISY  
AYQKSTQPTNPSASESPNASKEDQLKQYGLSRVSALPRDYGRLEVGTWLNKLTGGAMRYFGKSRATAEERYIDGTNGGNTSNVRQLKRSIKQETLARQPLIFDPAAYEPPK  
NLIPRAEVKMLFDRYIDPLDAGNDAATQRTYSSFPDKDKEDVTCNADKTLCKNGYGTGSKSVLTNPFARGRTFLMTWSTYK

## SEQ ID 5657

ATGCCGCTCTGAAGCCCTTCAGACGGCATTGTGTTCCCAACCGCATCATCTGCCGCAAGCCTATGCCAATCCGTTTATCGCATCGGCAACTCAAAGAAAATCCATTTCAATCCACG  
CAGGGAAGCCGGTTTGTGATTTCGGTTATTTTGGTTGTTTCGGGTAATTTATGAGTCGTCAATCCCGCAAAAGCGGAATCAGTTTTTTT

## SEQ ID 5658

MPSESPDGIICFPKRILPQAYANPFYRIGNSKNPFHSHAGKPVDFGYFWLFRVIYESSFPQKRESVFL

## SEQ ID 5659

ATGCCCGCCCTTTGTGCTTACCGTTTAAACGCAATTCGCAAAATTAATAAATAATCTGAAAAAGCGGGTAAGCCAAAGATGGTAATCATCGTTGOCATCATGCGCAAACTGCGGAAGCCCG  
CCTATTACATGTGTAACCGGGCAGCCTTACGATGCGGAAGACAC

## SEQ ID 5660

MPALCAIRFNAPKLINNLKAGKPKMVIIVAIMRLAKPATYIVKTQGPYDAERH

## SEQ ID 5661

ATGTTTCACGGTTTAAACCGGACAACGGCACTGCCTTTATCGGGCAGTGCCGTTTGTCTGCCGCCGAACGTTTCGGACGGCATATTTTGACTTTGGAAACAAAAATAAAATACCCATAAA  
AATTAATATATATGACAAATTGAAA

## SEQ ID 5662

MFHGLKRTTALPLSGSAVLSAARTFGRHILTLKQIKYPKKLTYYDKLK

## SEQ ID 5663

GTGCCAAACGTTGCTAAAGCCCGCGCGAAGGACACGATATCGTCGTCGTGATTCGCCATGAGCGGGGAAACCAACCGCTCGTTGCGTTGGCGCACGAAATGCAGGAGCATCCCG  
ATCCGCGCGGAGCTGGACGTGCTTTAGCTACCGCGGAACAAGTAACCATCGGCTTTTGGCAATGGCAATGAAGGATATCGCGTGGATGCCAAAGCTACACAGGCTGGCAGGTCTCCCT  
CAAAACCGATACCGCCACACAAAGCCCGCATAGAAAGCATTGATGACGAAAAATGCGCGCGACCTCGCGCGCGCAAAAGTCGTATCGTTGCCGGCTTCCAAGGCATCAGCAGTGAA  
GGCAATATTTCCACGCTAGGACGCGCGGTTCCGACACTTCGCGCTTTCGCGCTTGCAGCGCTTCAAGCGGACGAATGCCAAATCTATACCGACGTAGACGGCTTTACACACCGGACC  
CCCGCTGCTACCGGAAGCGCGCTATGGATACGTTTGAAGAAATGATCGAATCGGCCGCTCGTTGCGAAAGTTTTCGCAATCCGTTCACTAGAAATTCGCGGAAAAATACAA  
AGTCCGCTGCGCTACTGAGCAGCTTCAAGACGCGGCAACGGCACCTTAAATACCTTTGAAGAGGACGACAACTGGAAGAGCTGCGGTAAACCGTATCCGATTCGATAAAACCAA  
GCCCGCATCAACGTCGCGGTTGCGCGATAAGCCCGCGCTGCGCTATCAGATTTCGCGCGGCTCGGATGCCAATCGAAGTCGATATGATTATCCAAATGTCGCGGACGGAAGGCA  
CAOCCGATTTCCTTTCACCGTACCGCGCGGCGATTACAAACAGACTTTTGGAAATCTGTCGGAACGTAAAGACAGTATCGCGCAGCTTCTATCGACGCGCAGCACCGGTGTCGAAAGT  
CTCCGAGTCGCTTTGGGTATGCTTCGCACGTGCGCGTAGCCGCCAAATCTTCCGACGCTCGCGGAAGAGGCGATCAACATCCAAATGATTTCACCTCCGAAATCAAAGTTTCCGTA  
TTGATTGACGAAAAATACATGGAACGGCAACCGGATTTGCATAAAGCCTTTGATTTCGGC

## SEQ ID 5664

VAKRVAKARAEHDIIVVVSAMSGETNRLVALAHMQEHDPRELDVVLATGEOVTIGLLAMALDKIDVDKASYTGWQVSLKTDTAHTKARIESIDDKMRADLAAGKVIVAGFGQISSE  
GNI STLGRGSGTSVALAALKADECQIYTDVGVVTTDPRVVPPEARMDVTTFEEMI ELASLGSKVLQIRSVFAGKYKVLRLVLSLQDGGNGTLITFEEDNMRRAAVTGIAFDKQ  
ARINVRGVDPKPGVAYQILGAVADANIEVDMI IQNVGSEGTDFSTFVPRGDYKQLEILSERKDSIGAA SIDDDTVCKVSAVGLMRSHVGVAAKIFRTLAEIGINIQMISTSEIKVSV  
LIDKYMELATRVLHKAFLDQ

## SEQ ID 5665

ATGGCTTATGTGGTGTGGTCATGTTTGTGTCGCTGTTGAATACCTGATTCCAGCCCTTTGTAATTTTGTTTATGCCGTGGAGGAGATGATGATCTGTCT

## SEQ ID 5666

MAYVVLVMVFSLSLFEYLIPSLCKFLCRGGDDDL

## SEQ ID 5667

GTGCGAGGCCCAAGGCACTCACACTATCGGTAATCTGTTTGTGTTAAAGAGCGTTGCGAAATATATAAGTATCCCTTCGCGCTGTCTAAGATATCTCTCGATATTTCCGACATCCCGTCT  
ATACTTTTCAGTTCTGCTCCGCGCTTCGGCAGCGCGGAAGAACGCAATATACGCCCGAGGGGAAACAGTCAATACTTTTCAGCGGATTTTTCGGGGAAATTCGTCTATGTCGCTGTCG  
A

## SEQ ID 5668

VRGPRHSLSVICFVKERCEI IKYFRLSKISLSDIPCYTTPQFVRRFGSGEEPNTYFAGENSQYFQDRDFPGRIRHVAVG

## SEQ ID 5669

TTTTTCTCTGTGAACACCACAGGCTGCACCGCGCGCGCTCAGGCGTTTCGGCAGCGCTCAGCATAGACACGACACCGGCAACGCAATATTCGACACCGCTCCCGCTCAGCGG  
CCCAAGCGCGCACTGCCCAACACAGCTTGAAAAATCCAAAGCCACCGCGCGCAAGCGCCACCGCGGACAGAAACAGCGCGTAACCGGAATCCCGCGCATCATCTTTTGTACCGCAAGT  
TCGTGAGGCCCGGACACAAACACATTCAAAAACGCAACACCGCAACCAACAGTCCCGTCCCAACCGCCACCGCGCGGAATCCCGCTCCGACACCGCACACGACGAGCCG  
CGCCGCTCCGAACGCAATGCAAAAGCATCATGCAACCGCAACGCAACCGCAGCTCAAAAACACCGCCCGCAACAGGGTCGATAGGATATTTCTCGTTCACAAACATCGCGCTC  
CCCCCTCTCCGAAGCAGGCGCATATACCGCGCACCGCTTGCGCCCGCGGAAAAGTTCACAA

## SEQ ID 5670

PPVVEHRLHRRARQAFRQQRHQPFGKRIFRHRLPAQPAQGGTAQQOLENPSHRRASRHAQKQVRTRMPPHLFRVQFQARRHNIQKRKHTEHKPNSAVPTATPAESAVRHRHQF  
RPSERTCKGIMHRQKQKQKQPRKQGRIRIFLVHKHRRPSSSEAGRIIPRTALPPARKVAQ

## SEQ ID 5671

ATGCCCTCGGGCAGGCTACGGATGTGCCCGCTATTTATGTACGATTAAACGCCATGTTTACGCTTTCTTGTGTGGGATGGTCGGGCGAGCATGGTTGCTGGAAAAAGCGGCTATTATTA  
CTATTTTTTACATGAAGTTCAAGAAGGACTGCGCTTTCCCGCTGCGCTTTGACAGCGGTCAGCGAAAAAAGCTGTTCTTTCAGATTTT

## SEQ ID 5672

MRSGRPTDVPYPLCTINAMPHAFICIGRAAWFAGKAALITIFMKFKNGLRFPACRLTAVSEKPVLSDF

## SEQ ID 5673

GTGTGGGATTTGTCGGGCGAGTGGTTGCTGGAAGCGGCTATTATTACTATTTTTTACATGAAGTTCAAGAACGGACTGCGCTTTCCCGCTGCGCTTTGACAGCGGTGAGGAAAAA  
CCTGTTCTTTTCAGATTTTTCAGAAATGCCGTCTGAAGCGTTTTCAGACGGCATAGGACAG

## SEQ ID 5674

VWDWSGSMVNCWKGYYTYFLHEVQERTALSRLPFDGQKRTCSFRFLTKCRLNGFTAYGQ

## SEQ ID 5675

ATGCCCTGATTATATCCGCACTCAGCGCGCGCGGACAGCGCTGCGCGATATCAAAATCACCCCTATTTCCTGCCGATACGAGCGGTTCTGCGCTTATTGAATGCGGTAAATACCAAGTGA  
TTTGTACCGCTTCGTTGGAGCAAAATGCCCAACCGTTTCGACAGCGCAAAACCAAGCGTGGGTAAACGGCGGAATACGGTATGCTGCTGCTCAACCGCTTTGCGTATGCGCGCGAAGC  
TTCGCGCGGCAACAGTCGGGACGACACAAAGAAATCCAAACGCTTGATCGGCGCTTCGCTGCGCGCGGTCGTGATATGAAAAAATCGGCGAAGCAAAATCCTGATTGATTGCGATGTG  
ATTACAGCGGACGCGCGGACGCGTACGCGCTTCGATACCGGTCGCTTTCGCGCTGCAAAATCGCGCTCGGCAAACTGGTTTCAGACGGCATTTTGAAGTAAACCCCATCTTGAAGCTG  
TTGCCCGGTATCAGCGGCGTAGTGAACGGCGTGCGCTTTTGGATTTCGATATCCGGAAGACTCGGCTGCGACAGTATGTGAACATCGTCATGACCGCATCGGGGAAAAATCATCGA  
AATACAGGGAACGCGGGAAGCGCGCATTCAGTTTGGACGAGTTGGGCAAACTGCTTGCCTGCGGCAAAAGGCAATAGCGAACTGCTGCGTTATCAAGAAATGCGTTGTCGCTGCT

## SEQ ID 5676

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IQADGGTTFASITGAFVALQIAGKLVSDGILSENPLLEAVAAVSAGVNVGVLDDLDYDPEDSGCSDVNIIVMTASGKIIEIQGTAEAGAPPSLDELGKILVALAKRIGELLFYQQNALSWA

## SEQ ID 5677

ATGTACAACATCTGGTCTGCGGTGACGGCAGTGAAACGTCATCAATGCCCTGAAACACGCGCGGAGCTTCCCGGGTCAACGGTGGCGCTGACTTTGGTACACGTTGCCAATC  
CTGCCGAATATATGGCGCTCGCCCCGAATTTTGCACACGAAAGTTACGAGGCGCGCGCTCGCGCAAGGCAACGAGGTTTGGATGCCCGCGAGCGCACCGCCCCGGAAGTGGGTGT  
GGGAAATACCGTCAACACCTGCTGGTTGCCAATAAGGGTGGCGGAAATGGCGAGGATTTGGTCGATTATGCCGATGAAACGGTGGCGGCTGCTGGTGTGGGCACGACGGGCGC  
ACCGGCTGATGCACCTTTTATGGGAGTTTCCGCGAACGGTAATGCCCAAGCCACCTGCCGCTTTTATTATCCGTAGCAAGCCGAGAGGCG

## SEQ ID 5678

MYKHLVAVDGSSETINALKHAELAGVNGARLTLVHVANPAEYMLALAPEFLQHSYEAATAVQNEVLDAERTARELVGNTVKHLVANKGAREMAQDLVDYADENGAGLLVLGTHGR  
TGLMHLMGSPAETVMRQSHLPLLIIRSKAREA

## SEQ ID 5679

GTGGCTTTGGCGCATTAACGTTTGGCGAACTGCCATCAAAAGTGATCAGCCCGTGGCGCGCTGCCCAACACAGCAGGCGCGGACCGTTTTCATCGGCATAATACGACAAA  
TCTCGCGCATTTCCGCGCGCACCTTATTGGCAACGAGGCTTTGACGGTATTTCCACACCCAGTTCCCGGGCGGTGGCTCGCGCGCATCAAAACCTCGTTGCTTGGCGGACG  
CGCGCGCTCGTAACTTTGGTGTGCAAAAATTCGGGGCGAGCGCCATATATTCGGCAGGATTTGGCAACGTTACCAAGTCAGACGCGCACCGTTGACCCCGGCAAGCTCGCGCGCTG  
TTTACGGCATTTGATGGAGCTTCACTGCCGTCAACGGCAACGACAGATGTTTGTACATATCGTATTCTCTCTTTGACCGCTCACGGTGGCGCTCTCTCAGGTTTGGCAAGGAGT  
CTGCGCGTTTCAATTATAGACCGCGCTCGGGCTTTATACAACAGCGCAACAGCGTACTGCTTTCCAGTA

## SEQ ID 5680

VALAHYRPGETAHQKQVPGAPVRAHQHQAQTVTFIGIDQILRHFAITLIGNQVVDGISHQTPFGGALGGIQLVALRDGGGLVTFVLQKFGGERHIFRIGNVYSQTRTVDPKLGCV  
PQIDGRFTAVNGNDQMFVHIVFSFCTVSRCLRFPAQRQSAFFHYRPAVGLYTTAEQPDPCFPV

## SEQ ID 5681

ATGCCCGGAAGCGTCGCGAAGAGGTCAAAGCGTTGTCGGACATGGTCGAATCTCGCAAGATTGGCTCAAATCAAAAAGTGAACGAAGCCGCGCAAAAAATGCC

## SEQ ID 5682

MPPRREEVKALSDMVESCKIASNQKVNESRQKNA

## SEQ ID 5683

TTGACCTCTTCGCGAGCTTCGCGGCATCGCCAGACTCTAGCGAGACTCTGCTTACGCGACTTTTTCACAGGCACAGCTTGCCTGGTGGCGGTGGCGGGGTGGCGCTCGTGGCGGTG  
AGGCTTTGGCGCGCACGGCATCGCGGCTTTCAGTTGATTGATTTGGACAACGTTGCCGAATCGAATGCCAACCGCCAGCTGCACGCCCTGACCGCGACTTCGGCAAGCAAAAGTTAC  
CGCTTGGCGCAAGCTATTACACAAATCAATCCGCAATGCGAAGTATTTGAAATGGAAGATTTGTTACCGAAGCAATTTGCGGAATACTTCGGAAGAGTTTGTATTGCTCATCGAC  
GCGATCGACCAAGTGGCGGTCAAAGCGCAATGGCGCTTATTTTGTGGAACGCAAAACCGTTTGTCTCAGCGCGCGCGCGCGGACAGAAAAATCCCGCTGATTCAAACCGCG  
ATTTAAGCGCGGTAAACCCGACCCGCTGCTTGCACCTCGCTACACCTTGGGAAACGCTACGGCTTCAGCGCGGATCTAAGGAAAAAATGGCGGTGGCGGTGCTGATTGACCGA  
AAATATCATGCGCGCGCAATCGCGCGCAGCGTCTTCTGCGATGCCGCGCGCAGGCTTGTCTATCGCGCGGTATGGCGCAAGTATGCTCGTTACCGCTTGTGCGACTGATTGCGCA  
CAGCGCGCGGTGGAACACATCCGCGGCAAAAA

## SEQ ID 5684

LTSSRRPGGIARLYGDSALTHFSQAHVCVVGVGGSWAVEALARTGIGRLTILDLNVAESNANRQLHALTGDGPKAKVTALRERTIQINPQCEVFEIEDVFTEDNLPEYFGKGFDFVID  
AIDQVRVKAAMAATYFVERKQPFVLSGGAGGQKNPALIQTDLSRVTHDPLLANRLYTLRKRYGFSRDTKEMRVPCVYSTENIMFPQSGAACSADAAPQLSCAGYGASMLVTSFGLYCA  
QAQVEHLAGKK

## SEQ ID 5685

TTGACGTTCAAATGAAATCGCGCACGATGGGGTCGCGGAGGATTTCAAACGCAAGTTTCAAGACAGATCATCATCTCTCCACGGCATAAACAAAATTTACAAAGGCTTGAATCAG  
GTATTCAAACAGCGACCAATAACA

## SEQ ID 5686

LQVQTEAHGVAEDFKTHVFKTDHLLHGIKIKYGLSEGIQTATQIP

## SEQ ID 5687

ATGCCGCTGAAACAGGATTCAGACGGCATTTGAACAAACCGGCAATCAAGCTGTCGGTTAGAAAAACCAACATCGGCACGCCCTAAACCGTATTACAATCTACTCTTTCAAATA  
TTTGCAAT

## SEQ ID 5688

MPSETGFRRLNKRGNQAVGSEKPTSRALKPYSQSTPFQNICI

## SEQ ID 5689

TTGCATTAAAGCCGTTATAATGCCGTCCGAACATCTGCCGACCATATGCGTGAATGCCGCGAGATTGTTTCTTTTGTAACTTATATTAATAATCACTTACCAATTCACGCCAT  
GCCGCCATCCCTGCCCTATCCGACCATCCGAGCACATGTCGATGGGTATTCGCCAACCCGTTACCGATTTCGCCGAGGATTTGTTATCCCGCCGACCGCG

## SEQ ID 5690

LHLKAVIMPSEHLPDHIMRECRQIVFFCKLILKFTYQFTPCPSLFPYHPHSTLSHESYANPLPICRRICLSRPT

## SEQ ID 5691

TTGTTTATCCCGCCGACGCGTGAAAGTCGTATTGGCAGTTTCAAGGCCCTTTGGATCTGCTGCTTACCTTATCCGCAAGCAGAAATCGATGTTCTCGATATTCGATGGTGAA  
TTACCGGCGAGTATCTGCACTATATTGCCAAATGGAAGCTTATGATTGCGCGCGGAATATCTTTGATGGCGGCAATGCTGATTGAATCAAAATCGCGCTCTGCTGCGCG  
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GATTTCGCGTGGGCTTACCTGCGCTGAAATTCGAGCGGAGACGAGCTGCCGAGGTTTACATCGCGATTGATGCGAGCATGGTTGGCATTTCTTCTCGGCAAAACATACGCGCA  
GCCACGAATTAATCAAGAAACCTTTCCGTCGCGCGCAATGACGCGAATCTGCCGCTTTGAACGAACACGGGATATGCAAGGTTTACGCGCTTTCAATCCGCAAGCGCGCGC  
TTACGTGATGCTCACTTATCGCCCTGTTGGAGCTTGCCAAAGAAGGATGGTCGAATCTGACGAAGACGCTTTCGGAGAAATCCGAATCAGGCTCAATCATGAGGGGCGCATTC  
GACGGCATTTTCGCGACACGGGCGGGCGCATGCTTC

## SEQ ID 5692

LFIPDPALKVVLGSPQPLDLLLYLIRKQNDVLDIPMVEITGQYLHYIAQMEAYQFLAAEYLLMAAMLEIKSRLLLPRTEAVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGR  
DPAWAYLPLEIAETKLFVYIADLMQAWLGILSRKHTRSHEVIQETLSVRAQNTAILRLRIENHIGICRPHALNPEQGAATVIVNPLALLELAKBGLVIGVEDGPGREIRISLNHGAHS  
DGIFGTGGGRDVF

## SEQ ID 5693

ATGAGGGGCGCATTCAGACGGCATTTTCGGCACACGGGCGGGCGGATGCTGTTCTAATACGCCCAAGCGCGCACCAAGAAATCGGGAGACACGCCATATGACCGGCATCATACATTCGC  
TGCTCGACACTGACCTCTACAAATTCATGCTGCAAGTAGTCTGCAACAGTTTCGCGACAGCGACAGCTTTACGAATTCGCTGCGCAACGCTCGACCGCTCTATCCGCTTGGCGA  
CATCAGGAAGACTTGAAGCGGAACCTGACGCGCTTGGCGGCTGCGCTTACCCACGACGAACTCGGCTATCTGCGCTCCCTGCGTTTCATCAAAAGCGACTTTGTCGATTATCTCGAA  
CTCTTCCAGCTCCAAACGCGCTTTGTCGAAGTCGCGACAGACGATAAAGGCGCTGCAACATCCGTATCGAAGCGCGATGATACAGGCGATGTTTTTGAATCTTCATCTCGCCATTC



TCAACGAACTTTACTTCGCCGGCTGGAAACCCCTGCCGTTATCGAAGAAGCGCAACGCCGGCTTCAAGCCAAAGCCGCGCCTGAAAGAAATCGCCGCCGACAGAATCCGGACGAACTGCCCTTCCTGATTTCCGACTTCGGCACCAGCCGCCGCTACAGACTCGCGTGGCAGGAACAGCTATFCGCGCACCTGCTCGAAGCGCCCCAAGCATCGTGCGCCGCAACAGCAACGTTTACCTCGCCAAAAAATCTCGGCATCAACCCCCATCGGCACCATCGGCACAGCAATTTCTCCAGCCTTCCAAGCCTCGACGCTGCGCCTCGCGAATTTCCAAAAGGCGCGCTCGAAAGCTGGGTGCACGAATACCGGGCGATTGGCGCTTGCCCTTGACCCAGCTGGTGCGTATGGATGCCTTCTCGCGCATTTTCGACCTCTATTTCGCCAAACTCTTTGACGGGCTGCGCCACGACAGCGGCGACGAATACCGGGCGATTGGCGCTTGCCCTTGACCCAGCTGGTGCGTATGGATGCCTTCTCGCGCATTTTCGACCTCTATTTCGCCAAACTCTTTGACGGGCTGCGCCACGACAGCGGCGACCTTACGTTTGGGGGACAAAAGCCTACGCCCACTATCAAAAGCTCAAATCGACAGCGCACCAAAATGCTGACCTTCTCCGACGGGCTGGACATCGAAGCCTCTTGGGCATTGCAACCAATTTTCAAAGGCCGCTTCAAAACGGCTTCGGCATCGGCACCAACCTCACCACGATATGGGGCATACGCCCTTGAATATCGTGTGAAACTGGTGAATGCAACGGGCAGTCCGTGCCAAGCTCTCCGACTCGCCGGGCAAAACCATGACCAACACAGCACTTCTCGCCTTACCTGCGCCAAAGTGTTGGCATACCCGAACCTAGAACGCGG

**SEQ ID 5694**

SEQ ID 5694

MRGRITQAPASARGAGAMCSNTPQAATNRRETHMTGIITHSILDLDLYKPTMLQVVLHQPPQTHSLYEFRCRNVSTVYPLADIREDLAEALDALCRLEFTHDELGYLRSRFRKSFDFVDYLE  
LFQLQRRFVEVGTTDDKGRNLNRIEGPMIQAQPFPIFLAIWVNELYFRLETPAVIEEGERRLOAKAARLKELIAAQNPDPEPFLISDFGTRRRYKLANQEHVINTILLEAAPSTVIGTSNVY  
LAKKLGITTPIGTMAHEFLQAPALDVLRLNFKAALESWVHEYRGDLGVALTDVVGMDAFLRDPDLYPAKLFDGLRHDGSDPYWGDKAHAYHQLKIDSRTKMLTFSDGLDIERSWALHQ  
YFKGRFTGTGFGIGTINLDMGHTPLNIVLKLVECNQGSVAKLSDSPGKMTWTNNSTFYLAYLRQVGPGEPRPT

**SEQ ID 5695**

SEQ ID 5695

ATGAAGTCTCGGCTTTTCGGTTAAATTCAAATCAGGCGGTATTTTAAAGATTTTATGCGGCGGAAACAGGAATGTACGCTTTTTCGCGGTTTACGCGCTTCTAGGTTCCGGTATGCGG  
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CGGTATGCCCCCATATCGCTGTGTGTGAGGTTGTGTGCCGATGCCGAAGCCGGTTTGAAGCGGCCCTTTGAAATATGTGGTGCATGTGCCAAGAGCGTTTCGATGTCCAGCCCGCTCGGAGAAGGTTCAG  
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CGGATGATGCGGTTCCTGCCACCGACGCTGTAGTCGGCGGCGGTGCGCGGAAGTCGGAATCAGGAAGGGCGGTTCGTCGCGGATTCGTGTGCGGCGGCGATTTCTTCAGGCGCGCGGCTTTG  
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CGATACGGATGTTTCAGACGGCTTTATCGTCTGTGCGCAGCTTCGACAAACCGCGGCTTGGAGCTTCGAGAAGATTCGAGATAACGACAAGTCGCTTTGATGAAACCGCAGGAGCGCAGATA  
CGCGAGTTCGTGCTGGGTGAAGCGCAGCCGCGCAGCGCTCGAGTTCGCGCTTCCCTCATGATGTCGGGAAATCGGATAGACGCTCGAGACGTTGCGGCGAGCGGAATTCGTAAAGG  
CTGTGCGCTCGCGGAACCTGGTCAGGACTACTTCGACGACTAGTGAATTTGTGTAAGGTTCAGTGTGCGAGCAGCGAATGTATGATGCGCGGTCAATATGCGCGTCTCCCGATTTCTGTGTGGCGG  
CTTGGGCGGATTTAGAACACATCGCGCCCGCCCGTGTGCCGAAATGCCGCTTGAATGCGCCCTCATGAT

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SEQ ID 5696  
MKFGLSVKPSGGIILDKFMRRKQELYAFSAGLRRRSRFGYAEHLAQVGEZGAVVGHGFARRVUGELGDGLPVAFDQPHDIQGRMPHIVGEVGDAEAGPRAAFELIVQCPRAFDVQPVGEGQ  
HFGAAVDFELLIVGVGFVAPNVRVAAVVAQPVKEFGELEIEIAQEGHILTHDVGGQNAQIAPVPHVPAFERGLELLEIPQAHVBLEGLELEEFVRHAGDGGDAEFFGEVNVACAHDWGGGFEGQ  
ADDVFLPRELVAARAENVGNQEGRFVRILCGDFFQARGFGLKPAPAFPDNGRGFPQAEVKFDNAGEDDEDKKHRLYHRAFDVDQTAFTVCAADPDKAALELEBEFELDKVAFDEYQGAQI  
AEFVVVGEAQPAERVEFGQVFPDVGKRIDGRDVAAEFVKAVRLKLVQDYLQHEFEVFSVEBQRMYDAGHMACLEPISGGGLGRITRERARPVCRKRLNAPPHD

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SEQ ID 5697

TTGAATTTTAAACGAAAGACCGAACTTCATGAACCTACATCAAACCGTCGAACCAAGCGCGCCGCCCTTTGCCGCCGACAGGCATCGCCGGCAGCCCGCTTGTCTTGCAGCCGACCAAA  
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AAGCGCGCGAAGTGTGGCGGACCGCGCTTTATCAACCTGCGCGTGGCCACGAATTTTCGCTCAAACATTCATCGCGCTTTGAACGATGCGCGCTTTCGGCGTAGCGAAAACCTGCCCAACCG  
CAATACCGCTCGTCATCGACTATTCCTCGCCCAATCTGGCGAAGGAAATGCACGCTCGGCCATCTGCGTTCACGACATCATCGCGGACAGTATTTTCGCGCGTGTGGAAATTTAGCGGGCAACACCG  
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TGGGACGCAACCGCACCGACCGTTTGAACGCAACCGCTGGA AAAACAGCTTCGCGCGAGCTTCTGAATTTGAAAACGTGCTGCAAAAGCGTGGCGGACACCGCGTATCCGCACTACCTCG  
CGCGCTACCTTTTACACGCGCGCAACCTGTTCACGCTGTCTACGAAGCTTGGCCGATTTTGAAGCGCAAGGCGCAAGCGCAACACGCGCTGCACTGGCAAACTTCACCGGCACAC  
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**SEQ ID 5698**

SEQ ID 5698  
 IMLTERPNFMNLHQTFVEHEAAAAFAAGIAGSPVVLQPTKNAEHGDFQINGVMGAAKKAKQNPRELAQKVADALAGNAVTESAEVAGPGF<sup>1</sup>INLRLRHEF<sup>2</sup>LAQNIHAALNDARPGVAKTAQP<sup>3</sup>  
 QTVVIDYSSPNLAKEMHVGHLRRSSIIIGDSISRVLEFTGNVIRQNHVGDWG<sup>4</sup>TQFGLMIVAYLVEQQKDNAEFAELADLEQFYRAAKVRFDEDPAFADTAREYVVKLQGGDET<sup>5</sup>VLALWQKFVDI<sup>6</sup>  
 SLSHAQAVYDTLGLKLRPEDVAGSSKYNDITSGDITVGLVDLLTEAVERATALVKEKNPELGADEAAKIGKTVGI<sup>7</sup>GAVKYADLSKNRTSDYVFDWDAMLSFBGNTAPYLQYAYTRVQSVFKAGE<sup>8</sup>  
 GYLPEDAKAEFIFGFTMMGKDGKPPKTRSGDTIVKLVDLLTEAVERATALVKEKNPELGADEAAKIGKTVGI<sup>9</sup>GAVKYADLSKNRTSDYVFDWDAMLSFBGNTAPYLQYAYTRVQSVFKAGE<sup>10</sup>  
 WDATAPTVLTFEPLKQLAAELLKFENVLQSVADTAYPHYLAAYLYQAATFLSRFTEACPILKABGASNSRLQLAKLGNWLKQGLDILLGIDVLDM

**SEQ ID 5699**

SEQ ID 5699

TTGCACAACAACCGTTTATATATATATACATAACGAAAAACGCCGGTGTAGCTCAGTCGGTAGACGACGCCATTCTGTAACGCGAATGTCGGGGGTCGATTCCCTTCTCCGCGACCAATAACCA  
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**SEQ ID 5700**

SEQ ID 5700

LHKQPFYIILTKNAGVAQSVBQRIRNANVGSGSIPFSGTNTKHRPSLGKPVLPFHSASDGIYIELATQTTPFRPLAQLRLTLP PPPPHTCRAARRNRPVHRTRPATPPPTRMDRDDRRLR  
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G

VKALFGPSGCGKTTVLRLLIAGLETPKSGKITRNPHTKGFLFOENRLEPNI.TAMQNTAIFMDNPDDEGKIVALAAKVGLTAGDLNKYPTTELSGGMAKRVAFRLRLILCGCDLALLDEPFGVLDR  
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NPVTVFIFLTVAVYAGLGAFAWHCQQQGRGRDPVWKTLPVLGAALFVHGAAALMPVIQDKILMGPGYSGSLIVMMMLFTYFAGSFYFPLRQVQLLLYPCAALMLLSGLVFPFGKSGYEITD  
FPFALHIGTSSLAYGLFGIATLLSVLSLLHRSIHRNPSKLAGFLPSLLSLEKLMFQAMWAGFILLTYSVVSQGTFFAEAVFGKPMFTFTHKTVFGILSNLIYGGLLKHSMATAWRCKKAAV  
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GGCATCGCGGCGAGGTTTCGCGGACATATCGACGATTTCTTCGTCGAATCCTTTCAATGGCAAGCATGTCGCGCGGAGGAACA

MIQNPFRCRLNASDGLILFAKELQAGFNDDVEAQLVAFHDFVVAFEHQTALEAHADFFYVVFIA PQRSQFARVDDHVVADMDGIAFDHAVGDHTACNVADLNGNGDLDTFDRTGNLFF  
LPGRKHAAHRRLLHVDGIVDDVVADFHVFTIPGKPARRGICTHVKADNERARSDGKVDIRFGNAAHAHVQHVHFLVGGQFPQAAQSLVRALNVCLDDRRQLGLGPAHTVEHIFQLRRI  
LFGKAHVAVPALAEEGDFAFPFLVRQYHRVTRRLRVGQAEQDFDGRAGFGNGFAVFIHERADFAECRTGQHQVAFQRTVFLNQCCGNRAAPVQVTRLDDAFGGCIDRCGPQYVPGFEQ  
YGFQEQVDVRSFPRGNVDLNRAPIVGDDFVLGQFLTDAPFGVGSVFIDFIDGNHNRRACRFSVGNCLDLGRHFAVVGDLKHNHDI GCFRAARAHSKSGKFVARGVQEGNHAAARGFDVVRAD  
VLNRAAARFALYHFGAADVVQQQGFVAVDVDAHGDNDGRTRQCFCGLRFRALAQEGFGVIGGGGFADVSEFFDDNQGGVLVDGLVDGNHHAFLHQGFDHFAFDRHFVRQIGNNGNPGNQLV  
YDGFGRCLBGLVLRLEFFPAALAAALYAAVAGAVIVTAPFCTAFGVAALTFLVIAAAVFFRFRCDRIDRVFVDDGRCGLRFLGRPGGTLASAGFGLCGFCLLPCLLFHHGPAFCIAFLF  
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VPRCRLRLNRGLGGLGFGYLLCQFPGRRNVDASAFACFPDYPVNGADPFGAADDGAAVAAVFLGQVGVQKFLVVPVQRGQIAAIVADAGFQFLSQVQVDFGAPLGGLKFLPGCVHTHLYP  
LYLSSVNNQCSRAVRMTAFVASSFTPVVISSSSTASSAKSSRVMPASARLSISASTPSRLRLISSTSPFSSSAALVNRHVASRARLSISTISQPPSSSSAAG

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**SEQ ID 5711**

**SEQ ID 5712**

**SEQ ID 5713**

**SEQ ID 5714**

SEQ ID 5715

**SEQ ID 5716**

**SEQ ID 5717**

**SEQ ID 5718**

**SEQ ID 5719**

**SEQ ID 5720**

**SEQ ID 5721**

SEQ ID 5722

**SEQ ID 5723**

**SEQ ID 5724**

MSEWRGFSNKGNTMNIHALLSQWTLPPFLPKRLLLSLLILLAPNAVFWLALITATARPVTNLDYLPAAILLIALPWRPVKIGVLAFWPAVLFDGLMHVQLPFFADLIGAINLVPPILT  
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VAESWGLPGNPQLQATFAKLLAQDRPSVWESGSPFFIGATVEGEMRELCAYGGLRGFALRRAPDEKPARCLPNRLKQEGYATFAMHGAGSSLYDEFSWYPRAGFQKIKTAENLIGKKEA  
PFSAAACATASCACRHFSSKNTTRDCPTG





## SEQ ID 5742

LQNNPPFYRKNRINFFIAADGGCASPQRCRARGFTAFAPVQGRAVSLFNAQPFHNGHPIILAPAAPACPAVRPRRLRIFSPQSFAPFFRIANLSVGVIGKIRLILLFISFTTIPKRPV  
LHLHQVQIGFAGGYLRHFPALIAVGFHTYTDFTPLRRRAQVARTCTVSLPHLRCDVIRHPNFMFRAVAVDDVKGLAVIDFGHRACVAVAGFRRCPSSANGRVETHVPCSAEYVEYGNRRPH  
RLTVISRTIQRAQKRGDGKPFHDFNLHIFQMMPSEHL

## SEQ ID 5743

GTGCGAAAGTCATCTATCCCTGCGAAGGGTAATCCTGACGTTAAGATGCCGCTGAAATCCGGTTCAGAGATGTTACAGCGCATCGGCATTGAAAAATATGCAGAT

## SEQ ID 5744

VRKSSIPAKGNPDVKMPSEIRPRDVQTASAFKAYAD

## SEQ ID 5745

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GTTATGCTAAAGAACAGCAGGATAAGGCGGATTTGCCGACTATGCCGACGCTCAATTCAGCGGAAAGGGAACGCAAGAGATTGTGAAAGCTAAAAATCCGCAAGCGCGGTGGCGGTA  
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## SEQ ID 5746

LKNMQIKKIMKWLFPVALLGALGYTGYDSEAVRTAVAVLDVLGTAGDVGFDAVRRRASAKSGHSTGTGTVSKVIDGDTLHVLDGDAKHKIRMAITDAPEMQAYGTRSDNLRAAEGR  
KVSVRVFTEDRYQREVAQVSAGKTDNLMLQVQDGAWHYKSYAKBQQDKADFYADADQIAERERKGLWKAKNPQAPWAYRRAGRSGGGNKIDWMSVGEMLGIW

## SEQ ID 5747

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AAGCAAAATATTGTTCCCGGCTGGGCAAAATCCCACTGCGCGTGAAGCGCGTGAAGCGCGCGCTCCCTTGTTCGCGCAAACTGCTTGCATGGGCGGACAGCCGAACTGCGTATCGGC  
TACACCACTGTTTACGCAACCAAAATCGTCGATGTCCACGGCTTGAATATCGATCAGCGCTGACAGATGAAGATGAAATCAACAAATCACCGCGCTACTCGAAAAACGGCATATTCGCC  
CGCATCGCGCGATGTGTTGATTTTGGGACGGAAGAGGTTGCGAAAGTCACTATCCCTGCCAAGG

## SEQ ID 5748

LGRSGKKIKGAVSTSKSGELLARYDI PVVSLNEVSLAVYIDGADEVNHALQMIKGGGAHLNEKIVASASEKPVCIADSKYVSLGKPLPVEAVESARSLSVRKLLANGGQPELRIG  
YTFYGNQIVDVHGLANI DQPLTMEDEINKITGVLENGIFARDAADVLILGTEGAKVIYPCQG

## SEQ ID 5749

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## SEQ ID 5750

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## SEQ ID 5751

TTGTGTGCGGACAGCATATCGGCAATCCGTCAGGCTGCCCCGAAACGGGATTTTACAATTCCAACGTTAAAAGTTCCAATATTTC

## SEQ ID 5752

LCAGQHIKSVKACPKRGFYNSNVKSSNIS

## SEQ ID 5753

ATGCCGCTGAAATTCATTCAAACATCAGGAACACAAACGATGACGAATATCCGTATCGGACAGGCTACGATGTCCACCAATTGACCGAAGCGAGAAAGCTGATACTTGGCGGAGTTG  
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CTCGCACCGCAGATTCGCAAAATGCGTCCAAACATCGCCGCGGATTGGGTATCGATATTTCGTGCTCAATTCAAAGGCAAAACCAAGAAAACTCGGCTATCTCGGCGGATGGAAG  
GCATAGAGGCGCAGGCGGCTATTGCTGGTACGAAAT

## SEQ ID 5754

MPSEIQFTSGTQTMNIRIGQYDVHQLTEGRKLILGGVEIPFEKGLLGHSDADALIHAVTDLALGAAGLGDIGSHFPDTAAEFKDDASRVLLRAAYQSVQAGWQVNVDTTVLAQKPK  
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## SEQ ID 5755

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CCGCGCGCAAACTGTCGCAACGGTGTGGCAAACTGTTGGAAACCGGTTTGGCGGCGGAACCGCAATATTCGTGTACAGATGCCGCCGCTGCTGCTGCGCTGGAAGCTCTGGG  
CGGTTGATAGAACAGGCGGCGCAAGCCGCGAAGGCGGATTTTGGCAGTTCCGCTTGGCGGATACGCTCAAGCGCGCAGAAAGCGCAAAATCAGTGCAACTGTGACCGTTTCGGGCTTT  
GGCAGCGCAAAACCGCGCATTTTCAAGCGGTTTGTGTCACCGCGCATTTGCTGCGGAAACCTTGGCGCGCAATACCGATGAAGCGTCCGCCGGAAGAACTGGGTGTGCGCTCGCT  
ACTGATACAGGCGACGCGCAATTTGAACTGACGCGAGCGCAGGACGCATACATGTCAGGCTGCTGCTCAATGCCGTC

## SEQ ID 5756

MKRKNIALI PAAGIGVRFGADKPKQYVEIGSKTVLEHVLGI FERHEAVDLTVVVVSPEDTFADKVQTAFFQVVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNLVHDAARCCLPSEALA  
RLIEQAGNAABEGGILAVPVADTLKRAESGQISATVDRSLWQAQTPQLFQAGLLHRLAAENLGITDEASAVEKLGVRPLLIQGDARNLKLTPQDQAYIVRLLNAV

## SEQ ID 5757

TTGCCACACCGTTGCGGACAGTTTCGGCGCGGCTGCTGCCACCGTTTTCACACCCGAACCTGTGAAATGCCGCTGTAACCTTATCGGCAACCGTGTCTCGGGCGAGACGACAAACGAC  
GGTCAAAATCGACGCGCTCATGCCGTTCAAAATCCCAAGTACATGTTCTAAAACGGTTTGTCTTCGATTTTCGACATATTGCTTGGGTTTGTCCGACCCGAAACGACCCCGATGCCGGG  
CGGGAAATCAGCGGATATTTTTCGCTTTCATGCGTTTTCGCCCGGCTTTTCAGACGCGACGGCTTCTTACGCCAAATACAGGCTTCGCCCAAGCGCTCGAGATATTCTTCGTGCGCGC  
CAGTTTCGGCTTACCGCTTAACTCACTTTCAGTTTGGCACCGAGTTTCATTTTCGCGAGATGCAACAGGTTTGGCTGTGCGTTCTTCCTCCTCGGTCTCCGCCATCAAGTCCGAATTGCCG  
CGGTCATCGCCAGATAGACTTCGCCCAAAAGTTCGCGATCGATCAATGCGCGTGCAGGACCGGCTGCTGCGGTGCAAGGAAAAACGGTTGCAAGGCGATCCAGGCTCGCTTTCGCC  
CCGAAACATTTCGCGCGCATTCGCCAGGATTCGTAACGGTGCAGCGGAGTTCTTCGACGGTTCGGCAGCCCAACCGCGGAACTCCATATTGAGGAAGCCACATCGAATTTCGCAAT  
GTGGATAATCAGTTCCGACCCGCGCAGAAATCGGCAATCTGCTGCCGACCTCTGCAACCGGCGCGGCTTTTCTCTTCCAAACCTGTATGTCGCAAGCGTGGACCGGCTGCCGCTCT



LPHRCGQFRRGSSVRRFSTPEPVEMSEBPYQVCRLRRRQRRSNRRRPHAVQKSQVHVLKRFCFRFRHIAWVCPHRNAPRCRRRESARYFCVSCVFPVAVFRRHGFLPTMTGFAQAVEIFVVR  
 QFGFTRLNHFQFGTEFHFGRGNRCRFGCRFLLAGLPHQVELPPRRHRQIDFAQKFAVDQCAVQDALAAVDGKTVAQGIQARFLPRKHFAHRHQIGNGAAEFLDGRQHPHAEHLHIEEAEHIEFGI  
 VDQNFRTAOKIGNPLADLCKRRRVFLPNLYRQAVDACRLFGHIALGVDIIEVQVFGHLAVDHFQTKGLDTVAAVGVIQAGGFCIEDDLACHHIGVFLLS

ATGATGACACGCGAAATCATCTCGATACCGAAACACCGGGCTGTATGCCGACGGCGCGACCGCTGTGGTCGAGTTTGCCGGTCTGGAATGGTCAACCGCGAAATGACCGACAAAAACC  
TGCACCTCTATGTCCACCCGAGCGCGATATGCCGAAGAGGGCGGACCGGTCCACGGCTTGACGATACAGGTTTGGGAAGAGAAAAACGCCGCCCGCTTTGCAGAGGTTCGGCAGCGAGAT  
TGCCGATTTTCTGCGCGGTTCGGAACTGATTATCCCAATGCCAAATTTCGATGTGGGCTTCCTCAATATGGAGTTCGCCCGGGTTCGCCGACCGCTCGAGGAACTCGGCTGCACCGTT  
ACCGATACCCCTGGCGATGGCGCGGAAATGTTTCCGGGGCAGAAAGCGAGCCTGGATGCCCTGTGCAACCGTTTTCCTCGACGCCAGCAAGCGGCTCTGCACCGCGCATGTATGTCGAT  
CGGAACCTTTTGGGCGAAGTCTATCTGCGCATGACGCGCGGCAATTCGACTGTGATGGGGAGACCGAGGAGGAGAAACCGACGCCAAACCTGTTGTCATCTCGGCAAAATGAAACTCGGGTGC  
CAAATCTTAAGGATGATTAAAGCGGATGAAGCCGAATCGGCGGCGCACGAAGAATATCTGACGGCTTGGGCGAAGCCTGTATTGGCGTAAGGAAGCGGTGCCGTCTGAAAAACGGCGGGGAA  
AACGCA

SEQ ID 5760

MMTRQIIIDTETTGLYADGGDLVFEAGLWVNRQMTDKNLHLVHPERDMPEEAARVHGLTIQVLEEKNAAPPAEYVGROIADFLRGAELIHNAPDVGFLNMEFRVGLPTVEELGCTV  
TDTLANAREMPGQKASLDALCNRFVSDRSKRVLHGALIDCELLGGEVYLAMTRRQFDLMGETEEEBRTAKPVASAEMKLGAKLKVIKADEAELAAHEEYLDGLGEACIWRKEAVPSENQGB  
NA

SEQ ID 5761

TTGAAAAAGAGAAAGAAAAAGCGATGGAGCGCTAAAAAAGCGCGGTTTGGGACTGGTTAAAGGCCGCCGTTTCGGGCCCTCTTTTCGCTACGCAGTTTCTCGGCGCGTTCAATGACAAATGTGTCA  
AAACCCGCGCTGTTTGTTCATGATCGGGTTTACAGCGTTGGGGCAAACGGCTTCTCTGCTGCGCGACAGATGTGAACTTGGGCGCACTCGTGTATTATTTCGCGTATTCTCGGTTTTCGCG  
CTCTTCGCGGACGCTGGGTAAACAAATTCGACAAAGCGCTTTTGGCGCGTGGGTCAAGGTCTGGAATATCATCATATTATGGCGGTGGCGGCATACGGGTTTATATCGCGTCAGCCCCGCTG  
GCTTTGCTCTGCGTGTPTTGCATGGGCGGCAATCGACGCTGTTCGGCCGCGCTTAAATATGCCATTCTGCCGATATTATCTGCAGCACAACGAGCTGATGATGGGCAACAGCCTGATTGAAT  
CCGGTACGTTTGTGCCCATCTCTGTTTGTGCAGATTTCGGGAACGGCGGTTCGCGCGCGCCGCTTATATTGTGCGGATATCGTPTTCTGCTGGTGGCGCTCGGAGGAACGGCGCGCAGCGCT  
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GTATTTCGCGCGCGTTCGGTACTGTGTGCCAAGTTCGGCAGGGAACGGCATGATTTGGCTTGGGTAACGTTGGTGTGCTGCGGTTTGACGTTTTGCGCGCTGTTTGGTGTGCGTGAAGCA  
CGGACACCGCTTTTGAAGGGCTGAACGGCATTTTGGTTTTCGCGGCTTACCGCATGCGGTGATGACGCTGATGACGCTGATGCGGCTTTTTCGCGGATTTTTTCGCGTTCGCGTCT  
TATACCTGGCTGCAACCGGACCGGACGAGACTTTTGGGCTTTCGCGCGCGCGCGCTTGGCGGCAACAAATATCGTTAACGGCATCTTTATGGTTTCGCGCGCGGTTTTGAGCGCGGATTTGCTGTTTT  
TGATGACGAGCATTTCCCTGCTGTATCTGATTTGCGCCTTGGGCAATATTCGTTGGCGGTATTTTGATTAAGCCGGAAGGCGGTTTTAGGCGCGGCGCAATCAGGAAAAAACT

SEQ ID 5762  
LKKRRKFTDAKGGGLGLVKSRFFGPIFATQFLGAFNDNVFKTALFVMIGFYGLQNGFLPAGQMLNLGALLFTLPYFLFSALSQLGNKPKDAVLARVWVLEIIIMAAVAYGYIRSAFL  
LLLCLPCMQAOSTFLGPKLYAILPYDLDDNELMAGNSIESGYPVAILFGQILGTAVAGAPPYIVGILVLVLVWVGCGAGSLPMPSPVAKAADTQIENIVRGTKSLIRETVRINPVFTAI  
GISWTFVPGAVTTPQTPFTQIHLGDNFENFNLALNSISIGIAAGSVLCAKFGPKRERILMAWTVTGALGLTVCGLVLVWLTHGHRFEGLNGIPWFLSQWAGYPMVAVMTLIGFGGFFSVPL  
YTWLOTAASSETFRARAVANNIVNGIPHVSAVLSAVLLFLFDSISLLYLIVALGNIPLAVFLIKRERRFLGAAAIKKPK

SEQ ID 5763  
ATGCTGTCGGGCACACAAGCGCATCAAATTATTTTGATTTTATTTTAAACAAGAATGCCCTGATGGGGCAAGCTATTCTTATTACACCAAGGACCAGTATGT

SEQ ID 5764  
MLSGTOAASNYPDFILTKNAPDGASYSYSDQGPVC

SEQ ID 5765  
ATGAAGAATGCTTTCCGGTATCGAATTATTTGGGCGGACAGGGTTGTATTTTTCGCCAAGAGGCCAAGCCTCGCGCTTCCTTGCCTCTCTCC

SEQ ID 5766  
MKMLSGNDLLGGQGCIFRQRGKPAACLPSF

NRMLSGMDLLGGQGCIPRQRGKPAACLPSF  
SEQ ID 5767  
GTGATGGAAAGTATGTTTATTCTGGTGCCCATCAGCATTTATTTTGGCATTTTGTTCATCGCGTGGTTTTTCTGGTGGTCGGGCAAAAACGGACAGTTTGACGATTGGAAGGACCGGGCAACC  
GCTATTTGATGGGATGATGCTGCAAGAATAACTGATTGAAAAAGAGAAGGAAAACGATGGACGC

GTGATGGAAAGTATGTTTATTCGGTGCCCATCAGCATTATTTGGCATTGTGCATCGGCTGGTT  
GCATTTTGTATGGATGATGATTGACAAAGTAACTGATTGAAAAAGAGAAGGAAAACGATGGACGC

SEQ ID 5768  
VMSMFTILVPISILLAFVIGWPFNWSGKNGQFDLEGPAHRILDDSTSKLIEKENDGR

SEQ ID 5769  
VMESEFLIVPISILAPVIGWFFWWSGKNGQFDDEGPAHRILADDSTSKLIEKEKENDGR

SEQ ID 5769  
TTGGAAGATGGGACGGGCAACCATGTCTCTGCGCGGTTCGGTCAGACGGAAATCCCCAATATGGCGCGTGGTCAAAGACCGTATCGAGCTGTTTTTTGACGAAGCCCCCGTCGGAACCTT  
TGCCTAAGCAATATCTGACCGGTCTCAGGGCAGACTTTTGTCTTGAACGATTGTATAGGGAATATG

SEQ ID 5769

TTGGAAGATGGGACGGGCAACCATGTCTCTGTCGCCGTTCGGTCAGACGGAAATTCCCCAATATGGCGCGTGGTCAAGACCGTATCGACTGTTTTGTGACGAAGCCCCGTGGGAACCTT  
TGCCTAAGCAATATCTGACCGGTGTGAGGCGAGACTTTGTGTTTGAACGATTTGATAGGGAATATG

TCGCTAACGAATATCTGACCGTGTCTAGGGCAGACTTTTGTTTTGAACGATTTGATAGGGAAT  
SEQ ID 5770

SEQ ID 5770  
I EDGTGNIHVLSPFGOTEIPOYWRVVKDRIELFFDEAPVGTLRNEYLTVSGQTFVLNDLIGNM

LEDGTGNHVLSPFGQTEIPQYWRVVKDRIELFFDEAPVGTLRNEYLTFSGQTFVLNDLIGNE  
SEQ ID 5771

SEQ ID 5771  
ATGGTGGCCCGTCCCATCTTCCAATTTAACGGCAAAACGCCCGCTCTGCAAGCCGTGCTTCCGATTCGTCGTCGGCAAGAAGGATGAAAAAGCCTATATGCCGTCCCGATTTGGTCATGAATA  
CTGAAATTAATGCATAAACTCCCAACCCCGCTTTTTCAGACGGCATCAAC

ATGGTTGCCCGTCCCACTTCCAAATTAAAGGCCAAAAGCGCGCTCGCAGCGTGC.  
CTGAAATAATGCATAAAFTCCCCACCGGCCCTTTTTCAGACGGCATCAAC

CTGAAATTAATGCCTAAATTAATCAAGGCTTTTTCAGATGGATCAAT  
SEQ ID 5772

SEQ ID 5772  
MVARPIQFNGKTPALQPCFRFVVGKKDEKAYMPSRLVMNTEIMEKFPTRLFSGDGIN

SEQ ID 5773  
GTGAAAAATGGCGGAAGTCGGGTATTTTGACGGAAAAAAGGGGGATATGCCGTTTGCCGGTGTTTTCCGGCTGGGGGAGGAGAAATTTCTTTGCATTTTCCCGTCCAAACTGGTACATTCGC  
CCTGTTTT

SEQ ID 5773

GTGAAAATGGCGGAAGTCGGGTATTTTGACGGAAAAAGGGGATATCGCGTTTGCCGGTGTTTTCGGCTGGGGGAGGAGAAATTCCTTTGCATTTTCCCGTCCAAACTGGTACATTGGCCTGTTTT

GTGAAAATGGCGGAAGTCGGGTATTTTGACGGAAAAAAGGGGGATATGCCGTTTGCCGGTGTTCGGCTGGGGGAGGGAGAATTTCCTTGCAATTTTCCCGTCCAAACTGGTACATTCGCCTGTTTT

OCTGTTTT

SEQ ID 5774  
VHMAKVCSTYGGKCDMRFAVGGNGRENFFAFTPSKLVHSPCT

VTMAKVGYPDGKKGDNRFAGVFGNGRENFFAFFPSKLVHSPCF

SEQ ID 5775  
ATGTACCACTTTGGACGGAAAAATGCAAGAATTCCTCCCTCCCCAGCCGAAAACACGGCAAACCGCATATCCCCCTTTTTCCTGCAAAATACCCGACTTCGGCCATTTTCACGCAA  
ACGCCCGATTAAAGCCAAGCAATTGCAAGATTTTTCG

ATGTACCAAGTTTGGACGGGAAAAATGCAAGAAATTCCTCCCTCCCCAGCGGAAAAACACGGGAAACCGCATATCCCCCTTTTTCCTCGCAAAATACCGGATTCGGCATTTTCACGAA  
ACGCCCCGATTAAAGCCAAGCAATTGCAAGATTTTTTTC

ACGCCCGATTAAAGCCAAGCAATTGCAAAGATTTTTCG  
SEQ ID 5776  
MYOFGREKCKEILPPPAENTGKPHIPLFSVKIPDFRHFHANARLSQAIARIFC

SEQ ID 5777

SEQ ID 5777  
TTGATAAAAGAAGCAGGCTATTCTAGCAAAAAATCTTTGCAATTGCTTGGCTTAATCGGGCGTTTGCCTGAAAAATGGCGGAAGTCGGGTATT

**SEQ ID 5778**

LIKAGYSSKKSLOLLGLIGRLRENGGSRVF

**SEQ ID 5779**

SEQ ID 5779

TTTGCAAGAGATTTTTCCTAGAAATAGCCTGCTTCTTTTATCAACCGTTTCAGACGGCTCCACTACTTTCOCGTCAAGGAAAGCAAAACGGATTTCGCAAGAAATCCGATTAGTATCCGTGTCC  
GATTCCAATGCGCTCTGAACCTTCCGGGATAGAAAAATGCCCCAAAAT

**SEQ ID 5780**

LORFFARIACFFYOPFOTAPLLSRQKONGFGTNPISIRVRFQCRLKLSGVRKCPKN

**SEQ ID 5781**

SEQ ID 5781

ATGTCCCAAAAATTGATCTTGGTTTGAAGTCGGGCAGCTCGTCCCTCAAAGGCGCGGTCTCGGATAACGGCAGCGGCGAAGTCCCTGCTGAGCTGCCTTGCCGAAAAAATCAACCTGCCCG  
ATGCCTACATTCACATTCAAGATAACCGCGAAAAACAAAGTCGATCTGTGTCGACACCCCGACCACACCGCGCGGTGGAAGCCCTGATGGAAAGTAATCGAAGCCACGGCCCTGCACAG  
CGCGATCGGCGCATTCGCGCACCGCGTGTGTGAGCGCGCGGAAGCTGTACAACGAATCCATCTCTGTTGACGACGAAGTATCGCCGGCATCGAAAAATGCATCCCGCTGGCTCCTCTGCAC  
AATCCCGCCCACTCTTGGGCTGCGTGC CGCGCAAAGCAATTTTCAAAGGCTGCCAACGTCGTGCTATTGATACCTCCTTCCACAAACCATGCCCGAAGTCCGCTACAAATACGCCG  
TTCCGACAGGAGTTGTATGAAAAATACGGCTGCGCCGCTACGGCGCGCACGGTACACAGCTACCGCTCTCGTTGCCGACGAAACCGCGCACTTCTCGGCAAGACAAAAAGACCTGGGTAT  
GGTCAATGCGCCACTTGGGCAACGGCGCATTCATACCGCCGCTGCCAACGGAGAATCGCGCACACCAAGTATGGGCTGACCCCGCTGGAAGCGTGGAATAGGGTACGCGACCGCGCAG  
ATCGATCCTTCCGATTCGCGCTTCCTCGCGGAAAAACGCCAATATGACCAATGGCCAAATACACGACATCGCTGAACAAAAAATCCGGCGCTGCTGGGCATTTCCGGCATCTGCCAAGCATCTGCC  
GCACCAATTGAAGAAGAAGCGCCAAGGGGCATAAAGCGCGCAAAATGGCCTTGAATATGTTTATCTACCCGCTTGCACAAATACATCATCGGCAGTATGGCGGTTGCCGACAGGCGGCTTGGACGC  
ATCGTCTTTACCGGCGGTATCGCGGAAACCTCGCATCATTCGCGACATCGCGACGCGTAATCGGCTACTTGGGCTTCTCTCGGTCTGAACATCGACCAAGAAGCCAACTGAAAGCCCGCTTCCG  
AACCGCGCGTGATTTACCATCGACGACGACGAAAGCCGTTGCCGTGTCATTCGACCAACGAAGAGCTGATGATGCCCCAGTACCGCCCGTTTGAGCGGTCTGC

**SEQ ID 5782**

SEQ ID 5782  
MSQKILILVNLGSGSSSLKGAVIDNGSGEVLSSCLAELKLNLPDAYITPKVNGEKKHKVDLSAHPDHTGAZEALMEELEAHGLDLSRIGAIHGRVVSGGELYNESLIVDDVEIAGIEKCIPLAPLH  
NPAHLGLLRAAQSIKFLGNVVVFDTSFHQTMPYEVAYKAVPQZLYEKYGLRRYGAHGTSYRFPVADTAHFLGKDKKDLRMVIAHLNGASITAVANGESRDTSMGLTPLEGVLNGTRSGD  
IDPSVFGLPAENANMTIAQITDMLNKKSGLLGISGLSNCRTIREEAAKHGKAKLALDMFYRLAKYIGSMAVAAGGLDALVFTGGIGENSDDIREKVIGYLGFLGLNIDQEANLKARFG  
NAGVITTDASKAVAVIPTNBEMLIAHDTARLSGL

**SEQ ID 5783**

SEQ ID 5783  
ATGAACATTATTCGATGCCATCATCAATTGGCTAACAAACCTGTTGTGCGGGTCAACTCCCATCTCTCAAAGCAACAATCGTGCCAATCAGGCAGGTGATGCTTTGGGAAGATATGTAAGAAAG  
ACTTGTTTTCCGGCAGTTTCAACCTAAATGAACCCAAACGCATAGCCCGACACGCCAAGATATTCATATTTGGGCAACAACCTCCAAACCTCTCTGATGCCATGTTGCGAAACGGGGATGC  
CATCGAAGTTAAGAAAAATTGAAGATTAAGATTCCGCATCTGGCGCTGAATAGCAGCAACCCAAAAATCAAAGCTCTCTGTTGATGACAGCATGCTTTACAAAGCCTGCCAAGATGCGGAAAAA  
TGGCAAGACGAAGACATTATCTATAATTGTGCGGCGTCGT

SEQ ID 5784

SEQ ID 5784  
MNIIDAIINLANNPVGVNHSQSNNRANQAGDALEEYVKDLFGSGFNLNETQRIARHAKVPSTYLGNNNSNPDPDAMLRNGDAIEVKKIESKDSALALNSSHPKSKLSVDDSMITKACKDAEK  
WEKKDLIYNCRRR

**SEQ ID 5785**

[illegible]

**SEQ ID 5786**

MLDNLITGRFSNVFKNIRGQAKLTEDNIKEALREVLRLALLEADVALPVVKEFVNNVKEKALGQEVAGSLTPDQAFIIGVNNQALVELMGKENKTLDLSSVPPAIILMAGLGQAGKTTTVGKLA  
RLKKNDDKKVLVVSADVYRPAAEIQRLRLAEQGVGFPPFSOTNQKPVETATAAVDYAKKHFYDVLMMVDTAGRLAIDDEEMNETKALHAVNVVETLFTVIDAMLGQDAVNTAQAFNEALPL  
NGVVLTKMDGDSRGGAAALSVRHVITGPKIPKIFGVGKINLEPFPDRLASRIIGMDVLTLLIEDVQKIGIDEAAAKMAKLIKQKGGFDLNDPFBQIQMRNMGGLLENLMSKMPGELGQISK  
QIPEGTAEKAMGKVEAIINSMTPKERANPALIKAGKRRRIAMGAGTTVQEVNKLKQFEQMQQMTQFSGNGLGKILRLAKGMKIGKMGFFGL

**SEQ ID 5787**

SEQ ID 5787

GTGGGCAATCAGTCAAGCTCTTCGTGTGGTCGGAATGACCACGGCAACGGCTTTGCTGTGGCAGTGGTAATCACGCCGGCGTTGCCGAAGCGGGCTTTCAGGTTGGCTTCTTGGTCGATGTTTC  
AGACCCAGGAGAGCCCAAGTAGCCGCAATTACGGCTTCGCGGATGATGTCGGAAGTTTTCGCCGATACCCCGGTAAAGACCAAGTCGCTCCAAGCCGCTTCGGCAACCCGCATCTGCCGATGT  
ATTGGCAAGCGCGTAGATAAACATATCCAAGGCCAATTTCCGCGCTTTATGCCCTTTGGCGGCTTCTTCTTCAATGGTGGCGGATGCTTGGACAGGCCCGGAAATGCCGAGCAGGCCCGGA  
TTTTTTGTTTCAGCATGTCGGTGATTTTGGGCAATGGTCATATTGGCGTTTTCGCCGAGGAAGCCGAATACGGAAGGATCGATGTCGCGCTTCGCGGTACCCATTACCAAGCCCTTCCAGCGGG  
GTCAGGCCCATCTAGTGTGTCGCGCAATTCCTCGTTGGCGACGGCGGTGATGGATGCGCGCTTGCCCAAGTGGGCAATGACCAATACGCAGGTCCTTTTGTCTTTTCCGAGGAAGTGCAGCG  
TTTTGTCGGCAACGAAGCGGTAGCTGGTACCGTGCBCCGGTAGCGGGCAGGCGCTATTTTTTCATACAACCTCTCGGGAACCGCGTATTGTAGCGCATCTTCGGCATGGTTTGGTGGAA  
GGAGGTATTCGAATACGACGAGCTTTGGGCAAGCCCTTTGAAATGCTTTTCCGCGGCACGACGGCCCAAGAGGTGGCGGGATTTGTACAGAGGACCCAGCGGATGCATTTTTCGATGCCGGG  
ATGACTTTCGTCGTAACAGGAGTGGATTCTGTGTACAGTTCGCCCGCGCTGACACGCGGTGGCGGATGCGCGCGATGTCGGCTTCGAGGCCGTCGGGCTTCGAGTCTTCCATCAGGGCTT  
CGACCGCGCGCGGTGTGGTCGGGGTGTGCGGACAGATCGATTTGTGTTTTCGCGGCTTTGCAATTTGAATGTAATGTAGGCATCGGCGAGGTTGAGTTTTCGGCAAGGCAGCTCAGCAGGAC  
TTCGCCGCTGCGGTTATCTCAGGACCCGCGCTTTCGAGGACGAGCTGCCGCGAGTTCAAAACCAAGATCAATTTTGGGACATTTCTTACTCGGAAAGTTTCAGACGGCATTGGAAATCGGA  
CACGGATACTAATCGGATGTCGCCGAATCCGTTTGTCTTCT

SEQ ID 5788

SEQ ID 5788  
VGNHQLFVGRNDHGNFVAVGSGNHAGVAEAGFVQVGLVDVQTEEAQVADYAFADDVGVFADTAGKDCQVQAACGNRRHTADVFGKAVDKHIQGGQFRAFMPLGGFFFNGAAVVQAGNAEQAG  
FFVQVHVGDLGNNGHIGVPGEEAEYGRIDVLAARHTYQPPQFGQAHTGVARFSVGDGGGCAVAGVGNHDHQQVFFVFAEEYRGVFGNEAVAGTVRAVAQAQVFFIQLLNGVFGVDFGHGLV  
GGIEYDDVQGAPENALRGTAQGEVGGIGVQSRDAPFDAGDDFVNNEGDFVVQFAAADDAVADGADAAVEAVGFEPFHQGFDRAGVVGVCQGIDFVFFAVYFECNVIGIQVVEFFKAAQQD  
FAAAVQIDRAFEAGRAAAVQNDQQLGHGFLTPESPRRHNRNTRILIGFVNPNPCFP

**SEQ ID 5789**

ATGTTTPTTCCACAAAAGATACACACACCGGCAACACCGCGTGTGTTATCTTTTCTATGCGCTATTTTTTAATCATCGTATTTTTTATCTTTTAAATTTC AATACGCAAAACCGACTTATACA  
CACGGFTTTCACATCTTTTGACATGCTTCCGTGTGATAGCGGATATTCGCGTTTTCTTATCTGACAAAAATGCGCGTC

**SEQ ID 5790**

MF FHKRYTHRQTPAVFI PSYAYFLI IVFLSFNFNTQFDLYTRFSLWTFASVCLADIAVFLSDKNV

**SEQ ID 5791**

TTGTCCAGATAGGAAAACGGCAATATCCGCTATACACACGGAAGCAGTCCAAAGATGTGAAAACCGTGTGTATAAGTCGGTTTGGCTATTGAAATTAAAAAGATAAAAAATACGATGATTAAAA  
AA

**SEQ ID 5792**

LSDRKTAISAIHTEAVQRCENRVYKSVCVLKLKDKNTHLKK

**SEQ ID 5793**

TTGTTCATACCACTCGATAAATCTGTCTGCTTTGACAAAACCCAGCAGCGGCTCGCTCGCGCTGCCTCGCGCGGACAGCAAAACACGCCCGGGCGGCCGGAACAGACCGGTATTCTTTCAAC  
AACGCCGTGATGTTCCGGCGGTGTGGCGGATACGTGCATCTGGGAAATAGCTGTTCCATATGCATGCGCTGATGCATCTCCGGCTGATTGAGCGGTGTAAACCGCCGATTTCTTTGCGAGGAATGT  
ACCACTGCGGATATAAATCTCAAACACAGAGTTTCTGCGGAAAGCTTTCTCAACGGCTGATCATCTGCTGCTTACCGCGCGGAGTATGCGGAAATCAATTTTCCGCTTTCGAAATTTTGGC  
TGCTTCGGCCGGCGGATTTAGAGGTCAGAGAAATGGTGCAGCGCGGCTGCTTTTTCGCTTTTTCGCCCTGCCAGCGCAACACCGCGCGCTATCAGCAATATGCTGCCCCAATGCGAATGCCACA  
GCTTTTCGAGCGGCTTTCTGCTTCGCTCGCTGTGACCAGCAGCATAAAGGCAGGAAACAGCATCAGCAGCGGTGACAGCGCGCAGCAGCAGATAATAGGGCAAAATCGCGGCTGGCGAGGTAA  
CGCGCAGCGGCAGCAGGATAAAGCGGAAAGCGTATTTGACGCGCATTCATCCAATGACCCGCCCTTAGCGAGGATATGTCTCCGAACGTGCGGATGCGAATCAGCGGCACGCGGTGCCCAA  
CGCCAAATGTAAAGTGCAGCAACCGCCCAACCGCATCGCCCTGTCACCGGATACCCCAAGGCAACGCCAGCGCGCGGCGACGCACGGTCCGACAATCAGTGGGACAGAAATACC  
ATPATAAAGACGAAACGATTTTACCGCCGAGAGGCTGCTGCTCTGCTTTTGGAAATA

**SEQ ID 5794**

LFIPDLKLVCFDKTQORLAAAAGVADGKHARRPEQTVFFQORLMPGRVGGYVDLEKAFHIDCLMHFLIERVNRHFFAGNAPVGIKIQNDRFVGHPQRRIHRHCIRQSGIGKHFVFRKFA  
CFGRRIEQENVORGRPAVCALPAEPRAAYQYYAAQCSCHSFRTAFLPASVDQQHGRNQHQQRVQRDDKEIQGMRRGEVNGDGKQDKAESVFDGHIPIARLRQDMSSEADGNQRHAGAQ  
RQSVKCTQANRILARITDIAQGRKRRRGDARSNDQCGQNTNKGDNDFAGEPALVLEI

**SEQ ID 5795**

ATCGCGACAATAATTATTGTGCTGAAACGGATTTCGATTTAGAAAAAACTGATTTGCCCTGTTCGCGGATTTTTTGATGTTGTGCGGACGGGCTTTCGCGCTGGATGCGAAGCATCTGCTGCCGC  
CGGAAAAGGCATTCGTGCCGGAGCTTACGTTGTCCGACGACGGCGTGAAACGTCCTTTTCAGGATTGCGCGACGGATATCATATGTATCAGGCGAAAAATCGTCGGCAAGACCGATCCGGCGGA  
TTTGTGGAAGACGCTTTCTTTCAGTAAGGGCGAAGAGAAGGAAGCAGGTTTTTCGGCAGGCGACAGCGTTACCATCACCAGGCGCAGGTTGCCCTTCCCTATTGCAAAAGGCTGTGCGGCGA  
CGGTATATTAATGCTTTTGACCTACATACGGGCTGTGCCAAGCGCGCTGTCTATCCCGCGGTGATACCGGTTTGATATTCTTCGGCAACCGCATCTTCATCCGCAACCGACAGAGCTG  
CATCCGCGAAAGACCGTTTTTTTGCAGCCTTCTCTCAAAACGGCAGCGGGCGTTGCCACCCCGAAGGGGACGAGGGCGGCGACGCGCGTTTCAAGCTGTCTTGGGATACGCTCAACGC  
CAATCTTTTGGCGTTTTTCTCGCGGTTTTGGGCTGAGTTTTTACCGCTTGATGTATGATCCCTGCTGCCGATTGTGTCCAGTATCGTGTGCGGTGACAAAAGGCGGGCAAGCGCGCGGCG  
TTTGTGCTGTCCGTCGTTTATGTTACAGGTTTGGCTCTGACTTATACGCTGTGTCGCGATGTTGCCGACATGACGGGCGCGCTGCTGACCGTATGTTGTGACAGAGGCTTGGGTCTGTTTGG  
CGGCATCGCCTTTGATGTTGCTGCGCTGTCTATGTTCCGCGCTGTTCAACATCCAGCTTCCCAACGCGCATACGTCATATTTCCAAACCCAGACGACGAGGCTCTCCGGCGGTAATAAT  
CGTTTCCGCTTTTATTATGGGTATTCCTGCGCAGCTGATGTGCGGACCGTGCCTGCCCGGACCTGCGCTTGGCTTTGGCTTATGCGGTGACAGCGGCGATCGGTTTTGGCGGTTTTG  
GCACTTTACACTTTTGGCGTTTGGGCACTGCGCGGTGATGTCATCGGCATCGGCACCTTCCGAGGACATATCTCGCTAAGCGGGGATTTGGATGTAATCGGCTCAAAATACGCTTTTCGCGTTTA  
TCTGCTTGGCGTGGCGTTTACCTGCCACGCCGATTGTGCCCTATTATCTGCTGCTGCGCGTGTACACGCTGCTGATGCTGTTTCTCGCTTTATGCTGCTGGTCAACGGACGCGAGCG  
GAAACGCGCTCCGAAAGCTGTGGCATTCGATTTGGGACGATATTGCTGATAGCGGGCGGTGTGTTTCGCTGCGCAGGGCGCAACCGGCAAAACGACCGCGCTGACCATTTCTTGACCTC  
AATCCGCGCGGCGAAGCAGGCAAAATTTGGAACACGGCAAAATTTTGCAGTACTGCGCGCTGAAGGCAGCGATGGATACGGCGTTGAAGAAACATCCCGACAAACCTGTGCTTTTGG  
ATTTTTATGCGCATGGTGATTTCTTCGCAAGAAATGCGCGTTTACACGCTCAATACGCGGAAGTGATCAGGCGATGATATGGAACCGTTTTTCCAGATGACGTAACCGCCAAAC  
GCTCGAATCATCAGGCTGTTTGAAGAAATCATGCTGTCTCGGCGCGCGCGGTGTTTGTCTGCGCGCGACGCGGACCGCGATGCTGGGTTTTGTGCAAGACGACAAAGCTTT  
ATCGAGTGGTATGAACAAACCGC

**SEQ ID 5796**

MRNTNLSYSETPDSIMKKLLCLFPAVLMCLGRGAFALDANQDLPPEKAFVPELTVADDGVNVRFRIPADLDGYHYHQAQKIVGKTDPADLLGGPSSGKEEKEDFFPGRQTVHHHEAQVAFPYAKAVGE  
PYKLVLTYYQCGAEGACVGYPPVDTEFDISGNGTYHPQDTEDEPASAKDRFLPQSSQNGSALPFPKGDGGDGRFLKSWDTNANLLAPFLAGLGSFTCAWYPIPLLPVSSIVVGDKKAGKARA  
FVLSVWYQGALAFYTLTVGIVAGLIGALLFTVWLQQAAMVLAASALIMLBSMGLFNIQLENAVQYTPQSSRISGGKIVYSPYIMGILSALITVPCVAPPLAFALGYTIGDVAFLGGL  
ALYTLALGTGVPYLLAIGTTPGGHILPKAGDMNAVKYAFGPIILAAVAVLYATPHELPIYLVVALTYTLMLVPAMLLVNGRRQRRKPAKAVAFALGSLLILGGANFGWQCGANGKTTALHHLFTL  
NPPAEAGKFPSEHGKMPADTAALKAMDTALKEHPDKPVVLDFYADWCISCKEMAYEYTLNQPEVHQAVDMERFPQIDVTANTPEHQALLKEYGLFGPPGVVVRADGSRSEPLIFGVKADKF  
TEWYEQNR

**SEQ ID 5797**

ATGTACGATGTCAATACCCACGATGTCGCGCGCTTTTTCGCCCGCGTGTGGCAGCAGCGGCTCAATCCGCTGCAATTTGGCGCGGTGGAACAGAAAGCCCTCCGCATTGTCGAAGGCCATC  
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GGGCATAGACCAGCGCGCAGCGCATACGCGCCATCCACGACACCTGTGCGCCAAACGCGGCTGGCCGGAAGCCGAACACGAAATGATGGAGGCATCTGGCGAAACACTGTGGACGGCGCAA  
CGCTACGGCACCAGTTTGGATGTCAATTTCTACATGACCCGACTGCGCAACTCATCGGCTTTGGTGTCAGAGGATCAAGCCAGGTTAAACCCGCATGAAATCGCC

SEQ ID 5798

MYDVNTHDVRVRFARVWQQRNLNPLQLGALSEQALRIVEAHPEYHRYLERIEDHLDTDWLPENGESNPFHMSLHLSVQBQAGTDQPEGIRAIHDTLCAKRGWPKAEHEMNEALAEFTLWTAQ  
RYGTGLDVNFYETRLRKLLGLGAEDQARLNPHETIA

**SEQ ID 5799**

TTGGCAATGGTTTACGGAATCGACTACTGCGCGATGCCGAATGCTATTTGAAGATAAAAAATCAAATTAAGGAAGGAATCGGCAACATCGCGGCATACAGTTTGCAGAAACCAAAGAGC  
TGGGCAGGGTCAACCGCATGTATCCGCTCAACATAACTTATCTGAGAGTACGGGGTATGTGGGGAATCGAAATCCATGGTTTGTCTTCACTATATTTACCAACGGAAATATGGAAAAAAG  
TTTCAATTTTCATGGCCATTATCAACGAAGACAAATGGAACAGTTTTAAACAATACAGACAAGCTGCTTGCCATACAGGAATCCAAACTGGCCATTTCOGACATTAAAAATTAATAATCCCAAC  
AACCCTGGCGGATTAAGAAATGCAAAACTCATCACTACCACCTTA

**SEQ ID 5800**

LAMVYGIDYCADAEYLKTKNQIKEGIGNIGGIQFAETKELGRVNRIDPLNITYTLRVRGMMIENPHFVFPNTYQRNMEKSPFMALINEDKWNFSFNNTTKLLAIQDSKLAISDIKIKNPN  
NPARLRNARKLITYHL

SEQ ID 5801

TTGCTTGATTTTGCAGGTGTGAAATTGTCGCACGAGCAGGCATGTTTTAGCTATTCGGAAATTCGAGGAAGGGTGCATCAACCTGTTTTGAAA

SEQ ID 5802

LLDFAGVKLSHEQACFSYSEIRGRVHQPVLK

## SEQ ID 5803

TTGGGGGAAAATGAATGCCGCTCTGAAAGGGGTTGTTCCGCTTCAGACGGCAATTTGCAGGCGGTGCGTATGGTCAGGCGATTCATGCCGGTT

## SEQ ID 5804

LGNECRLKGVVPLQTAFCRRSVWSGDFMRV

## SEQ ID 5805

ATGTCGGTTGGGCATTATGAGAATTTTCCCTCGGTTGCTGATTTTGCCCGCGCAGGTTGAGGAAGCCGGTTCATGCGGTGTATGCCPTTGACGAGCGGCGGACGATATGGCGGACGAGG  
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TGTGCGGTTGCGTTGGATTGTCAGCGGTTTATGATCTGCTCTCGGCGTTTTCGAGGATGTGGTTAAACCGCGGTACGCGCATTTTCGGCGATCTGACCGATTATTGCCGGCGTTCCGCC  
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CCGCGTGCATTCGGTATGCTGAAGCGGCGTTCGCTTTGGCGCGCAATGAAAGGCGGTATCGGTTTGGAACTCCGTATGATGTGTGTTGGGGCGCAGTTGATTTGCAGAACTGGAC  
CGGTGCCGATACGATGTGTTGCACAACGCCCGTTTGGATAAGAAGGATGTGTTGATTATGTTGAAACCGCGGTTGTGGAAA

## SEQ ID 5806

MSVGHYENFPVGSLLPRLRKLPPHVVAFARTADMDDEGSMPSPEARLSGLELRRLDVLASGRSAHFPLIARLDAAEVVFFGLDLQPPYDLSAFSQDVVKTYAHFGLDLDYCRSA  
NPVGRIMLALYKGTDAVCAVSDGICTALQLVNFQDVAVDWQKGRVYIPQDDLLKFGVSEBQIAGRAAARQRLMAYECRRAPRMLKAGSPLARELKGRIGLELRMTVLGAQLILQKLD  
ACRYDVFAQRPLDKKDLIMLKRALWK

## SEQ ID 5807

ATGCCAACCGACATACCTTCTCCATCCATAAACAATGCCGCTCTGAAACGGAACAAACCTTTTCAGACGGCATCAGATACCTCCAAGCTGCCGCGCAATCAGTGGTG

## SEQ ID 5808

KPNRHPTSLHQTCKRLKRNKPPSDGIRYLQAAGNQWM

## SEQ ID 5809

ATGCCGCTCTGAACCGGAACAAACCTTTTCAGACGGCATCAGATACCTCCAAGCTGCCGCAATCAGTGGTGTATGACCGTGCAGAACCGTGGACATGACCGTGTGCGATTTCCTCATCG  
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AAGCGCCATCGACCGATGCGCGGCATCTTACCGTGCAACGCCCTTCCACCAAGGGAATGCGCTGTAACCGCGTGCAGATACGCAATCGGTTCTTCGGTTTATCCAAAAGC  
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## SEQ ID 5810

MPSETBQTLFRRHQIIPSCRSQSVVMTVTVDMTVDFLIGICIAHAFNRSFKADFHACQRMVAVHERLAVGNIGYTTIDNLAGFRIVGPKHADFDNRRERARIFNTDQLRILLAERIVER  
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## SEQ ID 5811

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TATGCTGTAACCGATGTTGCCGACGCGAAGCGGTTGTCGACGCGAACCATCTTTGCGAGGATGAAATCCGCTTTAAAGCTACGCTGAAAGCGTGCAGATGATCCGATGAGGAAA  
TCGCACACGGTCATGTCACGGTTCGCACGGTCATTACCAACCAC

## SEQ ID 5812

VLECAQNSAVPERTNMAIAKNSVSLHYEMYDANNQLDKTEEPIAYLHGGYDGFPLFVEALHKGKADGTDVVALSSDDAFGEQDSELVRIEDAGAFPEVEVGMFPAADDPETGDDVV  
YRVTVDADKAVVDGNHPLAGMKIRFKATVESVRDASDEELAHGHVHSGHGYEH

## SEQ ID 5813

ATGGTPTTTGAGAGTGTGTAAAAAATTTTACACTGCAATAAATAACAAAAATTTACATTGAAATATGTGCCGTACAGTTTATGAACAGGTTAACGGTAATCGCCGCGCGCGGTTGTG  
TTAGAATGCCGCTG

## SEQ ID 5814

MVFESVVKNLHCKNITKIYIEICAVQFMNRLTVIGRRGCVRMRL

## SEQ ID 5815

TTGCAGTGTAAATTTTITACAACACTCTCAAAAACCATTCGACCCATCTGCCACTTCCCAATCTGCCTTAATAAATCATACAAGATACTGAATATATTAATCTCTATAATATTTATC  
CCTATCGGATTTTAAACAGCAAAACCGTTTACAGGATTTATCAATCCGCCCGCCAGAAACCTTTTCATTCAAACCTTTTCCCATCTGTACGACATTCGAATCCCTATTTCATGTTGCA  
TAATTACGCAATTCAGCGATGAATTTCAACCCGCTTG

## SEQ ID 5816

LQCKFTTTLSTKTIPTLPTSPICLAKSYKILNYLINIYPIYRIFNSKTVLQDLSIRPPENFSFKPFSHLYDIAIPYSMVHNYANSAMNPQGL

## SEQ ID 5817

TTGTGTCTTTGGCTTTGGCTGCTGCGCGGAGAAAAAGCCGCTGAAGCTCCTGCTGCTGAGGCTTCTCTACCGAGGCACTGCTGCGGAGCTCCGCTGCGGAGCACTGCCGCG  
AAGCTGCTGCTGTAAGCACTGCGCGGAGCTGCCGCTGCTGAAGCTCTGCGCGGAGCTGCTGCTACCGAAGCACTGCCGCTGAAGCTCCTGCTGCCGAGCTGCAAAA

## SEQ ID 5818

LLSLALACGGGKAAEAPAAEASSTEAPAAEAPAAEAPAAEAAAAEAPAAEAPAAEAPAAEAAATEAPAAEAPAAEAAK

## SEQ ID 5819

TTGCAAGCGGAAATGCTTATTTTCAGCTTCGGCAGCAGGAGCTTCAGCGGCGAGTGTTCGGTAGCAGCAGCTTCGGCGGAGGAGCTTCAGCAGCGGAGCTTCGGCGGAGGAGCTTC  
CAGCAGCAGCAGCTTCGGCGGAGGAGCTTCGGCAGCGGAGCTTCGGCAGCAGGAGCTTCGGTAGAGGAGGCTTCAGCAGCAGGAGCTTCAGCGGCTTTTCTCCGCGCAGGAGCCAA  
AGCCAAAGACAACAAAGCAGCGGCAACAGGATTTTTCATTATAGTAACCTTTAAATCAATTTAAATAT

## SEQ ID 5820

LQAEINATFAASAAGASVAAAASAGASAAGASAAAAASAGASAAGASAAGASVEEASAGASAAFPSPQAAKAKDNKAAANRDFILVTFKILNLY

## SEQ ID 5821

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AAGAAACACTATATCGGAGGATGACGGTACGCGAAGTTGCAAGAAATCCAAGGCTTCCCGACAACCTTCAAATTCATCTATCAAATGTCAACGACGCATACAAAAATGATTGGCAAGGCGGT  
CCCCGTCAACCTTGCTACGAAATTCGACGGCAATTAAAAAAACCCTAGAAGG

**SEQ ID 5822**

MQRSSPTTYNPMKIIISLFGSCGGLDGFKEAGFPIPAANEYDKTIWATTFKANHPKTHLEGDIRKIKREDFPEETIDGIGGPPCQSWSEAGALRGIDDARGQLFFDYIRILKSKQPKFFLA  
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VKAWEQEGFTVOASGROCOLHPOAPKMEKHGANDYRFAAGKETLYRRMTVREVARIOGFPDNPFPITYQNVDAYKMGNAVPNVNLAYETAAAAIKTKLER

**SEQ ID 5823**

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TTTCGTGCGCGCTATTTGGCTGGTGTGCTGCTGTCTGCGCGCTGGCTGATTTGGCTCGACCGCAACACCGACAACCTCGCTCTGTGTGATGTATCTGCGCGCAATTACCGTTTTTCAGACG  
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**SEQ ID 5824**

VRQYLPSYSRWCFPIINPGAIILHRQIFLEIMLPAAYGGFILTALLDRTPGSGNLKPAATLMAVLLVAVLLPFLPOLAAFFVAAYWLVLFLCFAWLWLDRNTDNFALLMLLAAPTVPQT  
AYAVSGDLNLRAQVHLNMAAVFVSVRVSVLLGTETLKECRKDPVPIPNVIYKNIAITLILHAAAEMLPACTAGFTALAVGFIILAKLRELHHKLLKHVETYYILLQLFAAGYL  
TGAAKLQNLPAAPLHLITLGGFTGGVMMVLTAGLWHSGFTKLDYPKICRAVSLFASAVSRAVLMMVNPIPTFTVPEILTAAVFMLYLITFVPIFRANAPTDDPE

**SEQ ID 5825**

TTGCCGCTGCTTTGTGTGCTTTGGCTTTGGCGCTGCGCGGAGAAAAAGCGCTGAAGCTCCTGCTGCTGAGGCTTTCCTCTACCGAGGACACCTGCTGCCGAAGCTCCCGCTGCCGAAGCT  
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GCAAAATAAGCATTTTCCGCTTGCAAAAAAGCAGGATACGTTTCAGTATCCTGCTTTTT

**SEQ ID 5826**

LPPLCCLNLNLPAAEKKPLKLLLRPLPRHLPLKPLPKHLPPKLLLLKHLPPKPLPLKLLPPKLLLPKHLPLKLLLPKLQNKHFPLAKKQDTFSILLP

**SEQ ID 5827**

ATGCCGTGACCTTCATACCGAATTTTCCCGALTCCTGCCGGCAGATGAAATTGCCGAACCTTCTCCGACGCTTTTAAAGATCAGCGCAACCGCTTACGCTGTCCACAGACATCATTTTGC  
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**SEQ ID 5828**

MPDLHTEFGRLLPADEIAEPSPTLLKQDRNRFPSAPDIILQPRSVESQVTHMRFCEYHRIPTVPGGGNTGLCGAAVSENGVLLNLKLNRIIRISINLSQNTCTVEAGSVLQTVQQAARASNR  
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CSEFELIGRFAAKLSSEFSKLPLPTHSEWHILLELTDSPDSNLDRLVEFLYKGGFTDSVLAQSEQRTHMVALRENISASQRLGTSIKHDIAPVIGRVADFVRQCAKDLEQNFKGIIQTV  
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SEQ ID 5829

ATGGAGTTTAGATTTTTTCCATCGCAGCTCGAGCAGCGTATTTAGAATTAGTAAAAGATAATCTAAAAGCAGTCGTAAATTATCGAGAGCAGACTATTGAACTTGTTCAAGCTGAAATTGAA  
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SEQ ID 5830

MDLDFHRTARYLELVKDNPKAVVINAETTELVOAEIESAVKIGGNYTKNDRTFKI IKS AVNFPADFILLOFNLKRPL

**SEQ ID 5831**

ATGACAAGGAATACACTGAAGATTACCTTGTTGGCTTCGCCCCGAGGTTTCGGGGTTGAAAAAGAAATGGGGAAGAAGAAAAACCACTCCGGCAATATTTTAAGGACTGTG

SEQ ID 5832

MTRNTLKITLLASPEVSLKKEKMGKKKNHSGNILLRTV

SEQ ID 5833

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## SEQ ID 5834

LGAELEITNSLWKPWNNSNIDYLTKNAEIRFNTKNESLLVKEDYAGGARPRPAYDLKDKVPEIPVLTPEKNITGTPSDIIFEGKALINLKHLDGHIQIVKNDPAKDAFRLSSKYRKGIYTL  
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.TGNVKGFGAGYATWHQLQDKGTGAYVDSMMQYQRFRRHINTEYATERFTSKGITASIEAGYNALLAEHPTKKGNSLRVYLQPPAQLTYLVNGKPSDSENAQVNLGSRQLQSRGVQAK  
AQFATNGVTFQPPVAVNSIYQKPPGVEIDGDRVINWKTIVETQLGVAAKIKSHLTLQASFNROTSKHHAHQGALNLTWTF

## SEQ ID 5835

ATGCGGAATSTTTGGATAAGTTCGCCCGTTACTTTTATGTGATAAGTTCTTCTTCTTCCAATATTCATAATTCTATCGCGGAGTTTTTTTTAAGCGGATAATTTTCATCATCAGTGAGCT  
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## SEQ ID 5836

MRECLDKFARYFLCDKFLLSNIHYFYRGVFFKRIISSSVSLVLS

## SEQ ID 5837

TTGTTCAGTTTTATGCTAAATCCACGCCCTATTTATTTTACTGTGACAAAGGAAATTTATATGAACTCGAAGCAAGCAAGCAGAAGTTAAAAAATCATTTATATATAAGTCTATTTT  
TTTCTATTCTT

## SEQ ID 5838

LFSFMLKSTPYLFLDKGKPFIMKLEASKQKPKSFIIISLFPFSL

## SEQ ID 5839

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TGTATAATTTGCCCTCGTTATTACAAAAATTCAGGAAAA

## SEQ ID 5840

VDFSILNKKCHLVQIPSTYFLFIKSKRLIFAILSSRFENVYNCPRYLQKQEK

## SEQ ID 5841

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## SEQ ID 5842

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## SEQ ID 5843

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GCGTGTCCCTGTCTACTCAGGCGACACGCTATGTCCGACTGTGCGGTTCGCGTGCAGATGCTTGCCTTATGCGCGCGCGTGCACGACCTTGC CGCACAAAAATCCCTCTGACACG  
CGACGCGGCAAAAGTGTCCCTCGAAGCGTGCAAAACAGTGTGCCAAAGCGTG

## SEQ ID 5844

VCTLCRTMLKHKGNHEPSSIFGQRRCLFGFRRLFRACARTRLPSSRYAACRRIRLHRRPNCRTLSGCTGLDPLVPVPHSGRHHVYVRLCGCRAPDACLMRRGARPCRTKPSDT  
RRGKSVPSVQTVQSL

## SEQ ID 5845

ATGTTTATGGCTATTGCGAACAAATAAAAAAGCATTTTACGATTTTTCATTGAAGACCGGATTGAAGCCGTTTGGTCTTGAAGGCTGGGAAGTCAAAGCAATCCGCGCGCGCGGTAC  
AGCTTAAAGAGAGTTATATCTATTGGAAGAAAGATGCGTTTATCTGGTTCGCTGCCATATTACGCGTTTGGCTACGCGTTTCGACACATCAAAACCGGATGCCGTACGTCGCGCAAACT  
GTTATTAAACAGTCGGAATCAATAAGTTAATCGGAAAAACCGAACGTCAGGTTACACCATCTGCGCGTGGATTTCATTTTTCACCGGAAAAATCAAGATGGAATCGGTTTGGCA  
AAAGGTAAGAAACAGCAGTAAACGACAAAGTATGAAGAAAGCGGACTGGAAGCGGAGAAACAGCGGTTGATTAAGCATACCGC

## SEQ ID 5846

MFMAIANNKAFHDFIEDRIEAGLVLEGWEVKAIARAARVQLKESYTYMKDAFYLVGCHITALTASTHIKPDVPRKLLKQSEINKLIKTERAGYTTIVPLDLHPSRGKIKMEIGLA  
KGGKQHDKRSKMEADWREKQRLIKHTR

## SEQ ID 5847

ATGCTATCAAAATCTGATTTCTCCAGTTGGATAGCGGACTGCGTGTGATGACCCAGCCCTTGTTCGCGCGTTTGAAGAACTTCATCCCGGTTGCAGATTGATGTGTCGACCGA  
AGTGGTGCATGCGCGGTGTTTCGAGCGTATGCGGAAAGTGAATGAGATTCTTGAAGAACTCCGTTTCGACACGCGTTCGAGCTGAAACCGGTTTGGCGGTCGCGGAGGTTGGGACGCG  
CGGATACGACAGGGTTATCGTGTTCGCGGTTCTTGAAGTCGCGAGTCATCGCGTGGCAACGGGCGATCGGAAAAAGAACCGGTTATGTCGCGGAAAGCGGTTATTTCTGTTGAACGAT  
ATACGACGGCTGGATAAGGAACGTCGCTTGTGTTGGTGGACCGATATACGGCTCTCGCGCATCAGAGTCAGGAAGATTTGACGGGCAATTCGGGATTTCCCGAGTTTTCATTGATGAAC  
GGCGCGGGAATTTCTGTCGAACTTTCGTTGAATCTTGAAGAACTGTTCTGCTTTTTCGCGCGGTCGCGAATTCGCGCGGCAAGCGGTTGGCGCGCAAGGCAATTTTCCCGAGTT  
GGGCAACACTATTCGAGGCGGTTTGGCAGTTTGGTGTTCGCTTCGCAAAAGATAATGAAATCGCGGAAAGAAATCAACTGCCCTTCAGACGCGCATGTGTCAATTTGTGCGGCAAA  
ACCGATTTCGCGAGGCAATGGATTGCTGTGCTGTCGCGGACAGGCTGCTGTGCAACGACGCGGCTGATGCATTTCGCGCGTCTTTCGCGGAGGAAGTAGTGGCGGTTTACGGTCTT  
CCAGCCGACGATACGCGGCTTTGAGCGACAGGCGAAAAATCGTCAGCTGCACCTTGAAGTGTTCGCGCTTTTCAACGTAATGCCGTTTGGGCGATACCGACTGCTTCAACAGGCT  
GTATCCCGAGAGATTGTGCGAGCGGTTGAAGAGCGGTA

## SEQ ID 5848

MSIKILIIISPSWIGDCVMTQPLFRLLKLHPGCTTIVDFAPKWSMAVFERMPEVNEILENPFHGALELKRWRVRELGRRGYDRVIVLPGLSKSAVIALATGIGKRTGYVGSRYFLIND  
IRRLDKERLPLMVDRTYALAHQSQEDFDGHSQPEFSIDERRREISVETPLNLKGPVLAFCPGAEPGPAKRWPARHFAELGKHYSAGWQVWLFSGQKINELAEINCLSDGMVCNLOGK  
TDLQANDLLSLADTVVNCDSGLMHLAAALGRKVAVYVYSSSPHTTTPPLSDRAKIVSLHLECSPCFKRECLGHTDCLNRLYPEKIVQAVEAV

## SEQ ID 5849

TTCCGCGACAGACCCCTCAAGGTTTCCGCGCAGCCTGTTCTGTACCGGCTCGCGGAATGGCGGAATTCGGGATTTTCGCGCTCAAAATTTATGATAGGATACGAGCAACAGATGA  
TTACCTGCTCTTCTTAACAAATCTGCCGTCAAAATGGGATGAAATCCGCCATTCCTCGTGAACCCCGGTTTGTAGTTCGCGCTTATGCCGTATCCCAATCTGACGGAATCGAAGCGCG  
GCAGTTTCGAGCGGATTTTGGGACAATATCGCGTGC CGCTGAAGAATATGTCGATTCGCGCGCGCATTCGCTGTGGAATTACGTTATCCGACAGCTTGAACGAGCTGGTGTGT  
GCCGCTATTGCCACGCTTTGGGCGAGATGTTGGCGGTGTTGCGCGTTAAGGAGTATGTCGCTGCGGATTTGTCGGAACAGAGTATTTGGAACAGGAATTTGCCCGCTCAAAAGGCT  
TGC CGCGAGCGTTTGTGTTTCGGAAGACGCGCGGATGCAATTTTTCGCTCAGGAATTGAATTTATCTTCAAGGCTCATCTGAAAACTTTGCCACGCTTTTGGAGCAGATTGGCACCGA  
GTTTCAAAAGCAGGATGGGACGCGCTTTCGCGATTCCTTACGCGCAACCGCGACTACAAGAGCAGCGCAGCGTTTGGCAACCCCAAGCGCTCCGCGCGCTTCCGCGCGCAAC

GGGCAGAACAGGTGTCTGTCATGATTCCTGCCACCGCGTCATCGGCAGCGAGCGCAAACTGACCGGCTACGCGGGGGGTTGAACCGCAACAGTTTTTACTGGCTTTGGAACGCGCGC  
AAGTTCAGACGGCATTTGTTT

## SEQ ID 5850

LPQDPQGFRRSLFLYRRAGHAEIGDFAVKFMIGIRSKRMITLPSLNNLPSKWEIRHCLSTRVFCGVMPYPLNITECAGQFERDFWONIGCAPESEYVIRRAIRRLLELRYPDSINELVC  
AALATPLGEMLAVFVGKGLCLLEFVGQKYLEQELAAVQKALRGFPVREDGRMQLRQELDLFKHGLKTFATPLBQIGTEFQKQAWDALLAIPIGETRSYKEQARLGNPKAVRAVAAN  
GQNKVSMIPCHRVIGSDGKLTGYAGGLNRKQPLLALERGEVQYALF

## SEQ ID 5851

ATGAATCCACTTATTCATCAAGCAAAGGAATCATCTATGCAAAACCGCATCTCTCCGCCGTACTGCTGGCTTTTTCAACCCGCTGCCCTTTCGCGGGGCGCATTCACGCTGCAATTTCGACA  
ACCCGTCGGAAGACGGCGGCTTACGCAAAACAGCTTTTGAGCGCGCTTACGCGCTTCGGCTGTTCCGGGCGCAATGCTTCGCCCGCGCTGCTGCTG

## SEQ ID 5852

MNPLIHQAKESMQTRILSAVLLAFSTAAPAGGAFTLQFNPSDEGGFTQNLISAPYFGCSGGNASPALSM

## SEQ ID 5853

TTGAGGGCTCGGTTGCGGCAATGCCATAATATACATATTTCCAAAGCATCAGGGAAGGAATGTTTCAACACACAGGACGACACATAAAGCGTCGCCCTATGAAAATTTTCAGACGGCGCT  
TCAAAGGGTCGTCTGAAACACAGATTTTTCATTTGCGCATTCGCGCATCATCAACCGTTTCGCGCATTTCTGCCGCGTTGACAGCCTATATGAATCCACTTATTCATCAAGCAA  
AGGAATCATCTATGCAAAACCGCATCTCTCCGCCGTACTGCTGGCTTTTTCAACCGCTGCTTTTCGCGGGGCGCATTCAGCTGCAATTCGACAACCGCTCGAAGACGGCGGCTTCAC  
GCAAAACAGCTTTTGAGCGCGCTTACGCGCTTCGGCTGTTCCGGGCGCAATGCTTCGCCCGCGCTGCTGCTGTTAAACCCCGCGCAGGGAACAAAAGTTTCTGCTGACCGCTTACGA

## SEQ ID 5854

LRVWLRQCLNIQYFSIRERNVSTHRTTHKASPYEKFQTAFKGSSETTIPAFHSGTSSNRFQTLPLP/LAYNESTYSSSKGIIVANPHPLRRTAGFPNRLCLRGRIHAIRQFVRRRRRH  
AKPAPERALRLR/LPQRQCFARAVVVKPARRDKFRPDRLR

## SEQ ID 5855

ATGAACCGTCGTCAATTTTGGGCGAGCGCGCTCCGCTCTCTTTGGCTTCCCGCGCTCTTTTCGCGGTCGCGCAGGACACCGCGACTACCACCATCATCAGGATATGACGCTGCCCGG  
CATCCGCTACACCGCGCTCCGCAAACTGCCGCACATGCTGGATGCCGACAGTTTGGCTGACCCACTGCTGCTGCTGCTCAGGGCGACACGCTATGCTCCGACTGTCGGGT  
TGCGGTGCGCGAGATGCTTGCCCTATGCGGCGCGGTGACGACCTTGCCGCGCAAAATTCGCCCTGACACGCGACGCGGCAAAAGTGTGCTGCAAGCGTGCAACAGTGTGCCAAAGCC  
TGTAAGAACAATCCGCCACCATGCGGAATGCAAGGCTGTTACGAGTCTGCTCGACTGATCAAGAATGCGAAAACTCGCGCGC

## SEQ ID 5856

MNRROPLGSAAYSLASAFARAHGADYHHHHDNPAAASAYTAVRQTAHCLDAGQVCL/THCLSLLTQGDTSMSDCAVAVRQMLALCGAVHDLAAQNSPLTRDAAKVCLKQKQCARA  
CKEHSAHAECKACYESCLDCKECKLAA

## SEQ ID 5857

TTGCTGCTGTATGATTCACCATCGCATCGCTGTAAACGTGCCGCTTTCAGACGGCTTTTGACTTATTCGCATTTCGAGCGCTTCTCCGGGAACGCGGGTGCTTGTGCTTTTCGCA  
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TTTGTGCGCTTACGTCGCGTTATTAACCATATCCGACTGGCGAGCTGTATTTGCGCGATTTCGCGCAGGGTTGAAGGAAACGCGCGGTTGAAGGAAACGCGCGGTTGAAATGCGCGCGGTTTAT  
GCTTTGAACGAGCGCGGCGAGGCGCAACGCGCGCGCGCTCGGTTCAACAAAAAGCGGCTTTTGGGACGCGCTGCTGCTGCGGCAAAATGACGATGGCGCGGTTGAACAGGCAAAAG  
CGCAGGCGGCGAAATGATTGAGGATTTGGGCGGAGCAGGGCTGGATTGAACAGCAGGAAGCGCGGCAAACTGTTTAAAGCGGTACCGCGGCGAGCTTCGCACTCTGAATTTGATTAA  
TACCGGCGCAGCAGAGGCTTCGATGAATTCAGACGCGATTGGGACGCTTCCGCTGCTTTCTGCTGTACGCGATTACCGGCGAGCGCAAGACCGAGTGTATTTGATGCGGATGGCGGAA  
GTGTTGGCGCAGGCGGCGAGGCTGTGTTCTGTTGCGCGGAAATCAACCTCACGCGCGAGCTTTTAAAGCGGTGGAACACCGTTTTCGCGAGTGGCGACCGCGCTGTGTCAGCGCGGA  
TGGCGGCGAGCGCGCAGCAGGATTATTCGCGCGGATGTTGGGCGAGCGGAAGCTGTTGATCGGCGCGGCTGGCGGTGTTTACGCTTTGCTGATGTCGGGCTGATTGTTGGTTCGA  
TGAGGACACGACGAGCGCTGCTTCAACAGACACAGAAATTCGCTTACACGCGCGGATTTGGCGGTGTTGGCGGCGAAGCAGGCGCGCTGTCGCTGCTGTTGGCGAGTGGCGCGCGCAGC  
TTGGAGAGTTGGCACAAGCGCAAGCGCGCTACCGCTGCTGCAACTGACCGAAGCGCGCCATGCTTCGCGCACTGCCACAAGTGGACATCTCAACATAGTGTCTGAAACTCG  
ATAACGGCTTCTCACCGCGAGCTTTCAGCTTTTGAACAGAACTTTGAAGCGCGGATGTCGCTGCTGTTTACCTTAACCGCGCGGCTTCGCGCTGCGCTGTTTTCGCGCGAGTGGCG  
CCATACCTTCGCGCTGCGGAACTGCTCCGCAAAATGGTGTGCAACCAACGCGCGCGCAACTGCGCTGCCACCATTCGCGACACCGCGAACCCTACCGCTTCAATGTCGCGACTGGCG  
AACCAAGACCTGACCGCGCTCGGACAGGATTCGACGCGCTGGAAGAAACCTTGGCGGCTTCTGCGCAAGGCGCGCTGCTCGCGCTGATAGGACAGTACGGCGCACAAAACGACT  
GGGCGATTGTTACCGCGCATTCGCCAAGCAGCAAAATGACATTTCTGGTGGCAGCAGATGCTTGCCAAAGGCGCATGATTTCGCGCGGCTCAACCTGTTATGCTGTTGAACGCGCGAGCG  
CAGCTGTGACAGCGCGGATTCGCTGCGCGGAAAGCTGTTGCGGAGCTGATGCAAGTGTTCGCGAGGCGGCGCGCGGCAAAACCGGCAAGTGTGATACAGACCCAACTGCC  
GAACACCTGCTTTCGCGCGCTCAAAGCGCAGGACTACGCGGTGTTTTCGCGAAACGAATTTGAACGAACGCGCAATTTTCGCGATGCGCGCTTTCGCTTTTCAGACGCGCGTCCGTGCC  
ATGCGCGCGCTGTTGCCGATGCGATGGAATTTCTCAACGCGCGCAAGAAACCTTCGCGCGCTTTCGCGGAAAGCGCTTCGCGGTTCGCTGCGCGCGGATGCTGATGTCGCGCTTC  
CGAACGCGAAGCTGCGCAAGTTTTCCTCGAATCAACATCCCGACAAGATTTCGACCGCGCGGTGAGTTTGTGGTGCAGGTGTTGCAGCAGAACCGCGAGCGGCAAAATCCGATGTCGCTG  
GATGTCGATCCGCGAGGCT

## SEQ ID 5858

LPACMIYHRIAVNVPLSDGLLTYSHSEPLPPGTRVLVPPFRNKTVMVWEITDIAPMDAARILSVQTVFVEEKPLSQSWRDLLAFTSRYYHYPTQAVPALPQGLKETRAVEMPQPLFY  
ALNEAGRAQTPPPARFNKAALWDALLSGEMTMAALKQANAQAALIEDWAEQGWIEETEAAPVLRPYRQASHSEFVLNTGQKASDEIQTALGRFSFLYIGITGSGKTEVYFDAHAK  
VLAQRQVLFLLEPEINLTPQLLKRVENRFADVPTAVLHRSMAAGRRTPQDYLRAMLQAKLVIGTRLAVFTPLPDVGLIVVDEEHDGSPKQDNELRYHARDLAVWRAKGGCGPVVLGSATPS  
LESWHKQSGAYRLLQLTERAHASALPQVDILNIGRLKLDNGFSPQALQLLQNFPAAGMSLVYLNRRGFAPALPCGDCGHTFGCPNCASRMVLRHQRARQLRCHHCDHREPIPFKCPDQ  
NQDLTAVHGHTQREVEFLRAFLPKAAVVRVDRDSTAHKNDWADLYRRIANDEIDILVGTQMLAKGHDFARLNLVIVNADGSLYSADFRAPERLFAELMQVSGRAGRADKPKVLIQTQLP  
EHPVFAAKQADYAVFAENELNERQMFAMPFPFGQTAVRADAPRVADAMEFLNAKETLAPLLPESVSRFGAAPMLHVRLEAERERAOVLESTSRQDLHRAVSLAVVQLQNRDQKIRHSV  
DVDQEA

## SEQ ID 5859

TTGCGTACCGTCGGTGGTCCGCTCGGAAGCGGAGCGCGCGCATATCGCGCGCAGGCGGCGAGGTGAGCGTGGTTCGACCGTGAATTTTCGCTTCGCCCAAGCTGTTGCTTATGAGGA  
AACCGACGACAGCGGGGTGGATTCGCGGCTGATGTCGCGAGCTTTCGCGACTTTCAGCGCGGTAAGCGTGAATTCG

## SEQ ID 5860

LRVGGPLGSGAGGISAHGAGQRCSTVNFASPKLFAVLEKPTSTGVDSAVMFGSLATFSVSVNS

## SEQ ID 5861

GTGCGCGATATGCGCGCGCTCCGCTCCGACGCGGACCCGACGCTACGCAACCGAACAGCTCTTTGAAGCGCGGCTGAAACGGGACGGCGAGTGA

## SEQ ID 5862

VRRYAAGSASERTTDTGTPNSSLKRALKRDQS

## SEQ ID 5863

GTGTTTCTGCTTCGCGGAGGACACGCGCGCGCTAGCCCGCGCGCGGAGTCCGTGCGGGTTTCAGCGCGCTTTGGCGGCGCTGCTCATTTGTCGGTAAATGCTGCGGCGAGCGG  
CGGACATCGCGGGAATGTGCGGACCAACCGAGTGCATCCGTCAGACCGATCGCGCGCTTTATGCTAAACGGTCAGGACGAAACTTTTGTGCTGCGGGCGGCTTTTACACGACA

GCGCGGCGAAGCATTCGCCGCCGACAGCCGAAGCCGTAAGCGCGCTCAAAAGCTGGTTTTGCGTGAAGCCGCGCTTCGGACGGGTGTGCAATTCAGCGTGAATGCGCCCCCGG  
AAGGCAGCGGT

**SEQ ID 5864**

VFPAPGRTRAARAEVRAGLQRAFGPRLASLGNACQAAIDGNGVDHPVHPVQTDRRVPIVNGQDETFCPCGRVLPQRGRSIAARTAEAVRRAQKLVIREAVFGRVVELQRECAPG  
KGS

**SEQ ID 5865**

TTGAGGAATATAACCGTGCCTCAAATTTACTTTCATACGCGTGAACGATTGGGTGCTTTAGCGCGCATCGTGCAACATCATACCGCTTGTACCGCAGCGTGGCGGTATATGAACCGACCG  
TGGTTATCTGTCGCGCGCGGATGCAAGAAGCTGCGGTGGCGGGCGCGAATTGAGGATTGCGCGGGGTGAGGCTGTGCGCTTGGCAGCGCGCAGGAGCTGTGATGCGGTGAAGCTGCCCGACCCCGG  
TTCAGACCGCTTATCAGCGCAATGGATTGCTTTCGAACAGGAAACCGTAGAAAGTTTCGCCGCAATACGGGACGGCGCAGGAGCTGTGATGCGGTGAAGCTGCCCGACCCCGG  
CGTATGGCGCGCGCTTGTATTATGCGGCTGCGGTACTGCGGATGAAGAAGTGGCGCACAATGGCGCGAGGCGCGCTTGGCGCGTGTGGCGTGTTCAGCATGACGCGCATCGGT  
TTGCCGTGTACGGAGCGTCAACCTGATGCGGCAATCCGAAATGATTACTGCGCATATGCTGCGGATGCTGCGCAATGCTGGCGCAGCGCTTAAATTCAGCGAGCGCGGT  
GCGCGCGCGGTGGCGCGGAGACAGCAATTTCCGTACGTGCTGACGATGATCGCGCGCTGACGCTGTTCAGGTTACGCAATGCTGCGTGAAGCAGATTGCCGCGCG  
GTTGGCTATGACTGCCGCTCCGTTTCAGCGCGCGCTCAAAGAGCTGTTGCTGCTACCGTTCGGTGGTTCGCTCGGAAGCGGAGCGCGCATATCGCGCAGCGGCGAGTTCAGCG  
TCGGTGTTCGACCG

**SEQ ID 5866**

LRNITVPSNYFHTTRERLALGGLIVQHHTALYRSVAVYEPTVVIVRRGCKLRLWAGRELRIAAEAVLGGQTLVDVINIPDSGLYQAQWIAFBEQETVERFAAQYGTQAQVDAVKLPHPG  
RMGAAPDYAAVLADIEVPHNAEALCGVLAWLQHDGIGFVYGVNLMRQIRKLTADMAADWSSAMLAQRINCSAALRRRLARQDTNFRLLTLDVRRML/TLQVTVNSVAQIAGA  
VGDCPSRFSARFKELFGCVPSVVRSEAPAAAYRTGQVSVGVPR

**SEQ ID 5867**

ATGCCCCCTTATACACCAATCCAACCCGGAGGTCTGCTGAAAATCAGCTTCAGGACATTTTCAGACGACCTGATTTCCAAAGTGAACAAAATGACCGAAACCCCAATCCCTAGAACTCGCCA  
AAGCGTTGATTTCCCGCCCGTCCGTTACCCCGACGACGAGATTGCCAAAATCTGCTTGCAGAACGCTGCACAAAATCGGTTTTCGGCTGAAGAACTCCATTTTCGGCGACACCAAAAA  
CATCTGCTGTTGCGACCGCGCAGAAAGCTCCCGTCTGTTTTGCGAGGCGATACCGAGCTTGTGCGCAGAGTCTCTGTGAAAATGGGATTTCGCCCGCTTCGAACCGACCGAGCGGAC  
GGAAGATTATACGGGCGCGCGCGGACATGAAAACAGCATCGCTGTTTCTGTTACCGCTGCGAACGCTTGTGTCGAACATCCCGACCATCAAGGACGAGTTCGACTCTTGATTA  
CTTCCGACGAGAGGGGATGCACTGGACGCGACGACCAAAAGTCTGATGTTGAAAGCACGCGGAGAGTTGATTGACTACTGATCGTCCGCGAACCGACCGCGTGGACAAATGGG  
CGATATGATTAAAAACCGCGCGCGCTCGCTGTCGGGCGAGCTGACCGTCAAAGGCAAGCAAGGCGATATGCTTATCTCTATTTCGGCGTGAATCCCATACATCTTTTGCCCGCGG  
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ACGTCAAATTTAATTTCCGCTTCTCCACAGAGTCCACGAAACAGGCGTGAACACAGCGTCCACGCGCATTTTGGACAAACACGCGCGTGAATACGATTTCAGTGGTCTGTTTCGGGACA  
GCCCTTCTGACCCACGCGCGGCAACTGACCGACGTCGACGCGCATTCGCGAACCTGCGCGTGTAGGCGCAATTTGTCACCAACCGCGGCGACTTCGGAGGAGCGCTCATTA  
GCCATTGCGAAGAACTCATGAAATAGGCGCGTCAATGCCACCATCCACAAATCAACGAAATGTCGGCTGGACGATATTCGAAGCTGTGCGCGTGTATGAGGAGTATTTGGCG  
GGTGTGTTGGCTGAAAAGCCGCT

**SEQ ID 5868**

MPVLYTNPTRRSENQLQDISDDLISKVNMTETQSLAKALISRPSTVTPDDRDCQKLLAERLHKIGFAAEELHFGDTKNIWLRRGTAPVVCFAHGTVDVPTGVEKWDSPFTEPTERD  
GRLYGRGAADMTSIACPFVACERFVAEHPDHQGSIALLLTDSDEGDALDGTTKVVDVLKARGELIDYTCIVGEPTAVDKLGDHMKNGRRSLSGSLTVKGRQGHLYPHLAVNPITHFAPA  
LLELTQEIWDEGNEYFPPTSFQISNNGTGATNVPGLNVKPNFRSTESTETGLKQRVHAILDKHGVQYDLQWSCSGPFLTHAGKLTDVARTAJAETCGVEAELSTTGCTSDGRFIK  
AIAKELIELGSNATIBQINENVRLLDIPKLSAVYERILARLLAEKAV

**SEQ ID 5869**

ATGCTGAGCCCAAAAGCTGCGATTGTTCAATATCCCGTTTTTCCAGTTTGGCCAGCTCAAAAAATACCAGCCGAGAGCATTCGCAAAATCAAAGCCGACTACAAGAAAACTGCGAGA  
TATGCGCAGCATGTATACAGCAGGTGCGCGCAGATTGAGCGAACCTTTCGCCCGCGCATATCGAACGCTGGTGAACGGCTGGCAGGTTCGCGCCCATTTCTGCGCTACTTCAAAATA  
CGCCCAATACAAAAATTCGCCCGCATTCCTGTGATGCTGCTCAACCGCGCGCGCTGAGCGTCAAGTTGAGTGGCATTTGCTACAAAGCCGAGCGTGTGCGCGATTGCGCTGCCGAGTAC  
AACCGCTGGCTGGATGATTTCGATACCGAAAAATACCGCGCATTCGATATGTCGCGACGCGCGGAAAGCGAATATGACGATTACCGCACCGTGCACAAACAAAGCAATCCGACGAGGT  
TGCAAAACGACGAAGACTTTTCTGCTGCGCAACACATTCGAGCGCGCAGATTGGGCAAGCAGGATGTAGCAAAATGGATAGCCGAAACCGTGAAGATTACTGCCGCTTACGAAGC  
CTGTCACGCGCAA

**SEQ ID 5870**

MLTPKSCDLFNIPFPQFAQLKKYQPEIPQIKADYKENWQIQQLIQVAAADLSEPPAPPHIERWCNMGVRAHFPAYFYKYQYKNSAAILSLILNRRRLSVSLDWHYKADVSPIALPEY  
NRWLDLDFTEKYAAPDMWHAESYDDYRTVAQQSESRRLLQNDDEFFCIGKHIERDDLQDVAKWLAETVEDLLPLYEACHGK

**SEQ ID 5871**

ATGAATCCGTTTGAACCCAAAGCGTTACCTTTGCGGAACCGATTGAATGCTGTATGCTGCCAGCGCAAGTGCAGCGTTTTCGCGTCAAGTTGCTATGTTGCGGCTATATCGCGG  
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CGCGCGCAGCCCGTGAAGCGGTGGACAGGCTGTTCGCCAACATATCGGCTGTACGACACAATTCGCGCGGCTGTTTCGCGCGAATTTGCGCAAACTCGAAGCAGACACAGCTTATATCCCC  
GATCGGAAGCGTTCAAAACGCTTGTGGAGGATATGATGTGATCTGCGGATTTGAAGAGCCTTTGTTGACATGGGCAAAACGTTTATCCCGAAGAGAAGCTGACCGAAATCGGCAAAA  
TCATGGCGCGCGCGCGTGCAAA

**SEQ ID 5872**

MNPFETQSVTFAEPIEMLYACHGKVRFPQGIAMLSGYIAENGCNQLVLQTRIQISRYFNVAAPLHHEDEENFFLLLYAPQAREGVDELLRQHIGLYDNWAAVSAEFKLEADNAYIP  
DAEAFKRFVEGYDHLAIEEPLFDMGKTFIPREKLTETGKIMARRCK

**SEQ ID 5873**

TTGAGACGATTGTTTCAGACGCGATTATTTGCAACCGCGCGCGCCCATGATTTTGGCGATTTCGTTGAGCTTCTCTTCGCGGATAAACGTTTTCGCCATGTCGAACAAAGGCTCTTCAATC  
GCCAGATGCACATCATATCCCTCCACAAAGCGTTTGAACGCTTCCGCATCGGGATATAAGCGTTGTCTGCTCGAGTTTGGCAAAATTCGCGGAAACACCGCGCCAGTGTGCTACAGCC  
CGATATGTTGGCGCAACAGCTGCTCACGCGCTTTCGCGCGCTGATTCGACGACGAGCGGAAAAAGTTTCTTCTTCGTCCTCATGTTGACGCGCGCGCGCAACGTTGAATA  
CCGGAGATTTCGGGATGTTTGAACAAAGCTGATTTCAGCGGTTTTCGCGCATATAGCCGCAACATAGCAATCTGACCGCAAAACGCGCGCACTTTCGCGTGGCAGCATACAGC  
ATTTCAATCGTTGCGCAAGGTAACGCTTTCGCTTCAACCGGATTCATGTTTTCGCTTCAACGGGAGCTTTTCAAGCAGTCAATTTATATAAAACAGCTGCACAAAGCAGCTGCT  
TGCTCTT

**SEQ ID 5874**

LRRLFPQALFAPARRHDFADFGQLLFGDKRFAHVBQRLFNRMHIISLHKAERFRIGDISVVCFEFGKFGGNSRPVVVQPDMLAQQLVHAFTGLRRVLQQQREKVPFVLMVQREGNVEI  
PGDLADGLQNLIAAVFGDIARQHSNLTAKTAHFAVAGIQHFNRPCKGNALGPKRIHVFLNGDSSSHFIKQPAQSRLSVF

**SEQ ID 5875**

TTGAACCGCGAACCGGAAAGGAGATATGAAGAGCAGCAGCAGACCATTTTGAACACACCGCCATCCCGAGGACATCGCGCTAATTAAGAGCGCAACGCGCGTTGGCGAAAAAAC  
GTTTTCTCCCGCTATAATGGGACACAAACCGCGCTTGCACCGCTTGAAGAAATATGGTAAGCAATTCGCCCAACTGGCGGTGCAATATCTGACCGGTGTTGCTTTTCAACCGAAAACTG  
CGCTGCCCGGAAGACGAAGTTTCGTTCTGATGGGCGTGTTTTACAGGCTTTGCAAAAACAGGTACCGCGCTGCACGAAAAAATATGCGCGTGAATAATTTGGCAGCGCGCAACG

TTTAATCGGCAGATTCTGCAAGGTATCGAAGAGCGGAGCCCTTGACGGCAANTATACCGGTCTGACCTGAGCAFTTGTGCGGATTACGCGGCCCTGGGATATTTTCAGGCGGCAA  
ACAACTGATTGCGGAAGCGGTATCCGAGATTACGGAAGACACGCTGCGCAAACTGATGCTGGGCGACGCGCGGAACCGGATTTGTTATCCGACGCGGAGAAACCGCATCAG  
CAATTTCTGCTCTGCGCAGATGGCGTATGCGAGACTGTATTTCCACGACATCTGTGCGCGGATPTCGACGAAACCGCCTTAGATGCGCGCTGCTTCTCCAAAACCGCAACGCGG  
TTCGACGCACTTCCGAGCACTGCCTATCGGACAGCAAGGAAC

## SEQ ID 5876

LNAEPKADMKSSQTPILEHTAI PRHIAVIMDNGRWAKRFLPRIMGHKRLDALENMVKHAKLGVQYLTVFSTENWRRPDEVSFLMGLFLQALQKQVRLHNNRLKILGSRER  
FNRQILQGLEAEAL TANNTGLTSLIAADYGGRWDLQAANKLIAEGVSEITDTLAKHMLGDAPEPDLFIRTGGETRISNFWLMAYALYPTDILWPDFDETALDAVASFPKRRER  
PGRTSEQLPIGQBN

## SEQ ID 5877

TTGATTAACCTGGTTTTCATATCAAAGATGATTGAGCGTGTGGAAAAGTGGCATGTATCAAACCTCTGTGCGCTGCAATTGCGCGAGGCTCAATTTATCGTCTGAAAATAGCTCCG  
GCTGT

## SEQ ID 5878

LINLVFISKIERVGVKVALYQTSVAPALRRGSTYRLKIASGC

## SEQ ID 5879

TTCACCTTGTATTCCGTA AAAACCGAATATTTATTTATCGATTGGAGATTACCATGAAAGCTTATCTGGCTCTGATTTCTGCCGCCGTATCGGTTGGCTGCCCTCTCAAGAACCTG  
CCGCGCTCTGCTGCCGAGGCACTCTGCGGTGAAGCAACCGCTTCCGAAGCGCTGCGCGGAAGCTGCTCTGCGAGATGCTGCGGAAGCCCTGCTGCGCGCAACTGTGCGCGCACTGT  
CGAATCCAAACGCAATATGCAAGTCAACACCAAGACATCCAAGTCAGCAAGCATGTAAAGAGTTTACCATCTACTCTGAAACATACCGGTACGCAACCAAGCCAGCATGGGTCAACAC  
CTTGTGATTGCCAAAGCTGAAGACATGGACGCGGTATTTAAAGACGCGTAGTGCTGCGCATACCGACTATGTCAAACCTGACGATGCGCGGTGTGTGCCACACCAAACTGATCGCGG  
GCGCGCAAGAGTCTTCCCTGCACTTTGGATCTGCGCAATTTGGCTGACGCGCACTACAAATTTGCTGCACTTCCCGGTCACGGTGCTTTGATGAACGCGCAAGTGAATTTGTGCGAT

## SEQ ID 5880

LHDFRKTYYTIDWRTMKAYLALISAIVGLAACSGEPAAPAAEATPAGEAPASEAPAAEAPADAAPAAAGNCAATVESNDNMQFNKDIQVSKACEPTTTLKHTGTQPKASGHN  
LVIAKAEDMDGVFDGVAADTDVVKPDDARVVAHTKLIIGGERSLTLDPAKIADGDYKFACTFPHGHALMNGKVLWD

## SEQ ID 5881

GTGACCCGGAAGGTGCGAGCAATTTGTAGTCCCGCTCAGCGAATTTGGCAGGATCCAAAGTCAGGGAAGACTTCTCGCGCGCGCGATCAGTTGGTGTGGGCAACACCGCGCATCG  
TCAGGTTTGACATAGTCGTTATCGGCGACACCTACCGCGCTTTAAATACCGCGTCCATGTCTTACGCTTTGGCAATCACAAGGTTGTGACCCATGCTGGCTTTGGGTTGCGTACCGGTAT  
GTTTCAGAGTGATGGTGAACCTTTACATGCTTTGCTGACTTGGATGCTTTGGTGTGAAGTCATATTTGCTGTTGGATTTCGACAGTTGCCGACAGTTGCCGCGCAGGGGCTTCGGC  
AGCATCTGACGAGGACGCTTCGGCGCGCAGGCGCTTCGGAAGCGGTGCTTCAACCGCAGGAGTTGCTTCCGCGCAGCGCGCGCAGGTTCTTGAGAGCAGGACGCAAAACCGATAACCGCG  
GCAAAATCAGAGCCAGATAAGCTTTCATGTTAAATTCCTCAATCGATAAAATAATATTCGCTTTTACGGAATCAAAGTCAACCGCCATTAACAAACCT

## SEQ ID 5882

VIREGAGKFVVAVSQFGRIQSGRLFAAADQFVGNNARIVRFDIVGISTYAVFYKAVHVSFGNHKVVTHAGFGLRTHGFPQSDGELFTCFADLDVFGVELHIVGFPDSCTVAGSRGFG  
SICRSSFGRRRFGSCPTGRSCLGSRRGRFLRAGSQTDNGGRNQSI SFHGKSPIDKIIIPGPTIKVQPLTKP

## SEQ ID 5883

GTGTTGCACAAACAGATGTTTCGGGGCGCATTTTGTACAACTTCATTTGAAATCAAAGCTGTTTGCAAGTTTACAATCGTTTACCCAAAAAGGGCAATCTTACCCGAACCTATT  
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GGGATGCGGCTCTTCCAACTTTGCGCGCGCGCAATCGAACTCTCCAACGCACTTACTCAAATGAGGATTTGGTTTTCGGCGGTTTTCGGTTTGGAAACGAGCTGACCGAAAC  
GACCGTATCGAAGCATCAAGCCCTGCCAGCTGCGGCAATACCGACGGGCAATCATCTTCAAACGCGATGCGCGCATATGTTTGCGCCAAAGACAAAGCTGCGCTCTTGATACATG  
CGTC

## SEQ ID 5884

VLEKQMFRRGILLQTSFEIKACLQVYNRLPKRRAILPRTYFFNIRAAVPRRANINGYLQHPCRFPYAFYF/TSSSSASANSGRSSNFAAESKLSNAALLKCRVLVFGGFSGFSTSLTET  
DRIEASSPASCNGTDGAILPKRDAAILFAAKRTSLPSSIAHV

## SEQ ID 5885

ATGAATTTGGAACAGTTGGCGAGCGGGAACGCGCTCTTTCCGACTTTTGAACAGCGCGGACAGTGCGCGCGTTGGATGCTGCGGTGAAAAAAGCTGCTGCCCAACTGCACCCCC  
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TTCGATACGCTCTGTTTCGGTCAAGCTGCTTCCAAACCGGAAAAACCGCGAAACCAATACCTGCACTTGTAGTAAGCTGCGTTGGAGATTTCGATTCGCGCGCGCAAGTTGGAA  
GAACGCGCATCCGAATGGCGGAGGCACTGGAGAGCTGGTCAGGAAGTACGGGGCA

## SEQ ID 5886

MNLBQLGRDAILSGILLQAGQWRRLDAAVKLLPANLHPHPTACTIEDGRLVLLAANMAASRLKMIAPSVLPQLAGLDASIRSVSVRLVPRPEKPPKTYLHLKAALESFDSAAAKLE  
ERHPELAELAEELVRKYGA

## SEQ ID 5887

ATGCTGACAAACATTCGCAAGAAATCTTCGCGAGCGCAACGACGCTTGTGAAACAAATACCGTAAATCCGTTGCCAGAAATCAACGCGCTCGAAGAACAGATGCAAGCCCTAAGCGATG  
CTGATCTGCAAGCCAAACTGCGCAATTCAAACACGCTCGCGAGCGTTCAGACTTTGGACGCAATTTTGGCGAAGCTTCCGCGTCTGCCGCGAAGCGTCCCGCGCGTACTCGGTAT  
GCGCCATCTCGACGTGCGAGTTATCGGCGGTATGCTGTCACGACGCGCAAAATCGCCGAATGCGTACCGCGAAGGCAAAACCTTGGTCCGCAACCTCGCGCTCTATCTCAACGCGCTG  
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CAGCGGACCTCGTGGATACCTATATGCGCGCGACAGCATGGAAGAACATGGGACATCCGACATGGAAGAACCGCTGCGCGCAATTCAGGCTTCAGGAAGACATCAATCTGCTG  
GAAGCGGCAATCGAT



## SEQ ID 5888

MLTNIARKIFGSRNRDLRLKQYRKSVARINALEBNQALSDADLQAKTAEFKQRLADGQTLGILPEFAVCREASRRVLGRHFDVQLIGMVLHDKIAENRTGEGKTLVATLAVYINAL  
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PPHLVRQETEEGEGDYVWDEKAHQVILSETGHEHAQILTMGLLAENDSLYSAANI SLMHHLMAALRAHSLFHKDQHYVIQDGETIVIDEFTGRILMSGRRWSEGLHQVAEKEGVEIKRE  
NQTLASITPPQNYFRILYTKLSGMTGADTEAFEPQSTYINLETVIIPINRFPVQRKDLNDQIPRABEKFPAVVKDIEBCHKRGQFVLVGTTSIENSLVSRLLQKAGLPHNVLMNAKEHREAL  
IVAQAGKVGALTVATNMAGRGTDIVLGNLKHQTDALRADETLSDEEKQAQIAALENGWQAEHDKVMEAGGLHTIGTERHBSRRIDNQLRGRSGRQDGPSSRFYLSFEDPLRLFLALDRA  
AAILNRLAPERGVATIEHNLTRQIEGAQRKVBEGRNFMRRQVLEYDDVANEQRKVTISQRNEILTSKIDIGLDMQIRSDAVSGPRGYLYAARQHGRMTGHPDTGKPPGCRITQASGRHPTILA  
EGGQCD

## SEQ ID 5889

ATGCCGTCAGCGGACCTCGTGGATACCTATATGCCGCCGACAGCATGGAAGAACAATGGGACATCCCGACACTGGAAAAACCGCTGGCTGCCGAATTCAGGCTTCAGGAAGACATCCAAT  
CCTGGCTGAAGCGGACAAATGCGATGACGGTCAAGACATCAAGAGCGCTGATCGAAGCTATCGAAAAACGAATATGCCGCCAAAAACCGAATTCAGGCTTCAGGAAGACATCCAAT  
CGAGCGCAACGTGATGTGTCAGGCAATCGACAAACCAATGGCGGAAACATCTTGCCGCCATGGACATCTGCGGACATACACCTGCGCAGATATGCCGAAAAAATCCGAAGCAGGAA  
TATAAACCGGAAGCCTTTACCATGTTTCAAGACCTGTGGAACGGCATCAAAATTCATATCGCTCCCTGCTTACTTCTCGGTTCAAAATCGAACAAAAACCTGTGCGCGCGGTTGAAGAGCAAC  
CCGTGCGGCAACATCCAGTCCATCCATTCGGAATCGCCGATATAGAAGAACTTTGGGTGAGTCCGAAACCGATCTGGTTACCGAAGCCTTTAATCCGATGGACGGATTTAGCCCGCA  
AGCCTTGGGAAGCGCGGGGCAAAATCGTCCACCGCAACGACCCCTGCCCTCGCGCAGCGGTTGAAATACAAACAAATGCCACGGCAATTCGGT

## SEQ ID 5890

MPSADLVDTYMPDSMEQNDIPTLENLAAEFRLQEDIQSWLKADNAIDGQDIKERLIERIENYAAKTELVGKQAMADFERNVMLQAIQNWREHLAAMDYLRLQGIHLRSYAQKNPQKQ  
YKREAFMFPQDLWNGIKFHIALSLTSVQIEQNPVAVEEQPVNGIQSIHSESPDIRELLGQSQDVLVTEAFNPDTDFSPLEARGQIVHRNDPCPGSGLYKQCHKLA

## SEQ ID 5891

TTGCCGTAACCGCCACATCCGACCGCCATTCGAAAAATCCCGATTCGTACCGCTCGTACCGAAAAACAGACATCCCGTCCCCCACCATCATGATTCATCCGACTTCATTCGACGAGCTTC  
TGGCCAAAACCGATATTCGCGCATCATCGACGAGCAGGTTCGCGTGA AAAAAGCGGGGCGAATAATATGCGGTGTGCGCGTTCACAGGAAAAAACACCGCTCGTTTCGCGTCACTCC  
GACCAAGCAGTTTATCATGTTTCAGTTGCGGGGCGCATGTTTCGCGGATTCGTTTGTGATGGAACATCAGGAGCTGTGCTTTCGCGAGCGGTTTCAGTTTCGCGACCGCTAGGT  
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ACCGTATCCGAATACCGCTTGTGGTATCGGGGATGTTGATGACAATGAGGGGCGCATACGACCGCTTCGCGCATCGGATTAATGTTCCCATCCGCAATCCGCGCGGCGAGTATC  
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CAGACGCGATTCATCTCAATACGCGAGGAGGCAAGCGGAAATGGTGAAACAGTTCGCGCTTTTGGTGAGATTACGCGCAGCGCATTTGCTTATTTGTAACCAACCGCTTAGCGA  
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AGCGCGCGCGAAGAGATTCGGA AAACTTCCAAATCGGCATCAAAAACTGCTCAATGAGTTAAAAACAGCAAAATTAACCAATTAACCAAAAAAGCGCTCAATCCGCGCTTAAATGAA  
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## SEQ ID 5892

LPEPPHPTAIKPNPDPVPSVPKTDIPSPHIMIPSDPIDELLAKTDIVGIIDBQVPLKKGANYMACCFPHKEKTPSPSVPTKQFYHCFSCGAGSAGFVMEHQGLSFPEAVQFLADRVG  
MIVPKVRGNDNPEVRAERKKQOTLEETAAADPYAQQLKFNPAKAYLDKRLGSAEVLIAHYGLGYAPDQWQPLAQVFPQYPNTALVDTGMVINDGRIHDPFRHRIMFPINRPNQVVI  
GFGGRVLDDSKPKYLNSTPPLFDKGNLYGLYEGRAAVKEAERILVVEGYMDVVALAQFVGVGVAALGTATTAEHVILMRQADSIYCFDGSAGRAKAMRALENALPOLKDDKSLHF  
LFLPEHDDSYIRAYGKAQFEDALLNQSKPLSEYVWEHLSGILHATQESKAELVTSPLLVQITAPALAYLLKQRLSELVGDIDPNLAQLLQEPKPRHVQKNYKLPPIISVKQPVMP  
TLVQRQIRSLILNPDWAAYIDLPLYALDGDFAFLANLAETIKNHPSVPATAQVLEHMRGSPYETINRIFRSALQSEMEGGGEGEDCENFQIGIKLLNELYSQIETLQKSLQSLGNE  
SEKKLLLSLLTAKQN

## SEQ ID 5893

ATGCTGAACAACCGGTAATAACCGCTATGTGGCTGCTGCCGCTGATGCTGGGACATGCTTTTACGCGCCGCAATGGCTGTGGGCTGCATTTTGGCGGCTGATTGCCCTGACCGCTTGT  
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TGTTGTTTGGCATTTTGGCTCGCGCTATGCTTTGTGTTGAGATTCAAAATGGAGGCTCAACCGCGGTTGGCAGGTTTATGCGCTCGGCTGGCTTTGCTCATGCCGTTTGGTTTGGT  
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CACCGGCAATCAGCCCGGCAAGAGCTGGGAAGGCGCAATCGCGGCTGCGGTTTGGTGGCAGTGTACAGTACTGCGGTACGAAGTCCGCGCTGCTGCAATTCGATACAGGCTGCTGCA  
TACCCTGTTAATCGGTTTGGTGTGACCGTTGTGACGCTATGCGCGGACCTGTGGAAGCTGCGCTCAAGCGCGCGGAGGCATCAAGACAGCAGCAACCTGCTCCCGGACACGCGCGC  
GTGTTTCGACCGTACCGACGCTGATTGCCGTTATCAGCGCTATGCGCGGATAATGTCGGTTTAAAT

## SEQ ID 5894

MLKQRVITAMNLLPLMLGMLFYAPQWLWAAFCGLIALTALWEYARMAGLCKETENHYLAATLVGVVAYAGGWMLENLVWYVVLAFWLAVMPLWLRFKWRNGWQVYAVGWLMLPWFPA  
LVSLRPHPDALPLLAVMGLVWADVCAFYSGKALGKHKIAPAISPKSWEGAIGAVCVAVYMTAVRSAGNLAFDTGWFDTVLGLVLTVVSVCGDLLESWLKRAAGIKDSSNLLPGHG  
VFDRTDSLIAVISVYAAIMSVLN

## SEQ ID 5895

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GAGATATCTACACCGATCGCAAGCGCGCTATATGTTCTGCGCGCAACTCATCAACATCGACACGCGCAAAACCTGACCGAAGAACCGCGCGGATTTGAACAAATTCGACTTCGCG  
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CCGACGTGACGCTTTACAGCTTTATGATGCCCATTTGCCGCTGACCCAGATGCCGCGCAAGCGCAAACTTTATGTTGTGACCGCGCGCTGCAAAAGCGTGGACGGAATGGATGCG  
TAAAGGCAAAATCCCGCTCGCGCGGAGCATCTGCGCAAAATCCCGTCCGCGGAAACCTTCCCTTGGCGCAACAGTTCGCGCTTCAACGCGCAGCGGACCTGCTTCCCAACCGCGCGCACC  
CAAGCGGTTACAGCGGATGCGGCACTGAGGAGAAATCATCCGCAAAAACAGCAG

## SEQ ID 5896

MTKLIKILPPTVPLLACGQTFVSNANAESAVKAESAGKVAASLKARLEKTYSAQDLKVLVSVEFPVKGIYBVVSGRQIITYTDAEGGYMFGELINIDTRKNLTTEERAADLNKIDFA  
SLPLDKAIKEVRNGKLVAVFSDPCFPCKRLEHEFEKMTDVTVYSFMPMAGLHPDAARKAQLIMCQPDRAKAWTDMRKGF PVGSGICDNFVAETTSLEBQFGFNGTPTLVFPNGRT  
QSGYSFMPQLBZIRKNQ



## SEQ ID 5897

TTGGACGGCAAAGCGTCATTGCGCTTTCTTCGCGCAGGCGAGTCCGCGATCCCGCTCTTGGTGTTCGCGATCGGTGACGGCGCGAGGTACGCGAATACACCGCCATCCTCGATCCTGTGCG  
GCTGCTCGCCCAAAACCAATCTGCACCTTCAGACGGCAAGACACACCGCAAAACCGCTCCGAAGCAGAGTCCCAAGAAATCAAACGCCAAAGCCCTCCGCAAAACCGGATAAAAAAGA  
CAGCGCAAACTCAGCGCTCAAAACCGCGCATACCGCAAAACCCATACCGTCCGCAAGCGCAACCGCTCAAAACAGATTGCGCGCGCCATCGGTCCGAACACCTGACGCTCGAACAGGTT  
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AAAACTGAAGCAAAAGTTCCGCGCGCCGAAGCAAAACCGCGGCTTCGACCCGAAACCAACCGCGAGTGTCCGAAACTCCGGCTTCGGCGCACAGAACCGCAACCGCGACCT  
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## SEQ ID 5898

LDGKAVLAVSSAQAVRDPVLVFRIGAGAVREYTAILEDPVGCSFKTSALSDGKTHRKTPAKAESQENAKALRKTKDKDSANSVAKPAHNGKTHFTVRKGETLQIAAAIRPKHLFLEQV  
ADVLLKANPNVSAHGRIRAGSVLHI PNINRIKAAAPKKIKABQPKPQAKPAETASMPSEPSQATVEKPIEKPEKPEKPEKPAKVAAPKAEPKPAVRPEKPAVSETPASATERQPGP  
VPAANTAASETAASAPRSPRRFCHRHADRRNR

## SEQ ID 5899

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CGCGAAATGGGACAGGTGCGACCTGCTGACCCGCAAGACGAAATCATCATCGCAAAAAAATGAAACCGCCCTGAAAAATATGTTTCAGGCGCATCTCCGCTGCCCGGCTCCATTGCGG  
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## SEQ ID 5900

MSKNQNHIEYQDDARPLTIEQARLRQLIIMGKERYITYSEINDALFDDMSDADQIDNIVSMISGLGIQVTEHAPDAEDILLSDNAVTDDEAVEEAALSSADSEBGRITDPVRHYH  
REMGQVLLTREDEIIIAKIKENALKNMVQASACPGSIAEILELIEKICKDEIRVDEVEAIIDPNEVLLNELGLHLETTAPEKPSNDSDENEDDESEEDADEISAANLAEIKQKVI  
GHFAQIKDYKKMKICLEKHHSHRKYDYLAYRDALANKLLEVRPATRQIDSLSSLRGKVENIRKLEIREIDICLDVHMERDYPIQNFLEPITNLQWIEEELIARGRVSNALDRPHAILL  
KQTELADMEKETRISIEBELKEINKMVSSEKETAQAQEMIQANLRLVISTAKKYNRGLQFLDLIQEENI GLMKAVDKFEYRRGYKPFSTYATWIRQAITRSIADQARTIRIPVHEIETI  
NKMNRISRQLQETGEEPSAKLAELNOMPEDKIRKIMKIAKEPISMETPIGDDDDSHLQDFIEDANNVAPADAAMTSLHEVTKEILESLETPREKVLNMRFGIDMNDHTLEEVGRQFD  
VTRERIRQIEKALRLKRLHPTRSRLRSLFDSSEKSL

## SEQ ID 5901

TTGAAATTTTGTGGCGCATTTTATGCGTCAAAATTCGTTAACAGACTATTTTTCGAAAGGTCTCGGCTACCGCCCAAAACCTTCGCAACTATAGCCCGCGTCCGCGAACTCTTAAACA  
CGCGACAAACCCCGCGCGCGACTACGCAACCGCTGCAAGCGCTGCTCTGTTGGAATCTGTACGCGGAGTTGTTGGGAAACCGGATGGAGTGTGGGATATGTGAAGCGGTTGTT  
TATTGT

## SEQ ID 5902

LKIFWRI FMRQISLTDYFCKGLGLRAQTLATLAAVRELLNSGQTPPPDYGKRCKACSLVEICQPELLAKRDGSGVGYVEALFIV

## SEQ ID 5903

ATGACCGCACTTTTAAACGAAACCAAGGAAANTCAGGATACGCGCTGATTCCTCTTCGCGCCCTGCAACACTACGCTTCTGCGCGCGTCAATGTCTTTGATTACACAGAACAGG  
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GCTGGGCATCAGCGCATATTTGATTTGGTGAAGTGGATACAAAAACAGCGCGTTCGAACTTGTGAATACAAACGAGGCAAGCCCAACCTGACCCGGGGATGAATCCAGCTTTGC  
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## SEQ ID 5904

MTALLTETQRENQDRILPLISALQHYAFCPROCALIHNEQAWAENYLAQGKALHERVDSDEPCTCKGVRFWTVHVLADKLGISGLDLVEVDFTGRKLPVEYKRGKPKPDGDEIQLC  
AQGLCLEMTGQTVSEALNWMQTRERVPVPSDGLRPLQ

## SEQ ID 5905

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AATTATCTGTGCTGTTGATTGGATAGTTAAAAATTTAGATAGAAATGTTGAAAGTAGAGGATGCTTTAAAGATATTATGATCCATATGATAGAGATGAATGGATAGAAAAAATTTTGTG  
TTG

## SEQ ID 5906

MKYLVGASWGGQGHQDQFFVFNQYVLEWESSQPDQFAKGEKIQVGDRIAIKRMKGSGSEIKILHIGIVKGVISITNKIICVVDWIVKNLDRNVSRCFKSIHDPYDKDEWIEKIFC  
L

## SEQ ID 5907

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CCTGCACATAAATGTTTTCAGCGCGTGAAGTGAACCGGTAACCGCGAATCAGGTACCGCGCAAGCGGTTTGGCGATTACAAATCAGCGCTGTTTCAGACGCGCTAAATGGCGTGA  
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## SEQ ID 5908

VMTTEVNSGQVRGPVQLAFAQSIDPIVPEVSIITRMAVTNEKLEKERTMGRKYIVPYVYRVHCFISANLAATGFSDDDLAKLWQALTMFPHEDRSAARGEMAARKLVVFKHDSALGSQ  
PAKILFPAVKVERVNGSGTPASGFGDYKLSVSDGLNVSVEZYL

## SEQ ID 5909

ATGAAAAAGGCTTGGAAACCATGTTCCAAAGCCTTTTCAAAATGCGCTCTGAAGCCTGTGCGGCGAGCTTCAGACGGCATCTTTGTTCAAACTCAATCTGCGCCAATGCATCTATCGGAT

## SEQ ID 5910

MKKANHVPSLFGMPSEACRGSFRRLCSNLNPAFPHLSD

## SEQ ID 5911

TTGCCGACCATGCGCGTTGCGTCAAAATGTCAGCTTGGATATGTCCAATCTTACGCTGTAGCATGGGATTACCCCTTATATATTGCGTCCCTAAGAAGGGGCGCAATATATAAGGTGTGGC  
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GCAATCTGCAACATTACAACCCCTTGCCTGATGTGGCGATTGTCTAAAGCGTGAATATTTCCGAAACTGGCTGTGCGCGCGCAAAATGTTATCGTGTGATTGAAGGGGCGGCGAGGTG  
AAAAGGCTCTTTGAACCCGTTGCGGAACGTTTGAAGTGTTCGCGCA

## SEQ ID 5912

LPTMAVASNVSLDMSNPVLRMGLPLYIASLRRGATYKVVQFVEDALRAVPADSFEPETAQKLKLFKAGAAITLIFYEDQNVVKGLEBQFPAYAAFPVWADQANAMVQYAVWTTLAAGVAG  
ANLQHYNPLPDVALAKANNIPENWLLRAQMVIGGIBGAAGEKVFEPAERLKVFGA

## SEQ ID 5913

TTGAGCCTTGTGCGTGGAAAAACGCCCGCTCTATTGCGCGCTCTTGTGTCAAACTGCCGTGCTGGGCAAAAGCGAAAAATCCAAAGGCTTGGTAACCGATGCTGCTGAAACGCAAAA  
TCCGTAAATTTTGTGAATCAGCAGCGAAACGAAGCCGTTACGAAATCTACGTCAAGAAAAAGCGTGTGAACTGCAAAACCAACCGCGCTTATGAAGCACTCGGCATTGAGTCTGA  
AGCCAAAACTGCCGGAAGCAGAGCCAAAGCCCGTGACATTACCGCGTGGATGTGTAAACCTTCTTCGATATCCGAACCTTCGGCGCGG

## SEQ ID 5914

LSLVGRKRRRLFGGSCCKLPWCARAKTSKGLVTDVCLRKIRNFVEISSENEAGYEIYVKEKSVLNLQNKRAYEALGIESEAKNRRRTKPKPVTLPFGCVKTSISSEPSAP

## SEQ ID 5915

GTGTTTACGCGCTCGGATGACGAACAAGAAAGCGCAAAATTTCAACGTATTGGAACAATTCGCAAAAGGTGCTCCGCTGCAAGAAATTCGCGCTGAACTCTCTCCCAATACCCGTTTTT  
ACATCTTGGGGCTTGCCTCCCAATGCTGCGCGGATTCTGTTGCGTTTGGCTGGACACCATTTGGGCGAGCTGGCGGAAAACTTGGCGCATCATTTGCAAGATTAGCCCTTGAGCCTTG  
TCCGTGGAAAAACGCCCGCTCTATTGCGCGCTCTTGTGTCAAACTGCCGTGCTGGGCAAAAGCGAAAAATCCAAAGGCTTGGTAACCGATGCTGCTGAAACGCAAAATCCG

## SEQ ID 5916

VFTPSDDEQESAKIFNVLEIQIGKRFQLEIAPELSPNTRFYTLGLAPNAARLSVRFWLDTTFFQLAENLAHMQDLALEPCANKTPPSIWRLLQLTAVLGKSENIQRLGNRLCPEQNP

## SEQ ID 5917

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CGGATGATATAGTGGAT

## SEQ ID 5918

MILASLVRYRYRLATETDETGNPKVPSYGFSEKIGWILVLDKEGRLKTVVFNLTADKKPQPKLMSVPRPEKRTSGIKPNFLWDRKATAYALGVEANKNKAKEKPTTPSEKTFEAPKQYHL  
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## SEQ ID 5919

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## SEQ ID 5920

LGMHLHDIDFDHGNTPHFRTPQMKDLIDVPPFYAEVKA

## SEQ ID 5921

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CGCGCGTGGCGTTATCGGAAGCGAGGCAACCGCGATTTGGGCTGGATGCTGCACGATATTGATTTTGATCAACGCAACACCGCGCATTTTTCGCGACGCAAA

## SEQ ID 5922

LYGSRRLPCAQTADGAQKTAAYKQDPKAVTHYLTRPAGFSDCQRVCDETFDORRLFRPYARSLKQMAKARIRVNRERRRYRKARQTAIMAGCCTLLILITATRRIFSARK

## SEQ ID 5923

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CTGTTTCATCCGGACAAACGCGTTGCGAGTCGGAATAACCGCGCGCGCTGTCAAATAATGCTTACTTTGCGCGGGTCTTGTCTTTGTAAGCGCGGCTTTTTCGCGCGCATCCG  
ATCTGTTTGGGCGCATGCAAAACGCGCGTGCCTACAATCAAAATGTTTGGCGATTTCATGACAGCAGGCATCCGATGCCGCCGACATATCGAGCGGCTTTTGCTATCCGATTTGG  
CGCATTTAGCGCGTAAC

## SEQ ID 5924

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ICLGAWQTAAAVQSKCLAISCRQASCRPTYRAGFCLSDLAAPFPVT

## SEQ ID 5925

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TCAAGAAACAGCTTTAAGTGGGATTGCGCTTAAACAAACAGCAGCGC

## SEQ ID 5926

MAYSADLRNKLHNSGLTKIRTRRAAGSTNGTEPIRALHHLRESFPLSRGGATPYRLLIRYITTDNAKTPAKPQRLTCQETRTGCFALKNKQAA

## SEQ ID 5927

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CGCCCGGCTTGAAGCCCTGTTGAACGCGACGCGCAGCGCTCAGTTTACACGCGCGCAGGCTTGGTTGACGTTGCGTCTGCCGACGAAGTCAGCGCGCTCATGTGCGCATCTGTC  
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## SEQ ID 5928

HPSEASDGIYKVLINTPQVLTILGSTGIGESTLDVSRHPEKPRVFPALAGHKQVEKLAACQDTFRPEYAVVADAEHAARLEALLKRDGTATQVLHGAQALVDVASADEVSGVHCATV  
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## SEQ ID 5929

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## SEQ ID 5930

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## SEQ ID 5931

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## SEQ ID 5932

NTDFADRASEREAEFLVEALAKHQPPSENTAGFSHCEDCGDIPEAKRKAVRGCTRCVVCHEYIQLKTK

## SEQ ID 5933

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## SEQ ID 5934

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## SEQ ID 5935

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TGAGGGCTGGCAAGATGGCACACGAAAGCGCTGTAACATGAC

## SEQ ID 5936

VKRQTKTATVLTALARTACTSTTVPSDTPIKTAVAVRIPVPSGLLVZEYERPERPAGGSPQLLNHAVRYGGYYRKLQIEGWQNWHTKGRLEKD

## SEQ ID 5937

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## SEQ ID 5938

NIEFVRAKRLRLWFLVLLWACGYRYAADKVEABQPTALIAAYRHSSMVAEQYALQLKKAQDERQRWYDFSQKQSTDLAAALSELDKTRNTLQE

## SEQ ID 5939

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## SEQ ID 5940

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## SEQ ID 5941

GTGCGTTCTTTACTCCAACATGCTTATGACAGCTGGTTTATGACAATATATACAAGCTGACCGCAATGTTCCAAAGCAAGCAGAGCGGAAGTCGCGAAGAGCATGGCTTTGATGGA  
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## SEQ ID 5942

VRSLIQHAYAEVLVDNIYKPDGNVFKQAREVAKSMALMETTDDLSRTLAILKEANQPQELLPLSOLYQKEIGLVPEVDKNTMIFLETQSSISQSSILSDIRSLINEKKYIAKRIK  
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## SEQ ID 5943

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CGTACGTTTGTGCACTGCTTCGCGAACATATTCAAATAGTTTGTGAATCATTTGAATCTCATCTCAGTGAAGTCTAAAGTTTCGAAAGATTTCAGATGAAATTCAGCAAAATCCC  
AAAGCAAT

## SEQ ID 5944

MSDIDDFKSYLESHQAAPFSAWGRFVAKIQLSNVISPVPVANFLKLEAKPGVKEISSALAKIGRKNYTSPTQMTDLVGVRVALLAEHIQIVCEIIESSSQWNAKSKDFADEIQONP  
KAI

## SEQ ID 5945

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## SEQ ID 5946

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## SEQ ID 5947

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## SEQ ID 5948

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KVSNG

## SEQ ID 5949

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## SEQ ID 5950

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## SEQ ID 5951

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## SEQ ID 5952

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## SEQ ID 5953

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TTAC

## SEQ ID 5954

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## SEQ ID 5955

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## SEQ ID 5956

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## SEQ ID 5957

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TCGGCGCATCGTTATCGCGCGGCTGCGCTGTTGACCGGAATCGGCATCGCTTCGCTTATGCTGCCAATAGGCAAGCAACCTCAATCCGATAGATGCAATTCGCGCGCAGGAT

## SEQ ID 5958

MSLIECKNINRCFGSENRVHILKDIISLSIEKGFVALIQSGSGKSTLNNILGCLDTAGSGSYRIDGIEPAKMQPDLEALARRRRFPIFQRYNLSLITARDNVALPAVYMGMGKES  
ARADKLLQDLGLASKEGNKPGELSGGQQRVSIARALMNGEIIPADEPTGALDTASGRNVMIRLIRLHAGHTVIMVTHDPGIAANANRVLEIRDEIISDTSKNPEIPASNVRIRKKA

SNFYYDQFVEAFRMSVQAVLAHMRSLTLMGLIIIGIASVSVVVALNGSQKILEDIISMGNTTISIPFGRGFGDRRSKIRITLIDDAKIIAQSYVASATPMTSSGGTLYRNTDLF  
ASLYGVGBQYDFVRGLKLETGRLFDENDVKEDAQVVVIDQNVKDLFADSDPLGKTLFPRKPLTVIGVMKIDENAFGNSDVLMLHSPYTTVMHQITGESHTNSITPVKIDNANTRVAREK  
LAELLKARHGTEDFPMNNSDSIRQVESTGTMKLLISSIALISLVVGGIGVMNIMLVSVTERTEKIGIRMAIGARRGNILQOFLIEAVLICIIIGLVGVGLSAVSLVNFHVPDIPMDI  
SAASVIGAVACSTGIGIAPGFMPANKAALNPIDALAQD

## SEQ ID 5959

ATGAGCCGTCATCCCTGCAACAGGCTGCCGAAAGCCCGCTTCGCTTTATTCGTTAAATAAAACCTGCCCGTTGGCAAAGATGAATCGTCCAAATCGTCAACACGCGCTTTGCACA  
CACCTTTTTCGTTCAATTCCAATCGCCCGCTGCTGCTGTTTGGCGAAGAGCATGACGAGATACTACTT

## SEQ ID 5960

MSRQSLQQAESRRSVYSLNKLFPVGKDRIVQIVHAVLHTPPFSNSQSAVVVLPFGHEDEILL

## SEQ ID 5961

ATGTTTGAGCCGGGACGCGCTGATCATCATCAAGAGCATACGCCGATGGCGGTTTGGCGAAATCGCTGAAAAAGAGTTGGCTCGACGGCGGGAATCCAAAGAC

## SEQ ID 5962

MFEPGRALIIIEHTPHGRFAKIAEKELASDGGNPKD

## SEQ ID 5963

ATGGGCGGTTTGGCGAAATCGCTGAAAAAGAGTTGGCTCGGACGGCGGGAATCCAAAGACTGATGAATGCCACCTCGCTTTTATCGACCCGAAATGAAACAGCGCAGCC

## SEQ ID 5964

MGGLPKSLKSNPTAGIPKTDCHPPYRPNETSAA

## SEQ ID 5965

TGGAAGTCGGTATCCGCTCGCAATCAGCCGATTCGCGGATATGTCGAGCAGATGGCGGCGCAGCGGAGGCGCATGGATTTGACCACCGCGGAGATGGTCGGCAGCTCAATCAA  
TTATTTTGAGTACGAGCAACTGCGCGAAGCTATGCCCTACCGACCGAAGCAACCGGAGCAATGTCGCGAATGGTTGGCGGTTGAAACCGGAGAGGCGATGAATCGCGCAATGAT

## SEQ ID 5966

LEVGTIRSIIRLDMFQMAAHGEAHGDFHRAKMGVTLNQIILDCEQLRESYALPTEADNPVEMLGGETGEGDESGND

## SEQ ID 5967

ATGAAACAAGCGCAGCTTAAGCTGATGACGTTGGGCAAAATCCAAATCGCTCGAGCTGCTGGTGAAGACGACGACACTTTGTTGGAGCTTGCCGAAGGCGGTGAGGTCAACGGCAACACTT  
TTGACGATGTCGACCTATGACTATTAAGGAGCTGCGCGTGCCTCGCGGAAAGCCGTGAACCGCGGAAGCGAAAGATAAGGTGATTCGCGATAAAATAAAAGGTGATGAGCTGGC  
GGAAAGCTGTGCAAAAGCAGACGGGTGTCAAAGAGCTTAAACCTGCGGATGTGGGATGAGCTGACGATGACGCTTGGCAGCTTGAAGTCCGATCCGCTCGCAATCA  
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## SEQ ID 5968

MRQAQPKLMTLGSKILLELVEDDDTLELAECEVNGNTFDDVDRMTIKELRVALRESRETAERAKDKVLIADKXKVDLEAEKLSKKQTVGKEPKPADVGIETLMQLSLPANKSVSARKS  
ADCAICSSWRRTARRMDLTARRWSARSIKLFWTASINCAKAMPYRPHRQTMCRNGWAVKREKAMPNAMIERLKAIVENQAEAMGRGARSAYLKQQAQELGISLATLYRLEAVSVKPTRK  
RRSDAGTELKPEEAKLISAVLAEMRRNGKRLMPVRQAVEMLRANGKIEAARIDGETGEVIPLESENTITRALREYKLSHSDQLLPDPVSRMKSHPNHCQIDPSLCVLYCLPRQKDTG  
LRVMKEBEFYKXKPRVVKIENDRVWRYTGTDSAGTISVRYYPGGETSANLCPFIYMQAKDICKDPPTVPRMVMIDPGSANTSAPFKNLCKPLDVHVQINKPKNPRAKQVEKAND  
IVETAFESGLRFTVEHDIDQLNALSERWMRYNGTQKHSRHGHTRYQAWNKIKPEQLILPPEAYCRELAVSAPKEAKVSADLEIRFGGRVYSVKGIRGILVGGKVLVGGKVLVGNPWEA  
NGARVATYDAEGNEVWSVPEVVFDEMGFKADAAGVIAEYKAPADTQDRHRKELDKLAMGAETLEAAAKRKGKAVFPFGKIDPYKHQEDTLAASNTLPHPRQGGQMDYNKNEVABQVLS  
KVEIAKRLKPRVEADGGDMQAVSVILKHYPESVTEGRLEAPERTTRCRKLKLLKTG

## SEQ ID 5969

TTGCCGACGCGGTTTGGCTGCGCTGTCGCTTTCGCCGTCGCTCGCGAGGACATCGGCAAGCAGGTTGGTTTTATAGTGAGTAAATTTAAACCGGTACGGCTGCTCGCTTGCCTG  
CTATTTGACTGCTGCGGCTTCGCGCGCTTGC

## SEQ ID 5970

LPTRFACRVGLPVRPEASDKQGGFYSGLNLRVGVASPCRTICTVCGFAALS

## SEQ ID 5971

ATGCCCTCGGACGCGAGCGGCAACCGACACGCGCAGCAACCGCGTTCGCGCAAAATGCGCTGAAAAAATTCAGACGGCATCTTCAGACACATTACCTGCAACCGGCAACACATTCCAAT  
CCAGACCGATCAGGCAATCAATACGAACGGCTGTTTACATACTTACACGCTTTCACCAACCGGTATCGATT

## SEQ ID 5972

MPRDGRNRHGTQTASAKMPSEKIQTASSDTLPANGNTFQSRPIRQSIRTAIVYLTFHQPVSI

## SEQ ID 5973

ATGGGCGGCGCATTTGAAATGGATGACGGCTTGGTATTTCGATAAAGATTACCGGATGTGTTTAAAGCGAAGTTTAAACCGGACAGGAAAAATTAAGGAATCGGT

## SEQ ID 5974

MGGALENDGLWYFDKDLDPVFAKFKTDRNLIKRIE

## SEQ ID 5975

TTGATTGGTCAATACCGAGGAAGTCCGTTTTTTTTCCCGCATGGGCGAGCTGATGATATAAGATTAAAGCGGAATTGGTGGAGCTTATCATTCGGTGTGTTATGATCTGCCAAA  
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TAAAAAGGCGGAGACGGGCTTTGTCGTCGTCGGCGGAAACATACGGATTGTGTCTGCTCAGCGGATATCTTCCGGAACGGTTATGCAGAGGATGAGCCTTGTCCCGTATATGTTTCA  
GGCCGATCGCATAGGCGTCCGGCCGTTCTGACGAACAAGTTTGGCGTTTGCACACAAGTTGCTGTTTGGATTGGGGAAAAATGCATGAGGTGGAATTAACGGAACCGATCCTTTAA  
CGGGGAAAAAGTCTGCTTCGATGGAATGGCGGGCATTGGAAATGGATGACGGGCTTTGGTATTTTCGATAAAGATTACCGGATGTGTTTAAAGCGAAGTTTAAACCGGACAGGAAAAAT  
ATTAAGGAAATCGTTAAATCGATACCGGTTGGTGAAGCTGG

**SEQ ID 5976**

LIGAIRRKSVFFPALGSLHAYKIKABELVGRYHSGCYVSANILLRTFTTVRFEKSGDMLNAKTAALKNGVTNPPPTGLFANKKAARRALSSWAETVGLCPASAGILPDGYAEDRCPVYVS  
GRCDKACGRSDQVLAFAPHLFVLWDGKMHVEVETITDPLTGEKSFCEWAAHWMKMTGFGISIKIYRMCLRRSLKRTGKILEKSVKSI PVGESW

**SEQ ID 5977**

ATGCCCGGACACGGCGCAAGAGCGGGCATTATTCGGCACACTGCGCTGATACCGTCCGAACACCGTTATCAAGGAAAAACCATTTGCAAAACCTTCTAGCTTTTATCTTCGCCATCCTGGA  
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GCCATCGTCGCGCGCGGTCGCTGACCAACCTCGCACCTGGCGGTTTGTCTGTACGGACTGAGCTTTTCCTTCGCGCTAACCGAACTGCGGCCCTATGTCGGCAGACATCGAAACCGCACCA  
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CGGCTTCGTCGCGACCGGACAGGCGTGGGACGCGCAATCCGCCGAGCTACCGTCCGCTGTTGTGTCGCGCATTCGGCATGCGGCTGGGAAAAACCGTTTCCACTCGTGGCAACCC  
CTCAAAATTTTCGCAAACTAATCAGCGGCAACGCTCTGTGAGCCATATTTCGGGCGCGTACCATTCGCCGACATTCGCCGAGACTCGCGGAACTCGGCTTCGAAAGTTATTTCGAAT  
TTTTCAGCGTTGTCAGCATCAGCTTCGGCGTGTGAACCTGTCGCCGTCGCCGTTTTCGACGCGCGGACCTCGTGTATTACTGTGCAATGATACGCGGCAACCTTTTGGCGGAACG  
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**SEQ ID 5978**

MPGHAHRKRLSARCACTVTRPLSKENHLQTLALFIFAILILVSLHEFGHYIVARLCGVKVRVPSVFGKPPFTRKRGTENWCLAPILPGGYKVMVDTRGEVSEADLPYAFDKQHPAKRI  
AIVAAAGPLTNLALVLLYGLSPFSGVTELRPVVGTVEPDTLAARTGPGQSGDKIQSVNGSVQDWSAQTETIVLNLEAGKVAVGVQTASGAQTVETIDAAGTPEAGKIAKNQSYIGIMPPFI  
TTVAGGVEKGSFAEKAGLRPGDR/LTAADGKPLASWQEWANLITRQSPGKIKITLYERAGQTHADIRPDTVEQPDHLLIGRVGLRPQPDRAWDQIRRSYRSPVVRPAGKWEKTVSHSWTT  
LKFPGLKISGNASVSHISGPLETIADIAQSAELGLQSYLEFLALVLSISGLVNLFPVLPVLDGHLVFTTVIEWIRGKPLGERVQNI GLRPLGLALMLMLMAAFAFNDFVRLIG

**SEQ ID 5979**

ATGGCAAAATGATGAAATGGCGGCTGTTCGCGGCTCGCGCGGCGAGCGGTTGGGGCGGATGTTCTTATCTGAAGCCCGAACCGCAGGCTGCTTATATTACGAAACCGTACAGGCGG  
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AAAGGGCGATTGATTCGCGAAATCAATTCGACACGAGACCAACAGATCGATATGAAAAATCCAAATTCGAAACGATATCAGCGGAAGCTGGTTCGCGCAGATTCGATTCGGCGAGC  
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CTTTAATCAGACAGGCAAAATTTCCATCAATACCGCGAGTCGGATTTCGGCTACACCGCATTAACCGCAGATGGAACGCGCAGGCTGGGCGATTCCCGTGAAGAGGGCGCAGACTGT  
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ACGATTTCGCGCAACCGGATACCGCGATTAAAGCGAAGCTCGACAGCTCGACCCCGGCTGACCAAGATGTCGTCGGCGGCTACACAGCAGTACGGATACCGCTTCAATCGCGTCT  
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GAAAAATCGCGCGCGCAAGCGGTTCTGACGCGTGTGGGTGCGGACGCGCAAGCGAGTGAACCGCGAAATCCGCGACCGGTATGAAAGCAGTATGAATACCGAAGTGAAGCGGGTTGAA  
GAGGGGACAAAGTGTTCATCTCCGAATAACCGCGCGGAGCAGCAGGAAGCGCGCAACCGCCCTAGGCGGCGCGCGCGCGCA

**SEQ ID 5980**

MAKMKWAAVAAVAAAVWGWWSYLKPEPQAAIYITVRRGDISRTVSATGEISPSNLVSVGAQASQIKKLYKLGQQVKRGDLAEINSTTQNTIDMEKSKLETYQAKLVSAQIALGS  
AERKYKRAALWDDATSKEDLESAQDALAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVAIVVEBQGTVNAAGSTPTIVQLANLDMMLNKQIAEGDITKVAGQDISF  
TILSEPTPIKAKLDSVDPGLTMSGGYNSSTDTASNAVYYARSFVFNPDGLATGMTQNTVEIDGVKNVLLIPSLTVKNRGGKAPVRVLGADGKAVERIERTGMKDSMTEVKSGLK  
EGDKVVI SEITAAEQESGERALGGPPRR

**SEQ ID 5981**

TTGTTGTTGAAATTAAGAGATAAAATGATTGTTGTTCCCGCTGCGCCCTGCTGGAAAAAGCGGTTTTTACGGTTTGGAAATGCTGTGTCGCTGGTTGATTGGAATCGACGGCGCGCA  
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GGGATTTTCAGACCGCATGTTTCCGACGCGCGGCTGTTGCTGAAATTCGCGCGGGTTGTTTCGCTGATTGAAGGGGTGCGTCTGGTGGCGCACACAGCCGTTTCGACTATACGTTT  
TTAAAGCATGAGTTTCATCTGTCGGGTATCGGATTTTCATCGCTGCTTTGTGCAGTGTGCAAGCTTTTCGCTGCGGTGATCCGCGAGTTTACAAGCAGACGCTGGACGGTATCATCGAA  
GTTTGGGGATGTTGTGGAAGACAGGCAATCGTCGATGGCGGATGATCGCGGTTGTGTGATTATTGGAATACAGCTGTGCGGCACACGGCTTGAGGAGTGGAGCAGGCAAGTTTCCG  
TTTGACGAATCCGAACCTTTTCTGCGCGCTTCCCGAAGGTTGAGGGAACAGCTGTACGCTTTGCGCGCAGGTACAGGTGTGCTGCTGTTTCGACGCGCGGGGAAAAATGAAATAT  
ATCGGTACGTTTGAACGCGCATATGCGGAGGTTCGCGCTTTGTGGAATTCGCGGAAAAAGCCCGCTT

**SEQ ID 5982**

LLPEFKENKMTVSRVPLLEKAPLRPGMFVAVVDLESTGGNLYEDRVTEVALVFGQGRAERYEWLVNPQKPIPKFVAELTGISDGMVADAPVFAIAGGLFVSLKGCVLVAHNSRFDYTF  
LKHEFHAGIGFSSPALCSVLQSRRLYPQFYKHSLDGIIERLGLVVEDRHRAMADVSALCDYLEYSLSAHGLEWRSQCRLTNPKLFPALPERLRQLYGLPDGTGLVACPDGGGKVNY  
IGTFERAYGEVAALLDSGKAPV

**SEQ ID 5983**

TTGCCCTGCGCTTCCGCTACTATTGTACTGTCTGGGGCTTCGTGCGATTGCTCGTATTAAATTTAATCCACTATATTGAACGACACCCGATCCGTTACGGGATATCGGTTTGCATGGC  
AAAAGTTGAATATGATTGATTAAGTCTGAGATTCTGATGAAGTGGTAGGTAAAGATATGGTAACGAATTCGCGAGGCAATAAAAAATCCCGAGGATTATTTCGGGATTTGGAATCT  
GGCACGCCACCGGGAATCGAACCCCGTTACCGCG

**SEQ ID 5984**

LPRLAVFLVSGASSHCPDLNLNLIHYIERTPHFVTVGRFAWQKFEYDSITSEILMKWVGKDMVTNCRGNKPNRGIISGIWNLARPRGIEKPLPP

**SEQ ID 5985**

ATGAAAAATGGTTTAAATGTTTGTAGAACATTACTCAAATTTGGTATTATACCTCTAAATATTGCAGTGGTAAACAGAAAAAGCAGAAGGAGCTTTGGAATATGCTGTATATCTGTACCA  
TCGGACAAAAATATAGTGGAT

**SEQ ID 5986**

MKNGFNCPRITITQIWTYTLNIAVNNRKAEGALEYAVISVPIGQNIVD

**SEQ ID 5987**

ATGCAGAAATATTTTACCGCTTTGATTATTCGTGGAAAAATCCCTTATTCCTCATCTGCAAGCGGATATGGGGTGGTGTTCGCGATCGGGTTTATCCAGCGCGGTGGCGGTGAAAAAG  
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AATCCAAAAAGCCAAAAGTGTCTCAGAGGAAAAAGGACTGATTTCGGTCAACGTGATGAAGCGGTCGAAGACCACGCGCGTATGTCGCGCAGGCTTGGAAATCAGGGCGGATGCGGTC

GTGATGGGTGCCGGCTGCCCTTAGACCTGCCGAAATGACCGAGGGCTATCATAAGGATGTCGGCTGCTGCCGATTCGTCCGAATCGCGGGTATTAATATCGTCTTGAAACGTTGGA  
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GTTTCCGCGCGCGCGGTATCCGACCAATTCCTAGACAGCTATATCAGGCGGAAGGCAAACTTCAGGCAAAACGCAAGCGCCGCGCGCTGTACCAAGGTTTAAACTGCCCTGAC  
CAGCTGCCGTCTCGCGAGGGCTTTCCAAAGCAGGCAATTCGTATTGATATCCAGCTTCTGCCGATTCCTGGAGAGGTTGATAAGGGGTGTGTTTTTCAGGGGAAAGACAGCTT  
CCCTTCGGTAATGCCATCCGACCGTCCGCAACGATACAATATCTGCTGACGGGAGCGAACCCTGTTGCAACGCTCGGACGC

## SEQ ID 5988

MONIFDPLIIRGKSLPIVQGHGVGSASGLSSAVARENGIGTASVDLRHLHEDLLAESQINPSEKYSLNCTALDREIQKASASEGKGLIIVNVMKAVKIDHAAYVRQACESGADAV  
VMGAGLPDLPEMTEGYHKDVALLPILSESRGINIVLKRMMKGILPDAIVVEHPAHAAGHLGASTVEGVNDKFDPKRVIRETFEVPKNLGLEGEKIPILLAGMANPEKVKTALKNWA  
SAVQIGTAFATVEEGDAHLNFKKTLASAETEKVVEFMSVAGLPARGIRTKPLDSYIRREGKLQANAKDPRRCTQGLNCLTSCGLRDGLSKAGQCIDIQLAAAFRGEVDKGLFPRGDKQL  
PPGNAIRTVRETIQVLLTGSEFVATLGR

## SEQ ID 5989

ATGCGGTCCGAAGGGCTTTAGACGGCGTTTTCAGGTTGTGTTCCGGAACAGTGTGAAAAAACGAGAGAAATAAAACGTTTATATA

## SEQ ID 5990

HPSEGLSDGVFQVVRNVEKTERNNVFI

## SEQ ID 5991

TTGCAAAACAAATGCCGTCCGAAGGGCTTTAGACGGCGTTTTCAGGTTGTGTTCCGGAACAGTGTGAAAAAACGAGAGAAATAAAACGTTTATATGAACAAATGCCCTCCGCA  
TTATGTCCGACATACAACAAATGCCGTCTGAAGCTTTTCAGACGGCATTTTTCAGGCTGCCCTTTCCGAA

## SEQ ID 5992

LQTKCRPKGTAFPRLCSTGVSKRRREIKTFLYEQNAFRIMSDIQHKRLKPPRRHPSGLSE

## SEQ ID 5993

ATGCGGTCTGAAGCCTTTTCAGACGGCATTTTTCAGGCTGCCCTTTCCGGAATGATGTTAAAAATAAAACGGATGAGATACATTTATTTTCGTCCGCAAAATCAGACCATCAGCCGGA

## SEQ ID 5994

MPSEAFQTAFFRLPFGMLKNKRDEIHLFSSDKSDHRAE

## SEQ ID 5995

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## SEQ ID 5996

LLYANSGRHCLITRRDGLICRTKINVSHPVYPLTSPKRAA

## SEQ ID 5997

GTGCTCAAAACAATCAATCAAGCCTTGGTACAAACACGCTGCGCGTGGGTCTTGATGGCGGGGCGGATTTTGTGCTCATGCCAGCGTCCGTATGTTTTTGTGCGGCAGCAGCAG  
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GAATCGGCAAAAGTGTGTTGCGGGCGGAGTTTTCAGCGCAACAGCCTTTGAACCTGCTGCTGATGACCCGACCCGCAAGGCGGACGATCAAAACGCTCCGCTCAAGCCGCTCGGAGC  
CGCAGAACCGCAGGGCGGAATAGGCGGTGTTCAAAACCTTCCGCGGCAACCACTGGTATGTCGGGTGGAGACCGCGGAGCGGTGTCGGCGTCCGAGAACAAATGGATTACCA  
GCCAGGGCAATGCGGTGATTTGACCCGATGGACAAACTTTCAATATGCAAGGAGCAAA

## SEQ ID 5998

VSQNPIKPKYKHWVFWLHAGPIFVVIASVAMFFVAQHAATDLVTDYDKGKHIDIQLHREBAVRRIHVQVLI SPDMAAKVFGGEFDGKQPLNLLMHPTRKADDQTVALKPVGS  
AQNGRAEYEAIVFKTLPANHWYVRVEDAAGVNRVENKNWTSQNAVDLTPMKLFPNAGSK

## SEQ ID 5999

TTGTACATAGCGGGAATATATTTGGGAAAGCGGATTTCTCAAACTTGAAACACAATGCCTTAAAAAACAAGAAAAATGACGCTGAAAGCAAAACCGCGCGGTAAACGGCAAA  
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TCCGCGTCCAGCGTATTCATCAATCCATCCGAAGGCGAAGCATCCATCCCAAAAGCGGAAGGACGGTTCGCAAACTGCGTATCGCGCGGTATTTGGCGGACCGAGTTTGTGTTTAC  
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## SEQ ID 6000

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AACIDACDEIMDKMGYPGGLIRYTTESALEHEYAEKDIKKRLLRPVAGYAVLAVVAAFLVGLSTRKMEVDILKDRGVMVRENAKHLENAYSLRIINNSEKEQLITASVRGFDIAL  
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## SEQ ID 6001

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## SEQ ID 6002

LYNFMRRPDLGEYISHFHQNALILPHRPNKIKILLKND

## SEQ ID 6003

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## SEQ ID 6004

MLSRKGRTRGKAAAGGGRGRIPLRAKPAIIPFEIKRYLCAGLLIAPVVELAPAVLPIRGCLFF

**SEQ ID 6006**

**SEQ ID 6007**

**SEQ ID 6008**

**SEQ ID 6009**

**SEQ ID 6010**

**SEQ ID 6011**

**SEQ ID 6012**

**SEQ ID 6013**

SEQ ID 6014

SEQ ID 6015

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SEQ ID 6016

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SEQ ID 6017

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**SEQ ID 6018**

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SEQ ID 6019

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SEQ ID 6020

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SEQ ID 6021

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SEQ ID 6022

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SEQ ID 6023

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SEQ ID 6024

MKKPTDITLPLQRRRLCAAGALLISPLAHAGAQREETLADVASVMRSSVGSVNPPLVFDNPKGEGERNLSAMSARLARFPVDEGERRRLLVNIQYESSRAGLDPTQIVLGLIEVESAFR  
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SEQ ID 6025

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SEQ ID 6026

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SEQ ID 6027

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SEQ ID 6028

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SEQ ID 6029

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SEQ ID 6030

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SEQ ID 6031

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SEQ ID 6032

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CRQSE

SEQ ID 6033

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SEQ ID 6034

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SEQ ID 6035

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SEQ ID 6036

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IPSIL

SEQ ID 6037

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SEQ ID 6038

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SEQ ID 6039

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SEQ ID 6040

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SEQ ID 6041

TGTGTCATCGCGCATATTGTTGTGAACACCGCCCGGAACCGGATATAATCCGCCCTCAACATCAGTGAAAACTTTTTTTTAAACCGGT

SEQ ID 6042

LFRHIVLKHREPEFDIRPSTSVKIFFLFG



## SEQ ID 6043

ATGGCGGATGAACAAACCGGTACGGGTGCCCCGCCCGGCTCAAAGGGAACGGTTCCTTAAGCGGTCAAGCACGGGGGAACGGTTCGGTACCATCGTACTGCTCGGCGCCGCT  
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## SEQ ID 6044

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## SEQ ID 6045

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## SEQ ID 6046

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VEKDFK

## SEQ ID 6047

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## SEQ ID 6048

LRLFEILPHAHENLRIFACVKTPIAADPQIABIELRRKALPRDFVVRQVCLIFVVFAREAVHNCFGCIKSPAGIAQVCPQQAVERFDRADTQTLADGSLFRLFRHVVRVPTAVRQ  
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ARHAQAVQTVCILRQAVGGFRPASARKFNRFGRSVVYSGLTIRTRRAAGSTGTEFVRVPLGRLEPPPLSRGGATRTGFCSSAILC

## SEQ ID 6049

ATCGCGTCCGAACGTTTTCAGACGCGATTTTGTGCTGCGGAACATACCGTGGCAACATCCGTGAGCAGAATCAAAAACAGCGCGATCATTTATTGTCAACGCTGCGCGCTCAGAG

## SEQ ID 6050

MPSERPSDGIPTCRKHTVGNIREQNKQKPHLLSTPAPSE

## SEQ ID 6051

TTGGAACCAAAATCGACGAGGCGAGGATGTTTGGGGATTTGGTGTCTAGCGGGAATACCGGTGGGGGAAAAACGCAATGTTACTCTGACGCGCGAGCGGTTGACAAATAA

## SEQ ID 6052

LEPKSTEARMFAGLVVMDTGGGKTQCYSDGAGVDNK

## SEQ ID 6053

TTGGTTTCCACAGTTTCCGCTCCAGATTTGCGAAAGCAACACGAGCAATTAAGTCATCGATTCTTCAAAACAGATGGTCCGTTTTCGCGCGGCTTGGACGAACAGAAAAACCTCA  
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CGCAGATTTCTTCCCAAGGCGAAGCGGCACTGGGTTTCCCATCGAAATCATCGCGGGCGCAAGAGGCGCGGCTGATTATACCGCGGTGATCCACCTTCCCCCTCGCGGGC  
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GCAACCTTTATGACAGCGCTTGTATGCCAAAACTTACGGTTCAAGAACTTGCCTTGTGGCAACAGTATCTCGGACGCGCGCGCGCTGATGAAATCGGTTTGGACATCGCCAC  
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GGATACGGAAGCTCGCGCTTACCTTGGTATGACAGTAAATGGTGGAAACGCCACCCCTGATTGCGGACGATGGAATATGAAAGCGTCCAATGGCAAAAAATCAATATGCGGTT  
AAAGTTGAAGCGTC

## SEQ ID 6054

IGSNFRLQICKSNQGLKVIDSPKQVMPFAAGLDEQKXNLSTSSQEQALDCLAKFGERLGRFPEQVRAVATNTFRVAKNIADFLPKAALGFPLEIIAGREEARLIYTGVIHTPLPCGG  
KMLVIDIGGGSTFVIGSTLNPITTESLPLGCVTYSLRFQNKITAKDPQAISARNEIQIRISKNMREGWDFAVGTSSAKSTRDVLAAEMPEADITYKGMRLAERI LEAGSVKAK  
FENLKPERIEVFAGGLAVMMAFEEMKLDRTVTVEAALRDGVFYDLIGRLNEDMRGTVAEPQHYHVSLNQAKRTAETAQTTFMDSLCHAKNVFVQELALHQYVIGRAAAALHEIGLDIAH  
TGYHKSAYILENADMPGFSRKEQTILAQLVIGHRGDMKMGIGIIGNEMLWAVLSLRALALFCRSRQDLSFPKNMQLRTDTSCGFTILRIDSKWLERHPLIADALEYESVQWQKINRPF  
KVEAV

## SEQ ID 6055

ATGCGGCTGAAGCCCTTCAGACGCGATTTGCGGCAACATCCGAAGGAGTTTACCATGATCCGTTTGACCGCGCGGTTTGGCGCGGCTGATCGGTTTATGCTGCAACACAGCGCGC  
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AAACAGGCGGATTTGAAGAAGACTACAACCTCCGCGCAACGAAGAGTTTGCTCCCTCCAGCAAAACGCGCAACCGCGTATGCTCAAAATCGCAAAACAGGAAGTTTACGATGTCATT  
TGCAGGACGTTGATTACGTCACACCCCAATACGACGTTACCGACAGCGCTATTAAGAAATGAACGCCCGC

## SEQ ID 6056

MFSEALQTAFRGNIRRSFTMIRL/TRAPAAALIGLCTTGAHADTFQKIGFINTERIYLESQARNIQTLDGEFSARQDELQKLRGLDLERQLAGGLKDKAKQAEEKWRGLVEAFRK  
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## SEQ ID 6057

TTGAAAAGGAGCGCAATCATGAAATGCAGGAGTGTGTGTAATAAAATGTAGCGGGGATGTGGAAGTAGTCGAACGCGAGGTTCCGCCCTTGAATACGGCGAGGCATTGGTCGAAG  
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## SEQ ID 6058

LKRSALMKQAVVVNKNVAGDEVVEVREVRPLEYGEALVEVEYCGVCHTDLHVAAGDYGEKPGRVLGHGIGLVKEVADGVNKLKVGDRVSIAMLPQSCGSEYCNTRGRETLCRSVLNAGY  
TADGGMATHCIVSADYAVKVPPEGLDPAQASSITCAGVTTYKAIKVSGRVPGWIAIYAGAGLGNLVQYAKKVPFTHVVAIDINDRLAFKGTADLVVNAKEDAAKVIQKRTGGAHAA  
VVTAVSAAAFNSAVNCVRAGGRVAVGLPFESMDLSIPRLVLDGIEVVGSLVGRKDLBEAFQFQAGELVVPKVLRLALDEAPALFQEMREKKTGRVIMDKKBCGCDHHH

## SEQ ID 6059

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## SEQ ID 6060

MEYTLFLSKVFRVQVQSGPFRADALGISTAMASHVSHLENTVQAKLLHHNSRNLSTZAGEEYRQCSYALDITDDAAQKAAGTEKPGQLLRVIMPLWFGSQICNWLAEYRERYEV  
ALELILDNRRVDLIAEGVDLALRVSTLSPSLIARPLARIEFALLASPDFLRNGVPTPEVAGLPAVLPTTITNQKLDLTRKSDGKKYRLLELTPVIRTDNTIMMREMIKAGACIGVQPL  
WAAEHLRCCPLRVLLPGYAVPTDRLNAVYADRAFLSAKVRSFIDFLNEKIASRKGCRNAV

## SEQ ID 6061

CATTCCGAATCTGAACAGGATCAAAGCGGACGACCCAAAAAATCAAAGCGGAACAACCCAAACCGCAAGCGGAAACCCAAAGCCGAAACTGCATCCATGCCGTCTGAACCGTCCAA  
CAGGCAACGCTAGAGAAACGATAGAGAAACCTGTGCAAAACCGGTTGAAAACTGAAGCAAAAGTTCGCCGCCGGAAGCAAAAGCGGAAAAACCGGCGGTTCGACCGCAACCCAAAC  
CGCAGTGTCCGAACTCCGGCTTCGGCGACAGAACGCCAACCCGACCTGTACCCGCTGCAAACTGACCGGATCGGAAACCGCTGCGGATCCGCAATCCGCCCCCAAGAGCGCGCTCTG  
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## SEQ ID 6062

HSEBQDQSGSTQKQSGTQYANGETQSRNCIHAV\*TVQTNGRETDRETCRKTG\*KT\*SKSCRARSKSGTGRSTRQTQSRVNSGFGDRTTPTCTCRKYCRIGNRCIRIPPKPPL  
PSTRRTKPTPTFPNLLRKPVKLPNPLNLSNRFLPKKPKADCLTVCSAVRTPCCLPAEABH

## SEQ ID 6063

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TGGCGTAGCATTTGTGATAAAAGCGGGTCAATGTTAGAAATGAAGTGTATGACGCAATGATTTGATCGGCAAGGAAACAGTCCAAACCTAAATTTGTGCGCGTGAAGAT  
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## SEQ ID 6064

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IQQFVQYAKIAEQAGFGVQIYAVHGYLISQPLSPHNRRQDQWGSLENRRFLLETTTATRAAAGKDFLVGVKINSADFKGKGDESESVQVQKLSWGLDFIEVSGGNYESPQMLAA  
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IAENFAGKR

## SEQ ID 6065

TTGGTTGCGGCGAGCGGCATCTCGTCATTTTTCGCAAGGCAAAATATTTCGCGCGCTTTCATTTTGTCTGCGCGCTTCTGAGCGCGGTGCGGAGCTTTGTTCAAAGTGTCTTTA  
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CGGCAAGCGGAGACTGCGCGGAGAGCGGAGCTGTCTTAACTTCGAGCTCAACGCTTGGCGCGCTTCTTAACTTCTCTTTTGGCTTCTTTCGCAACAGCTGCCAAGCGAGCGCG  
CATCATTCGCGCAATCAA

## SEQ ID 6066

LGRQAASRHFQCGNKLPGGVPHVCRFLSRVGSFVQSVFSRPAFRFPFGPCRVPFGFSYSLGTCLCISRSIFDLAPRFPDGRSGRLGGRSRVFNIGNLGRFNLPGFLRTSQGSR  
HHCNQ

## SEQ ID 6067

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CGAAACCAAGAGCGGTAAGCGGAAGCGGCTAAGACACTTTGAACAAAGCTGCCGAGCGGCTCAGGAAGCGGAGCAAAATGAAAGACCGCGCAAA

## SEQ ID 6068

MKKLLIAAMNAALAACSQEAKQEVKEAAQAVESDVKDTAASAAESAAVAEEAKQVKDAADAKASAEAVTEAKDAAETKEAVSEAKDTLNKRAADAAQEAADKMKDAAK

**SEQ ID 6069**

TTGGGGCAATCAATAATTTTTTCATGTCCTATCCCTCTTGAGTTGTTGATTAAAGGTTTTCGTTAAAAACCGGACCGTGTTCCATCAATCGGCTGATTTTGGCCATCGCCCGAGAGAAAAC  
GGTTTCCCGTT

**SEQ ID 6070**

LRQSIIFSC L I L L E L L I K V L L K N R T V F H O S A D F A H R P E R K R F P V

**SEQ ID 6071**

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SEQ ID 6072

LDFSNLAEKVRAAGKLKRRGCVLQFSEFS

**SEQ ID 6073**

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SEQ ID 6074

MLKIPPAVLGGCILLAACGKSENTAQPQNAQAQSAKPVPVKYIDNTAIALGALGQSSSEGTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCHETDGDAPSQAENGVCHTL  
FARLVGNTAEDGGKLTDYILSHSALQPYQAGKSGYAAVONGRYVLEITDSEGAFFYFRREHY

**SEQ ID 6075**

TGCTGCACCAAGCGCGCAGCGCACCTTCCAAAAAATCGGCTTTATCAACACCGAGCGCATCTACCTCGAATCCAAAGCAGGCGCGCAACATCCAAAAAACGCTGGACGGCGAATTTT  
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GGTCGAACGCTTCGCAAAAAACAGGCGCAGTTTGAAGAAGACTACAACCTCGCGCGCAACGAAGATTTCCTTCCTCCAGCAAAACGCCAACCGGCTCATGTCAAAAATGCCAAACAG  
GAAGGTTACGATGTCACTTTTGCAAGACGTGATTACGTCAACACCCAA

**SEQ ID 6076**

CCTTGAAHDTFKQIGFINFERIYLESKQARNIKQTLDGESFARQDELQKLOREGLDLERQLAGGKDKAKKAQAEKWRGLVEAFRKQQAQFEEDYNLRNNEEFASLQQNANRVIVKIAKQ  
EGYDVILOQDVITYVNTQ

**SEQ ID 6077**

GTGTACCGCCACGTCAAATCAGTGGTGATGATCGCAGCCGCAATCTTTTTCATATCGATCACCATAGCGCCGGTGATTTTGCCCTTCGCGCAATTTCTTGGAAATGGCGGGTGCTTCATCC  
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CGGGGATGGACAAATCCATCTGATTCGCGCGGCGACCCGACCAACCAACCAACGCTCCGCCGCCGCGGAGCAATCTCACGGCAGAGTTGAATCGCGCAGCAGATACGGCGGTTACGACCGCAGC  
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CGAGGAGTATAGTCTGAAGCGGGCGGAGGATTTGTTTGTACCGGAACCGGCATGGTACCGCCGTCTGTTGAGCGTAAAGCTGCAGGTTTCGCTTTCGTTGGTTCGCGGTACCGGGAGCGGCGCTG  
AAGGTTGAAGTGTCCGCGCTGGCTTTGAT

SEQ ID 6078

VYRHVKSUVVMIAAAFPHFHDHHTAGDFAFAHLENGGCFIQSTQLDFRHNQTFRAELGEGFFQIFARADQRADHFDVAVQNQTRDQGIIHRFRRQPDGNHTSARADAIHGRVBCGSRYGGYDRS  
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SEQ ID 6079

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**SEQ ID 6080**

MSKKRVLITGVITGTGPHLNGVYGAIRPAVRAAQNPDTESFLFLADYHGIKCHEQEMTHQSTQAVATWLACGLDPERTTFYRQSDIPEVMEMLNWILTCITAKGLANRAHAYKAQVQANAE  
NGQEDPDGFGVEMGLFSYPILMTADILMFNANEVVPGRDQIQHVHEARDIAGRFRNFRQELFTLPEVKIDENVELLVGLDGRKMSKSYGNTIPLWENDKKTKQSVNKKIITNMKEFGEPKQPD  
ESPLFEIYKAPSTPSETAEFTOMLADGLAWGEAKKLSAAKINAEALRERYNALTSNPSOITEILOAGAOKARKRARELLDKVRDAVGIRPLK

**SEQ ID 6081**

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SEQ ID 6082

MPSEMPSETWQAEVRTALGLFQRADADRIAYFIQQFARFFARFLIRACIQNLFDLRRIRGQCVVAFAPFCQFVDFPRRRKPFRLAPSQAVGKHLKFRFRFRRRGEGFIDFKQRAFVGLFRLA  
RLFHVGNDFVDRFLGFFVFPKRNGLAVGFHGFASVQTDQEFDFVDFHFGQEEFLFETVVEAAGNVARHFDVLDLWAPDGFVGVHEQNVGSHQNRITEDYTHFHEIGVPLFVFRIGLNG  
GFVGVGAVHQTFLGGDAGQNPVQLHFFGNVALAVEGGALGVESACKPSGGNGLGLVNLHLVAFDDAVVIGEEBFGIGVLRADGGADGADVQMRGAGGGYAGQNSFFAHRNVLTA  
MPSEREMRRLLYPICHIHPADNRLPHIKKI

SEQ ID 6083

ATGCGATACGACAAATTAACCGCAAAATTCACAAACAGCCCTTGCAGAGCTCAGAGTTTGGCGTTGGCTGCGGACAGCAGCTATCTGGAAGCAGGTTTCGTACTGAAAGCCCTGCTTACG  
ACCAAAACAGCGGAGCTGCCCGCTCTTGGCTCATCGCGGCTGAACGTCGCGCAGGTTAAACAGCGTTTGCAGCAGCATTTGAACAGCTGCCGAAAGTGTCGCGACAGGTGGTGAGAT  
TCTGCCAGCGCGCAATTCGACGGCGGTGTGAACCTGATGGACAAAGCGGCAACCAACCGCGGATGCCCTATATCGCCAGCGAACTTTCTGCTGCTGCTTGGTGACAGCAACGATGCG  
GCGCGCAAAATCTTTGAAAGAACCGGTGCGACCGCAAAATATCAATGCCCGATCGATGCGGTACGAGGCGGACAAACCGTGAAACGATGCGAAGACCAACGCGATGCTTTGA  
AAAAATACAGCTCGATCTGACCAACCGCGCCGAGACGGTAAGCTCGACCCGTTATCGGTGCTGATGATGAAATCGTCGCGGATTCAGGTGCTCAACCGCGCAACCAAAACAAACC  
CGTGTGATTGGCGAACCCGCTGTGGTAAACCGCCATCGTCGAAGGTTTGGCGCAACGCATCGTCAACGCGGAAGTACCTGAATCCCTGCGTAACAAACGCTGCTGGTTTGGATTG  
CGCGCTTTGATTGCGCGTGCGAAATACCGTGCGCAATTTGAAGAACGCTTTGAAGGCGGATTTGAACGATTTCGCGAAGACGACGCGCAACACCTGATTTCATCGCATGAAATCCATACCT  
TGGTGGCGCGCGGCAAAACCGACGCGCGCATGAGACGCGGCAATATGTTGAAACCGCCCTTGGCGCGCGGCAACTGCACGTATCGGTGCGACTACTTTGGACGAATACCGCCAAATACAT  
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AAAAAGAAACCAACCGGAGCTATGGACAAATTCGACCGCGCTTGTATTCAGCTTCGGATTGAAAGGCGCACGTTGAAAGAAAGAGCGATGCCAGCAAAACGTTTGGAACTGAT  
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AACCGGCAAAACAACTCTTGGCTAATAATGTCGCGCGGAGGAAATCGCAAGATGTTTCCGCTATGACCGGCATCCCGGTGCAAAATGATGGAAGGCGAAGCGCAAACTGCTAAA  
GATGGAAGAGGATTTGACCGCGCTAGTCTGCTCAAAACGAGCGGTGCGCGCGCTGCTGATGCCATCCGCGCGACGCTCCGCGCTTGGCGATCCGAAACAACTTACCGGACGCTTC  
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CGGTGCGCGCTTAATCGCGCGCTTCCGCGTTATGTCGGATACGAAGAGGCGGCTACCTGACCGAACAAGTCCGCGCAACCGGTACAGCGTGATCTTTTGGACGAAGTGGAAAAAGC  
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ATGGCTTGGATCAGGCAATATCCGCGATTGCGGAAATCCAGCTCAAAGGTTTGGAAAAACGTTTGGAAAAACAAACCTGCGCGTACTGTTTCCGATGCGGCTCTGACATCATCG  
CAAGCCGCTTTTCGACCGGATTTCGCGCGACGCTCCGCTCAAACGCGCGATCCAATCGGAAATCGAAACCCCGCTGCGCAAGCCCTGCTTGGCGGAACTATCGCGCGGAAAGCGAAATC  
AAGGTAGAAGCGGCGGACGAGACTGAAATTTGCC

SEQ ID 6084

MRVDKLTAKPQALAEQSLALADSSYLEAGFVLKALLDDQNSGAAALLAHAGVNPQVKRQLQHLNSLPKVSQCGEILPSRELQAVLNLMKDAATKRGDAYTASELFLALVQND  
AGKILKEAGATFQNTAINDAVRGGQNVNDANAEDQDALKKYLTLDTQRARDGLDFVIGRDEIRRAIQVLQRTKNNPVLIGEPGVGRTAIVEGLAQIRVNGEVPESLRNKRLLVLDL  
AALAGAKYRGEFERLKGVLNDLAKDNGNTLIFIDRIHTLVGAGKTGDAGNMLKPALARGELHCIGATTLEDEYRQYIEKDALEERRFQKVLVGEPSVEDTIALRLGLQERYEIHGI  
DITDPATVAAAEISDRYITDRFLPDKAIDLIDEAASRVMEKEITKPEAMKIDRLIQLRMEKAHVEKEDDAKRLLEIDEIDGLQKEYADLDEIWKAEKASIDGAANTIKKQIDEVKI  
KIBQAKRQDLALASKIMYEDLEHLEKQRAAERADTSTKPAKLLRNNGVAGERIAEVVSRMTGI FVSKMMEGERDKLLKMEVILHRRVVGQNEAVRAVSDAIRRSRGLADPNKPYGSP  
LFLGPTGVGKTELCKALAGLFDSEDLIRIIMSEYMEKHAVARLIGAPPYGVYEGSYLTBQVRRKPYSVILLDEVEKAHPDVFNILLQVLDGRLIDGQRTVDFKNTVIVMTSNIGS  
QHIQMQGTQDYEAUVKEMEDVKEHFRPEMINRIDEVVFVHGLDQANIRSLAKIQKLEKRLERLQNLRLTVSDAALDILAKAGFPDIYGARPLKRAIQSEIENFLAKALLAGNYAPES  
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SEQ ID 6085

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GCAACCTCGCGCGTTCGCGCTTGAAGCACCTGATGAAATCTTAGTCGATGTCATCCGCAACCTGCCGACTTCGCAAGGTATTGCGATTGCAAGGGGTGTATTCCGACGCAAGCCAT  
TGTTCTACTACTATCAGACAAAGGTTTGGCGGATATTCAGGTAACGATGCTATATCGGCAACCGCGGTGTCGAGCTGATTGCGATGCTATGCGAGCGTGTCTCAACGACGCGGACGAA  
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GTACAGGGAACGCGGTTAATTTGATCAAAACCGGACATTTCCGCTATGTTACGCTGCTTACGTCATCAGATTGAAGAGGCGATGGCGAGGTTGGCAAGATTCTGCAACCTTACCATC  
AG

SEQ ID 6086

MDKFPKSAKLDHVYDIRGPVHKALQLEEBGNKILKLNIGNPAPFGPEAPDEILDVIRNLTSPQGYCDKGLYSARKAIVHYQNKGLRDTIVNDVYINGVSELIAMSHQALLNDGE  
ILIPADPYPLWTAATLAGGTVRHYLCDEENGWPNLADMEAKITSKTKAIVVINPNPTGAVYSKEILLLEIAELARKHGLIIPADEITYDKLLYDGAHVHYHIALAPDLITVTFNGLSKAY  
RVAGFRQGMVINGPKHAKGYIEGLDMLSSMRICANTPMQHAIQTAGLGYQSI NEFILPGGRILLEQRNRAWELVNQIPGVSCVKPMDGAMVYFKIDTMYRIRIDMKFVYDILLVREKVL  
VQGTGFNWKPDHFRIVFLPVVHQIIBAMGRILARLQFYHQ

SEQ ID 6087

TTGGGCAATGGGTGGGAATGACTCTTTTTCACGCAAAATTAAGCATCAGGCGGGGTTTTCAGGCTTTTACCTGCCCTCTTTCGCGCGTTCGCTGACGCTTTTGGCGCTATATCC  
AGTTATCGGTATCCACTTCGTTCAATCAGACAAACGTTGTTTCGGGATTTTACCAGCAGCGGTGCCAGCAATTCGATTACGCCCGCATCAGTTCCGCTTTTTCGCGCGGACGCTGCGT  
TTCCTTGGCGCGGTTACTTTAATATTGACA

SEQ ID 6088

LGNGWECTLFAKFKASGRGFQAFYFLSLRSLTLLEPISQLSVSTSSITTTVVSGFLPSTRASNSITPPISSAFCAAVGASLEPPTLILT

SEQ ID 6089

ATGCTTTATGTCATATTAAGTAACCGCGGCAAGGAAGCACCAGCTGCGCGCAAAAGCGGAACTGATCGCGCGGTAATCGAATTCGTCGACGCGTCTGGGTAAATCCCGGAA  
CAACGCTTGTGCTGATGACGAAGTGGATACCGTAACCTGGGATATAGCGCGCAAAAGCTTCAGCGAACGCGCAAGAGGGCAGG

SEQ ID 6090

MPYVNIKVTGKEAPTAQKAEILGGVIELLARVLGNPETTVVVVIDEVDNDWDIGKSVSERRKEGR



## SEQ ID 6091

ATGATTCGGCCACCTCGACCCCTGTCCAAATCACCGCGGGCTCGGCGCGGAATGGCGCGGAGGACATTTCCGTTACCGCGTGGCGCGCTCGCAGACGCGCAGGCGGAACACATCA  
GCTTCCTCGCCAAATCCGAAATACAAAGCCGAAGTCCACGACAGCAGCGCGGGCGGATCATCGTTTCCGCCAAAGCAGCAGCGATTGGAAGGGCGCAACCTGATTGTCCCGGACGATCC  
CTATCTCTATTTTCCGCAAGTCCGCGGCTGTTCACCGCTCGTCAAAGCGCGCGGCGGATCCATCCGACCGCGCTCGTGAACCGGGCGGACCGTTCCCGCAAGCTGTGAAATCGGC  
CGCAACGCTTACATCGCGCGGAACACCGTCTCGCGAAGCTGCGGCATCTTGGCAACCGCGCTCGTCAAACAGATTGCAAACTGGGCGACGAGTCTGCTGCATCCCAACCGCGCTG  
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TGCAAAATCGGTTCCGACACCGCTCATCGCGCCAAACCGGCATCTCAGGCAGCGTAACCATAGGCAGCTAGTGCATCATCGCGCGCGCGCTCGGTACGGTCCGACACATCGAAATCGCG  
ACAAACCAACCATCGCGCGCGGACGCTCCGTTCACCAAGCAGCTACCGAAAGCGGCAACACCTTTCGCGGCTCTCCCGATGTCCGAGCATAAAGATGGGCGCGCAACCGCTTTACAT  
CCACCGCTTAAAGCAATGAACAAACGCTCAAAACGCTGGAACAGCAGCTTTCAGACAGCAAGACACGCA

## SEQ ID 6092

HTPATCTLSQITARLGGEMRGEDISVTAVRPLADAQAETHISFLANPKYAEVHDSAGAIIVSAAKADGFEGRNLIVADDPLYLPKVARLPSFWKARGGTHPTAVVEPGATVPASCETG  
ANAYIGANTFVLGGCRILANAVVQHDKLGEVVLHPNAVYYGCTLGRHVEIHSAGVIGADGFLGAFAGDSWFKIPQTGAATLDDVBEIGSNTNDRGASDITVVGNGTKIDNQVQIGHN  
CKIGSHTVIAAKTIGSVTIGSYCIIGGGVTVGHIELADKTTIGGGTSVTHSITSEKHLAGIFPMSEKKNARNNAVYIHRLESENKRLKTLQQLSDKDTQ

## SEQ ID 6093

ATGCCGCTGACCGCTGTTTTCAGACGGCATTTTTCAGGATTGGATTGATTGTTAATCTGTTCTGTTTGAATAACCGTCTGAAACCCCTTATCGCAACACTTCATTACAGTGGATTAAAC  
AAATCAGGCAAGCGCGGCGGCGGACAGTACAAATAGTACGGCAAGCGGCGCAACCGCTGACCGATT

## SEQ ID 6094

MPSEKCSGIFYPGFDFNLFLKLYRLKTLIATLHYSGLTKIRTRRAADSTNSTARRANAVPI

## SEQ ID 6095

TGAAATATTGCTATCTTATCAACAAAGTTCCTCGCGCCAAACGCTCCGCTTATTCTGAAATAATCAAATCGATACAAAGACAGTTTTTCAGGCGGCAATCCGCTCTTCACACGATA  
CATATTTGTTATAGCA

## SEQ ID 6096

LKYCYLIKQVASAQTSASFSEKPKSIQKDSFQAANPSSHDITTFVIA

## SEQ ID 6097

ATGAAGAAAACATTGACACTGCTCGCGGTTTCCGCACTATTTCGCACATCCGCACACCCCCACCGCGCTCTGGTTCGAAACCGGCCACACGCAAGCGCGGAATACCTTAAAGCGGACTTGG  
CTACGGCGAATTCGCCGAATCTGAACCCATCGCAAGACCGCGCTCAGCAGCTTTCAGCAAAACGATGCAAGTGGTTACGAAAAGAGTAAGGAAAACATGATTCAACGCGGCACATACAA  
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CCTGACGCAAGCTATTGCGAACAACCCGATGTTCGGTAAAAACATTGTCAACGTTGGGACAGAAAGCGCGGACACCGCATCATCAACAAACCGGTCGACAAAACCTGGAAATCGTCC  
CGCTGGCAATTCGCCCAACATTACGATAGCGCAACGCTTCAAAGTCCGCGTTCTGTTCCGTTGGCGAACCGCTGCCCCAATGCCACCGTTACCGCTACATTGACGGCTTCGACACCGCGA  
CCGACGCAAAACGCAAAACCGAAGCCCAAGCCTTCTCCGACACCAACCGCGCAAGCGCAAGTGACATATCCCTTCGCGCAAGGCTTTTGAAGCGAGTGTGCAATCAAAAGCC  
GATTTCCCGCATCAAGGCTGTGCCAAAACAGCGCACTACACAACTTTAACCTTCAAAATCGGCCATTTCTCACCAT

## SEQ ID 6098

MKKTLLAVSALFATSAPHRVWVETANTHGGELYKADLYGKFELEPIAKDRLHPKSKPNQVLVTEKKGEMMIQRTVYNYQYRSNRPVKDGSYLVTAEYQPTFRSKNKGWKQAGLKEH  
PDASYCEQTRMPKGNIVNVGHESADTAITKPVQNLIVPLDNPANIHVGRFVKRVLPFRGEPLNATVTATFDGFDTSRDKTHKTEAQAQSDITDGKGEVDIIPLRQGFPAKASVEYKA  
DFPDQSLCQKQANTTLTFQIGHSEH

## SEQ ID 6099

TGTGATTTGAACAAAGGATGCCGCTGAAACCAATTTTCAGACGGCATTTTGTGTTGGACGGAATTAATGGTGAGAATGGCCGATTGGAAGGT

## SEQ ID 6100

LNFEQRMPSSETISDGIFVWTELNVEMADLEG

## SEQ ID 6101

ATGTCGTGGATGGTGGATGCCATGAAACCGTGGTGAACATTCCGCGCGGGCGTATTTACCGGCAACCGGTTGAGTTCGCGCGCTCTTTCGCGGCTACCGAGGCTACCGGTTACGGCG  
TGAACCTCGCGCGCTCCAAAGCTTTGGAAGAACTGGGCAAGAGTGTGAAGGCGCAACCTACGCCATTCAAGGTTTCGGCAATGTGGGTACCAACCGGCTATTACGCGCATCAATCCGG  
CGGAAAGTGTACCGTATCTACTGTGACGTTGCTATCTCAATGAACCGGCTTGGATATGGAAGCGCTGTTTAAAGAGTTCCAAGAAAAGGCTTCATCAACCAACAAAGCGGTTAC  
GGCAAGAAAATTCACCAAGCCGAACCTTTGGCTTTGGATATGGAGTACTCGCCCTTTCGCGCATGGAACAAACAGCTGACTTCCGAAAACCGCGGTAAGTCCCGCGGAAATTCGTGGTTG  
AAGGCGCAACCGCGGCTACGCGCGGAGCGGCTTATCTGCATCAAAACCGGCTATTGTTGCTGTCGCGCATTTTGGCAAACTCGCGCGCGGCTGCTGCTTCTTTCAGAGTGGGT  
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## SEQ ID 6102

MSMVDAYENVVRHSAPGVFTGKPVFPGSLARTEATGYGVNLAQVLEKLGKDVKGATYAIQGFNGVYHTGYAHQSGAKVVTSTVDVAIYNENGLDMELFKFQKGFITNKAGY  
GKEITNAELLALDMDVLAPCALENLTSNAGKVRKIVVEGANGPTTPEADVILHQNGVLVVPDILANCGGVVSYFENVQNLQGYWEPDEVQKEIVVLRRAFRDIWNLAQBYDVLRL  
TASYHMSIRRVKAMLRGWHY

## SEQ ID 6103

GTGCGAAAACAGGCGAATACACAACTTTAACTTCCAAATCGGCCATTTCTCACCATTAAATCCGCTCCAAACAAAATGCCGCTGAAATGGTTTCAGACGGCATCTTTGTTCAAACAT  
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CCGCTAAATACCGCGCGCGGAGTTCACACGCTTTTCATAGGCAATCCACATCCACGACATATTTGCGGTTGTTTCATCTCGCGCGGGAATATCGAATTTTTCGCGGATC  
AGCGGGGCAATCGCTTCGCAATAAGCGCGGCGGATGCGTTCCAGTTCGCGCTCGGAATAATTCGCGCGGATCCAAGG

## SEQ ID 6104

VFKTGLHNFNLNPRFSPILPSKQKRLKMFQTASVQTSIPAAQLHRFFNTADTHHRRGTQIDILLRQVNPNAERAAQDDFFLNFVKLPILALQVHLEIGNDHAAAVQCNIGH  
DQYAVLMQDNGVGRSRAVCAFNDHFRADPTGVFGSLVPCARGEVYHIQSQKFGVGNFVAVTGVGDEAFFLELFKQRFHIQAVFIVDSNVNSRYGNDFRAGLMRVLAGVVAHIAETLH  
GVGCAFHIAQPFQSLDGGGEVHATVCSLGRQRAAELNRFAGKYARRGMFHHVFIGIHPHNFVAVGHVHGGNIDFFRRSAGQSLRHKRGRCVFPVPRNRADPR



## SEQ ID 6105

GTGCGTTCCATCCCGGTGTGAATCTGGACGAAGTCAAGGCACTGTCGATTGGATGACCATCAATGCTGCGTTGACGCGATTCCTTACGCGCGGCAAGGCGCGTTACCTTGGATC  
CGCGCGATTATTCGAGCGGAACTGGAACGCATCGCCCGCGCTTATGCCGAAGCAITGCCCGCTGATCGCGGAAAAAATCGATATCCCGCCCCGATGTGAACACCAACGCGCAAAA  
TTATGTCGTGGATGGTGGATGCCA

## SEQ ID 6106

VRSHPGVNLDEVKALSIWMTIKCVAGIPYGGGKGVTLDPDYSEAELERIARAYAEIAPLIGENRYSRPRCEHQRYVVDGGCL

## SEQ ID 6107

ATGCTGTGATCGCGTTGCAAAAGAAACCTCAATCCGTTTGAATTCGCGGAAACAGGTCAAACCGCTCGACCGGCTGAAAAACCGATCCGCGCGTTTATGAAATCCTGAAGAGTCCGA  
CCCGCGTGTGGGAAGTCAAACTCGACGACGCGACGCTCAAACCTTTACCGGTTACCGTTCCGCTCGCTTCCATCCCGGTGTGAATCTGGACGAAGTCAAGGCACTGTCGATTGGATGA  
CCATCAATGCTGCGTTGACGAGCATTCCTTACGCGCGCGCAAGCGCGGTACTTGGATCCGCGGATTTCCGAGCGGAACGGAACGCATCGCCCGCGCTTATGCCGACGCGAT  
TGCCCGCGTGTATCGCGAAAAAATCGATATTCGCCCGCCCGATG

## SEQ ID 6108

MSDAVAKETLNPFEIARKQVKTACDLKTDPAVVEILKSPTRVLEVKLDGTVKTFGTYSRAFFSRCEGSRSGTVDLDDHQLMCRHSLERRQRRLYLSARLFRGTGTGTHRPRLCRSD  
CPADRRKKSIFPPPM

## SEQ ID 6109

ATGACGTAACAATCCCATCGAAGCCAAAGACATCCAAAACTCATCCCCACCGCTACCGCTTCTCCAGCTCGACCGCATTAACCGCTTCGAGCGGATGAAAAACCTGACCGCCATCA  
AAAACTGAACATAAAGCAACCCCAATTCGAAGCGCATTTCCCGCACTGCCCGTTATGCCCGCGTACTCATCATGAAGCGATGGCGAGGCGTGGCGCATGTTGGCGATTGTTAGCGA  
AGGCGGCGCAAGGAAACGAATTTTCTTCTCGCGCGCATAGACGAAGCCGTTTCAAACGCCAAGTCATCCCGCGGACCACTCGCTTTGAAGTCGAACCTCTGACCAAGCGCGCG  
GGCATCGGCAAAATCAACCGCGTTGCCAAAGTGGACGGAAGTCCGCGTCGAAGCGGTGATTATGTCGCCAAACCGCGTGGT

## SEQ ID 6110

MDVQLPIEAKDIQKILPHRYPLQLDRITAFEMKTLTAIKNVTINEPQFQGHFPDLVPMFVGLIIEAMAQACGTLAILSEGGKRENEFPFFAGIDEARPKQVIFGDQLVFPVELLTSRR  
GIGKFNAAKVDGQVAVEVIMCAKRVV

## SEQ ID 6111

GTGATTGACGCGGTGCGCTGGGTGTGGGCGAGGCTTCGCGCAAGCAGCTTCGCGCGAGAGTATGACGAGACGTGATTTTAAACGGTGGCGGACGCGCGCTCTCGCGCGAGGCGTTCGG  
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GACCGTGGCGCGCGCGATATTACTGATTGTTCTTGGGTACGGCGTGGGCGCGCGCGCTTATGCCGTCATTGAGCAGGGGATGATTTTCGCGCATCATCGAAGCGCGCGCGAGGATG  
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ACTCGAAGAGCGCGCGCAAGCGCGCTTACCGCGAGCGAGGAGCGTTCAGCGCGCGCAACTGCGCGCTTTCGCGCGGAGCGCTTTCGCGCGGAGCGCGCTTTCGCGCGGAGCGCGCTT  
AAGAACTTTCGAGCGCGCTCAACGCGCAAGTTCGAACCTTCTTCGCGAGCTTTCGCGCGGAGCGCTTTCGCGCGGAGCGCTTTCGCGCGGAGCGCGCTTTCGCGCGGAGCGCGCTT  
TGGCGCGTCCGCGCGCAAGAAACAGCACCATTCACCTCTCTCGCGCGCGGAAAGCGCTTACCGCGCATGAGCGCTCTGCTGCGCTGTCAGCTTCAACCGCGCGCTTTCGCGCT  
TCTGGACGAAGTGCATGCCCGCTGACGAGTGCACACCTTCGCGCTTTCGCAAGCTGCTCAAGAAATGTCGCTGCAACCGCGCTTCTTACATCTCCCAACCGCGCTGACCATGGA  
ATGGCGGAGCAGTGTGCGGTAACCATGCAGGAAAAAGCGGTGTCGCGCTTGTGCGCTGACATCAACAGCGCTTGAAGTGGCGGAAGCGGT

## SEQ ID 6112

VIDAVRWLGEASAKQLRGESMDVIFNGAATRRPAPRASVELVFDNSDHSLQGAWGQYAEVSIKQLTRQESTYFINNQTVRRRDIITDLFLGTGARGYAVIEQMSIRIIEARPEEL  
RAYIEEAGVSKYKERRKETEGRLKDTREHLQRLGDLQNELARQVEKLEQAEATERYKSLTAQLNQDLDLYAQWQSLAAADKATQHQSLQAQDDETAQVQALNNEVHALQTBES  
QQQAVHLSNKRGLREQLARLEBQIRHRQNLHQRIERDKQAAQQLQRIQEBQQQIRVQLEENELQVEKQTELAEWAMQVABHEERLPELEEVQATLNAAPQTQDEANRIRRELALKQ  
QQLAHABQTVAKHEERKRLKQENQALNLPDEABTAAQEAALLQSRQEHYEQIIEAEEALHAAREAPQTASNRFSQSLQKHITLQAQQQALSQILSQQQAADFWQATDHAAAPQLWQ  
HTTAPAEWQHLSVILAERLHARSVPNSFPVPAPILPQGAANLSDGLSGGIIKSLPQALLNQIQAPFPPTALHMLDGLVLCAPDLSYALAHQNDLGTQIWLTPBGHQVDRVSVLLYAK  
PAQESLIAQKARLDGIAALENLAPGLSAAEAAPQTEAAVCSSEVQKMLMQQQOHTTROYSAQOQTAEELARTWQGIIRREHIERELAQLAEQTLVQHTSDGLSDDIATLQEAALZ  
EHQOQTFAHSRQEQGRKQALQALLLEANRQYGLAEVAVHKLWQKQNYRQIARLEQDTLDWQERRQELALAYETEFQNDQHIKLDLDELTVHTLDEZYIAVQEKLAQIQEQGREQYAR  
VQTQLTKLPQLQAAQTALLOQEQEALINAKRYHQNLTERAADLDVLEALAKESAIVLSSISGLTRQIEALGAVNLALQLEBEAREDRGYRSQSEDVQAALALLEEALIAQIDDKTKARF  
KETFDVANGKVYTPFPFLFGGGEATLKMIGDILLTAGVSTIMARPPGKKNSTIHLLSGGKALATNSLVPALPSLNPAPFCLLDEVDAPLDDANTSRFKLVKMSVQTFLYISHNLIME  
MAEQLVGVTHQKGVSRVVAVDIKQALEMAEAV

## SEQ ID 6113

ATGATTTTATTTTCAAGCGGCACAGCATCCGCTGAAAAAGCAGCGCGCATCCGAAAGCAATGTCCAATTAATAAGATATAGTCATCATTTTATTTTAAAAATTTAATTGGAA  
CATCGCGCGGATTTCAAAACCTTGCAGACCCCGCATAAAAATCCGAAACACCGCGCGAAAAACCTGTTGCGATTGTTAATAATCTATACATTAGAGCGCTGTGCAACAGCATGT

## SEQ ID 6114

MILFPKPHSTRKKAARIRKANVQLNKDVIILFFKNLIGTSPGQTLARPHKIRKHPKNLRLLLIYTLZALCKRC

## SEQ ID 6115

ATGAATGCAGCCATCGAACACGTCACAGCCGTCGCTTCGATTGGACGGCACACTGTGCGATTCCGTCGCCGACCTTGCCGCCGCCGAGAACGGATGTTGGAACAACTCGGTATGAAAC  
CGCTGCCGCCCAAGTGGTTCGAAAGCTACGTCGCGCAGCGCATCGGCAAACTGGTTCACCGCGCTCTACCAACGACCGCGAGCCGGAAGCCGATTCGGAACGTGGGAAAAGGTTTCGT  
GTCTATATGAAATACCTACCGCAGCATTTGAGCGCTCTTACCGGCCCTATCCCGAAACGAGCCGGCTGGCATTCCTCAAACTCCTTGGGCATTCGCTGTTAATCATTACCAACAAA  
AACGAAATCCTTGCCGCCGAGCTTCTAAACAACTGGGACTCGCGACTTTCAGCCTGATATCGCGCGAGACAGCTGCCCGGAAAAAAACCCAGCCCGCTGCCGCTGCGGCACGCGCG  
CCGAGTTTGGGTATCGATGCCGCCAATATGCTTATGGTGGCGGACTCGCGCAACGACATCATCGCGCAAAGCCCGCGCTGCTGAGTGTGCGGCTTACCTTCGGTTACCGCGATAT  
GAGCTGCTCTCCGCAAGCAGATACGACCCGCCCGGACCGGATTATCGCGCGCTGCGCGAAATTTACGAAACCTGCAACCGCAGAAAAACAAGACGAAGAA

## SEQ ID 6116

MNAIEHVQAVFDLDTGLCDVFDLAAAAEAMLEQLGKPLPAKVVESYVGDGIGKLVHRVLTNDREADESELWEKGFVSYMKYRDLHSVTRFPYPETEAGLALLKSLIGLPLVITRHK  
NETLAELLKQLGLADYFSLILGDSLPEKKPSPLPLRHAAEVLGIDAANMLMVCDNRNDIATAAGCLSVGVTFYVGDMLLSQDDTTTRPDRIIGALPEIYENLQPKNDKE

## SEQ ID 6117

ATGAAACCGCAAAATCCCTACGCGCCCGCGCGATGGACATCCTCTCGCGCAAGAAGTCAGCGCATCGGTCTGAAACGCAAACTTGACCCGCAAGCGGAAAGCGAAGAGGAGTTGGAAA  
ACGTGTTAAACGAATTTGCCGAAGCACTGGCAGTCGATTTGCGCTACGCGCAAGCTTATATCCGAGCAAAAGCCGCAAAACAGGTTTCATGAGGCTGAAACAGCGCTTGGCGCAACA  
GGCAGATGATGAAAAACCCGCGCAACCTGCTTCCGACCGCTCAAGCGAAAGCAAGCCCGCATAGCCGCTGTCGTAATAAAATTCAAACATCCCGCCGCAACCTCAAAGAAAACAAA  
AAACAGGCGGTTTCTCGCTATCGCGGTTTGTATGCCGATACCGTTTCAGACGGCATTGAAACAGCTTGGGACGAAAAATTGGGAAGACAGCTGC

## SEQ ID 6118

MKPQKSLRARAMDILSRQEVSRIGLKRKLAPHAEELEENLVNEFAERNWQSDLYAEAYIRSKSRKHSLRLKQALAQOQIDERTSRNLLPDRSSEKQAAALVLRKKFKHPAANLKEKQ  
KQARFLAYRGFDADTVQTLKHAENDENWEDSC

## SEQ ID 6119

ATGTCGGAACAACCGAAAAACACCGCCCTCCCGCATCGAAGACGAACGCAAAACCCGGTTTACCGTATGGGACGGCGGTTGCCGATTCATGCTCGCGCTTGGCGCGCGCTGCTGG  
CACTCGTGTCTTCTGCTTTTCGCTTTTGGCTTTTC

## SEQ ID 6120

MSBPKEKHASPIEDERKNPYYRMGBAVAGFMLAVWAGVLALVFFLVFRPHLS

## SEQ ID 6121

ATGACACACAACGCCCACTGCCCTTCCACGAACTCATTATGTCGCAACTGATGATCGCGGACACCGCCAAATTTTCAGCGGCAACGTACACGGCGGGAACCTCTGCTCTGCTCGACACAGG  
TTGCTTATTCCTGCGCCAGCGCTTACGCGGCAATTTATGCGTTACCCCTTCGCTTGACAAAGCTCTGTTTAAAGAACCCATCCACATCGCGGATTTGGTTACCTTTTACCGCGCTGTCAA  
CTACACGGGACGCACTCGATGGAATTCGGCATCCGTGTGCAAGCACAAACATCCGACCGCGGAATCCGCCATACCAACAGCTGCTACTTACAGATGTTGCGGTTCAAGACGCGCAAA  
CCGCTCCCGCTCCCTCGCTGGAATTCCTGACCGACCGCCCAACGCTGCCCTACGAAAAAGCCAAAAACGACAGAAATCAGCTCCAGGCTCCGAGAGCTGCTCTGCGGCTGC

## SEQ ID 6122

MTQORQLPSHELIMSELMPPDTANFSGNVHGGELLILLDQVAYSCASRYSGNYCVTLSDVKLFPKEPIHIGDLVTFYAAVNYTGRTSMEIGIRVEAQNIRTEIRHTNSCYFTHVAVDGK  
PVPVPLBLILDRQRCRYEKARKREISLQASGDVSCG

## SEQ ID 6123

ATGCTTGTCTGCTTTTCAGACGGCATAGGCGCGCTGACGAGCGCAGGACACGCTCTCGGAGGCTTGGAGGCTGATTCTCTGCGTTTTTTTGGCTTTTTTCTGAGCGGCAGCTTGGCGG  
TCGGTCAGGATTTTCAGCGGAGGACCGGGACCGGCTTTCGCTCTTTCAGCCCAACCATCGTGAAGTAGCAGCTGTGTTGATGCGGATTTTCGCGGTCGGGATGTTTGTCTTCGACAC  
GGATGCCGATTTTCATCGAGGTGCGTCCCGTGTAGTTGACAGCGCGCTAAAGGTAAACCAATCCCGCATGTTGATGAGGTTCTTTAAACAGGACTTTTTCACCGAAGAGGTAACGCAATA  
ATTCGCGCTGTAACCGCTGCGCGCAGGAATAGCAACCTGGTTCGAGCAGGAGCAGGATTCGCGCGCTGTACGTTGCGCTGAAATTTGGCGGTGTCGCGCATCATAGTTCCGACATAATG  
AGTTCTGCGGAAGCGAGTTGCGCTTGTGTGTCATGGTGTACCTGTTTAAAGAAAGGCTGTTTGAATGGGTGCGGGAAATTTAGGGAATGGGGAAGTGAATTCAGCTTAAAGAAAG  
CTATGGAGGATAGTCTGCGGAAATGGCGCGCGATGCCCTGTGAAGCCTTCAGACGGCATTTTGTTCAGGAAAGCCAAAAACGAAACCAAGAAAAACAGAGTGCCAGCAGCGCGCGC  
CAACGGCGAGCATGAATCCGGCAACCGCGCTCCCATACGG

## SEQ ID 6124

MLVLSFRHRPSPAAGHVSGLLEADFSAPFGFFVAALAVGQDFQRDGDGFVFDNRHREVAAGMADFAGADVLCFTDADPHRGASRVVDSGVKGNQIADVDGFFKQDFVNRKGNAI  
IAAVTAGAGIGNLVBEQEPAAVYVAARIGSVRHEQFCHNEPVGRQLALLCHGVPLRKGVLRKWRNFRWEGSGIQAQKSYGGTVCRNGPPMPSEAFRRHPVQESQKRTKKTSTPTA  
QTASHNPATARPTR

## SEQ ID 6125

TGAAAGCCGAGAGTTTGATGTGGGTGAGCGCATTAATGTCGAAAAATAAAAAAGAGCGTATTTTAAACGAAATCCCGCCGACCAACCCCATATCTTCCCGGCAAAACCTTACCGCA  
TCCCGCCCGGTGCGCGAGGATTTTGCATATCCCGCCATCCGATTAATAACTTTTCGCTTTCCCACTTTTC

## SEQ ID 6126

LKPESLMVRRIMVGKKNKEAYFNGNPAAPPHILPAKPYRIPPRCGRILHIPAIRIKIPAPFTLS

## SEQ ID 6127

ATGCCGTGAAACCGCCCTCCCGCTTTATGCGGACACGCGCGCGCGCACACGCTCGTCTGTTCCGCCAAACCTCCGCAATCCCGGACACCGCCGCTTATGCGCGCGCTTCCGCAAG  
GTTCCGCCGTTATCGGATTTGGATTGACGATGCGGAACAGACAAACCGCGCGCGCGCTTCTACCGCAATCCCGCGCGCACTCGCCCAAGGCTGCGCAAGCGCGCGCATCCCGCT  
CTACACGGCGCATGCTGCGCGGCTTGTCCGCTCGCGCTCCCGCTCAATATCCGCGCGCTCATCGCGACGAATCCCATACTTTTCCGACAACTCGCGCAACCGCTTGGGAC  
GAATTGGACAAACACGGCATCGCTTAACCTTCGTCACACGCGCTTCCGTTTTCGCGAAAAACCGACCTGACACAGACACAGGTACGGCACACCGGATTTCAACCGCTACCGCAAGTAT  
GGCTCGACCGCTTTTCCAGCAGCCCCCGCGGTTTCGGAACCTATTTCGCGCATACCGCAACCTTCCCGGAAACCTGCGCGCGCGCGCTTTCAGACGGCATCTTCT  
GCCGCAAAACCGCGCGGAAACCGCGGCTTGGCGGAGTGGCGCGGCTTCTCGAACAGCGCGCTTCTACTCGGTTTAAAGGATTTCCCTTCGCGCAAAACACTTCGCTGATGGCGCG  
TATTTGAGTGTGCGCTGCATCTCGCGCGCTGCTCGCGCGGAAAGCTTCGACGCGCTGTAACGCGTGGGCGGACAACTCATCGCGCGGATTTTCTTCAACTTGCCTTGCAGC  
ACGCGGATGACGACCTTCAGACGGCAATCCGGAACACACCTGCGCTGACGCTTTGGCAGCAGGCGCGGACCGCATTCGATTTATCGATGCGCGGATGCGCTGTTTGCACAAAACCGG  
CAGCTTCCACCCCGCTGAGACGCTTGAAGCGGATTTTCTGCGACGCTTTAAACCTTCCCGCGCGGAGGCGAGATATGTTTCCCGCGGAGCTGACCGATTTTCATGCGCGCAATC  
AACCAAGGCACTGGCGGCTTGGCGCTTCAGGACACCTGCGCGCATTTGCCCGCGCTCATACCGTACCGACCGGACCGGTACTTTTATCAACGCGCATTCGCGAATCGCGCACCT  
GTGCGCGGACACGCTTCACAGCCTTGGCGGTTTTCGCTGTCGATGCCAGGCTATCCCGCGCGCGCGCTGCGCGCGTA

## SEQ ID 6128

MPSETALFLYADTRAHLVWFRQNLRIIDNAAALCAVAGSPVIGIWIIDDAETDNPRAAFYRQSAEALQGLARRGIPLYTAASPAGLVRLAVRLNIRAVIADESHFTADKLADNALRH  
ELDKHGIALTVPNDRSVFGKTDLPDNGTAHTDNRVREWLDRFSKQPPAGSDLPAAAYRQPPENLPAPPAALSDGIFLPQNGGETAANRWRRFLQEAASYSLVKDPSPRKVTSILGA  
YLSVGCISPRILLARESLERRINAHADNIIIRDFPLQLALQHADDPSDGNPEHTLRLFLWQCGRTGPIPIIDAMRCLHRTGSLHPLRLSADPFCHVILNLPREGEIWFARQLTDFDAI  
NQGWRLLAASRHTCPDIAAASRYRDPDGTPIKRHIPELAHLSADTVHTPWRFAACSVDTHTGYPARPVAGV

## SEQ ID 6129

AGGAATACGACAGACATGACGCTCAACTCCCATCGAAGCCAAAGACATCCAAAACTCATCCCCACCGCTACCGCTTTCACGCTCGACCGCATTACCGCTTCGAGCGGATGAAAA  
CCCTGACCGCATCAAAAACGTAACCAATAAGCAACCCCAATTCAGGCCATTTCGCCGACTGCCGTTATGCCCGCGCTACTCATCATGAGCGATGGCGAGCGCTGCCGACGCT



CTGCCCTGGTGTTTTGGTGTGATGATCGGTTTCAGCGTGATGGCGAAGCGCTTCCATTTCACATTCCCAAAGGCTACCTCTACGCCGCCATCGGGCTTCGTGATTTTAATCGAACTGTTTAAC  
CAGATTTCCGCAACGCAACAGCGCGAAAAAGCACTACATCGGCAGCTCGTGTGGCGAAGCGCACCGCGCGAAAAAGCTTTTGGGTATGATGGGCATACGCGAAGCGTGCTGTGCTGATGCGGGCG  
GCGAATCCCGTGGATGACGCGCATTTTGAAGAAAAAGAAAAATCGATGATACGCAGCGTGTCTGACGCTTGCCGAAACGCCCGATTATGGGGTGATGATTCACGCGCGCGACATCGAACCGCT  
GGACATTTCCCAAAGCGCGGAAGAACAGTATGCCCACTGCAAAAACAGCGCTTACAGCGCGCTGCTCGTTGTGCGAAAGCGGGCGGTGGACGAACCGTGGGCTACATCAACAAAAAAGAC  
CTGCTGTCCCAACTGCTGGAAACAGGCGGCTTCGACATTCAGACGGCATTGCGCCAGCGCTCGTCTGCGCGACGGCACGACCGCTTGGGCGCGCTCGAACTCTTCCGCCAAAGCAGCG  
CGGATTACGCTTTGGTGGTGGACGAGTTCGGCGCGGTGTGGGTATGTGTGACGATGAAGAAGCTGTTTGAAGGCCATCGCAGGCGAGTTCCCGAAGAATTCAGCGCGGAAGAAGAACCGCG  
CGTTCAGGAGGAATCCCGATGAAGCCTGACGCTGGAAGCGCGTTTGGAAATATGTGAGCTGGCATCCCACTCAAACCTGCCGACGACGAGGAGGAGATACCGATTTCCATACCGTTGCCCGG  
CTGATTTTGGGAAGAAATGCAAAACCATCCCGATGTGCGCGGATTTTTCGCGGATTTTTCACGGCTGGCGGTTTGAAGTGGTTCGAAAAAGAAGGCGACGCGCATCGAGCGGGTCAAAATCACCAAAAT  
TGCCCCAAGAA

**SEQ ID 6146**

LRJLNRANTKIMDFSWLAEPHTWIGPATLLLEVVVGIDINLVFAVILANKVQPARDRARITGIGLAVVIRIIMLAFMAHITITLEPLQJIGGLAVSGKDMIMLAGGIFLLYKATTELHERL  
BENHRPAVADNQKQHAFPGWQVATLLIDAVPISDSVITAVAMVDHIVVAMGAVVAMAMVISASKLITFVPDRHPTVHMLCLGFLMIGFSLIAEAPFHPIPKGYLYAAGPSIITELFN  
QISQRNSRKNDYIGSSWRKRTAENVLGMGIGRESVLADAGESVDDAHFEENEKSMIRSVTLAERPIMGVMI PRDIERLDISQSRREEYQALQNTFYSRLLVVGKAGVDEPLGYINKKD  
LISQELTEGLGDIQTALRQPLVDGTTALGALELFRQSSADVALVDFEAGVLGMVTKMDLLEALAGEPPEFPEREEEPAVQENPDSELTVEGALYVELASQJNLPPQEEEDTDFHTVAG  
LMQLEQTIPDVGDFADFHQRVFPVEKEGQRIERVKITKLPEE

**SEQ ID 6147**

TTGAAACGTCFAATTAAAAATAAAGAATCAGGGTTAGCGTGAAATTATAAGGAATGCTGTAGTATTTTTTCGTGATTTCAAGAAATGGAACGGTATAAAAATCCGGTTAGGAAAGACAAGCAG  
CTGAATTGTATTTATTGAAATTTATCTTTATCAAGAGAACTTTTTTCATGTTGTTTCATATTTGAGATCGTTTTAAGAAACAAAATTGATATTTGCTTTCCGACAGGAGTTTAAAGACAGAA  
CCGGTTATATGATAGCATACAACCAAAAGCAATCCTGCAATGAAATATCAAGGTTGCTTTTTAAGAAATGGTACGAAAGAAATCTGCCGAATTAATCAAGGTTGCAATATCTAAAAATACAA  
AATAATAGCGGAGGAAAGTTTGACCAACAACCAATTGGTTGCAGGACTAGGATTCGGTTTTTGGCGGTATCTGTTTCCGGGAGGGAAAGATGCTCAATTTGATGCTGCAGGAAAGTATTGA  
TGAAAGTTTTTTCCAAAAAGCCCAATCTACACCAAGTGTCGCAATATAACAAAAATGGATTTTTTCGAGAAGTTTCCAATATTAAACAATTTCCGTAATCGTTTGGCACATACGAAACCGAT  
TGTTTTGATTTTAAAGGTGCAATAAAGATACACGGCTAGCTAGAAATATTCACCAATCTAATTTTGAATGCTTAATTACATGGATGTAGATCTGCTTCAGTATTTAGCCATTTTACG  
GATCAAGTGATTTGCGGCTCGCATGAAATGCACAACT

**SEQ ID 6148**

LKRPQKKNKESRVSVNYKECCSIFSDFRMERYKNAVXDKAAELYLLNLSLSRELPHVVSIFETVLNKKIDICFRQEFKDRNRLYDSIQPOTNPALKYQGCFLRNGTKESAELIKVALSKIQ  
NMSGGKPTDHNQVWAGLGFGFWRYLFAGGKDAQFDAAGKVLMKVFPKPKSTPSVQYNQKWIFRELSNINNFRNRLAHHEPICFSFKGAIKDTGYARNIHQSIFELLNMDVDPTASVPSHPS  
DOVIAVCDRIDKL

**SEQ ID 6149**

[illegible]

**SEQ ID 6150**

LRFPHPFDKYTEEDSMKTKTVKQASKQASKQASKQASKQASKQASKQAK

**SEQ ID 6151**

TTGAAACATTTCAAAATAAGCCCATGCGTTCGGAATCTCTTTCAGAGGGCATGGGCTTTTGCCATTGCCCCGATAAGCTGTATAACTGTTTAAATTATTTCGACCGAAGGTACACGCACA  
TGAAGACCCCCGAGCAGAGCAGTAAGCCCGCCCGCGTCTTTTGTGCGTACTGTCTGTTCAGGCAGCT

**SEQ ID 6152**

LKHFKISPCRPNILSDGMAFCHCPDKLLNCLNYFDRRYTHMKDPEQSSKPARRFLCVLSVQAA.

**SEQ ID 6153**

ATGATGGAAAAACGAAAAACAATCCCGAGATGGCGTTTGTCCCTTGAAAGATGGCGGCTGGCACCCTTAAATCAGCCCTATTGGTTGACAGGCTGGGGGCCCTGCTGGTTTTAAAGTTTGCTATCTTCATCTTCCGAGCTGACGGCGCGCTGCTGCCTTTTATCAGCTGGTGGTGGCGCTGATATCGTATGCGGCCCGCTGCTGCACTTAAATTTGGCAAGCCGGAAGAAAAACAGCAAAAGCATCATCTTGATTTTTCATCATGGTGGCGACATCATCAGCTGGGCGCTTTGGCGTACGGTTTTCGTCAGCGCTTTCGTCGGCGCTCCCGTGTGAAGCGTTTGAACAGGACCGCATGCAACATTGTTTACCGCGCGGAAGTCGTGGTTCGAAGATTGCAAAAGCCCCGAAAGGGCTGCAAAAGCTGTGCTGGTTTGGCATCCGCGCATTGCAATTGAAAGAACCTTGAGGATGCGGATGAGAAGAAACAAGACGCTGGATTGTGCCCTGAAAGGTATACGGCCGAGTATGCGCTCCGACGGCTGGCTGCCGTTATTCGCAACAGGAAGCAGAAAAAATCCGCAAACTCTGAAACCCCTGAAAGTCTTGGCGGATGCGAGAAAAACAGCGTTGTGGGACATCTGAAACAGGCAGGTCTCCCGAAGGGGAGAGCTGTATTACCTCCGCTTTACACGACAGGCAGAGGAAGGATGGATAGTCATTACCGATAAAGGGGCAACCAACAAAGGCTACGCGCGCATAGACGGCTTCATCATCCCT

**SEQ ID 6154**

MNENGTTFPRWRFALKSAGWHLLISLVLVAGLAALLVFKVWYPYPYABLTGGLSLYQLVAVDIVCGPLTLTLASPKKTKARNVDFSMVGITQLAALAYGLHSVSLARPVVEAFEQDRFT  
 IVTAAEVVVEDLHKAPEGLQSLSWFGIRRIALKEPEDADEKNKTLDLSLKGIEPSMRPDRMLPYSNKAERIKRHLKPLKVLADARKTTVADILQAGLAEGEELYLPFTSSRQKENIVI  
 TDKGNTKGYAPIDGFIIP

SEQ ID 6155

ATGCCGCTCTGAATGCCAGGGTTTCAGACGGGTGTCGCATTTTAAAGCAGTCTCTATCTGTTGTACAATGCGCCCTGTTTTTACGGTTATTTT

**SEQ ID 6156**

MPSEN#OGFRRCRILSSLYLLYNAPCFYGYF

SEQ ID 6157

TTGAAAGCGGGTTATCCGGTATACCGGAGGACACGAAATGAACGAATATTCCCAATTAATCAAGCATCCCGATATTTCCCTTTCCCGGATTTTCAGACGGCATCGGGGTGCGCAATCGCGCGA  
CGGGCGAAATTTTGGCGTATGTCGCGCAACACGGGTTCGGACAAGCTGAAACACCTGATTTCAAAGGCGGGCGGCAGCGCAAAATATTATGGCGCGCGAAACCCGCTTGGAAACGGCGCGACAT  
ATTTGCTGGCTTGGTATTTTATTAGTTAAAGAAAACAAAGAGCACTGGCGCGCTCTCATGACGATGGGAGCAGGGCAAGCGCTGACCGAGGCGCGCGGCGAAATCGATTTATCGGCTTCGTTT  
TGCGCTGCTGTTCGCGAAGAGCGCGCGCGATGACCGCGATGTCTGACGATGTGTAAGAGCTGCGCAAAATCTGGTTGTGTTGAACACCGCGCTCGCGGTTCACGTTAGTCAGTCAGCGGT  
GGAATTTCCCGTCCGCGATGATTCGCGCAAGGCCCGCGCTGCTTTGGCGGTGGGCTGCGCGATGATAGTCAAACCTGCATCGCTCAGCGCTTTGAGTGCATGCGTTGGCTGTACTGCG  
CTACGAAGCGGGCGTCCCGCAGGATTTGCTTTCCGTCGTGACGGCGCGCGCTTCGGAAATCAGCCATGAAATTTGCCACGAACCCGACCGGTGCGCAAAATCAGCTTCACCGCTCGACCGAA  
CGTGGCGCGAAATTTTTCGCGCGCAGCGCGCGGACATTAAAAAACTCAGTTTGGAACTGGGCGGCAACCGCGCGTTTATCTGTGTTTGACGATGCGGATTTGGACAAAGCGCGCTCGAAGCGC  
CGCTGCGCAGCAATGTTCCGCAAGCGGTGACAGCTCGCTGTCACCAACCGGTTTACGTCCAATCGGGCATTTACGACGATTTTGCGCGCAAAATGAGTGAAGAAAGCAGCGCTCGCA  
ATTGGCGCAGCGGTGGGACCAAGGTGTGAACCAAGGACCGCTGATTTGAGGAAAAAGGCTGAGAAAAAGTGAACGACACATCGCGACATCTCCAAAGGCGCGGTGCTGTCGACCGCG  
GGCAACGACGCGGTTGGGCGGAAACGTTTTTTGAGCGCATGTCTTAAGCGCGGTTTACGGCGCAATGGCGGTAGCTGCGGAGGAAACCTTCGGGCTTTGTGTCCGGTGTCCGCTTTT  
AAACCGAAGCCGAAGTCACTCAGAGCTGCGAACAATACGGAATACCGTTTGGCAGCTTACTTTTCACTTCGCAACACCGCGCTCAATGGCGGTGCGGGAAGTCTTTGGAATACGGCAGTGT  
CGGCATCAATACGGGCTTAATCAGTAATGAAGCGGCACCGTTCCGCGGGGTGAACACGCAAGCGGTTTGGAGCGTGAAGGCAGCAAAATACGGTGGCGGACGAATATCTAGAATGAAATATTG  
TGCAATGATGCGGGG



## SEQ ID 6158

LKAVIPTTGGHEMNEYSQILKHPDISLSPISDGI VGNPATGEILAYVRNTGSDKLNLIQAAAAQKLNAAKTALERADILMRWYFLVKENKEALRLMTMEQKSL/TEARGEIDYAA SF  
VRWFABERRIDGDLTVSVKASQKLVVLKQPVGVTAATTPWNPFSAMILKAAAPALAVGCAMIVKPSLTPLSAYALAVLAYEAGVPQDLLEPVVSGRASEISHEPATNPTRKLSFTGSTE  
VGAKIFAGSAADIKKLSLELGGNAPPTVDDADLDRAVEGALASKFRNSGQTCVCTNRVYVQSGTYDVFCRKLSEKAAALKLGDGLDEGVNQGPLIEKAVEKVEQHIADALSKGAVCLTG  
GKRSLAGSTFFPEPTVLSGVTAQMAVARESTFGPLCFVPRFTEAEVIRAAINTEYGLAAYLFTSDTARQWRVGEVLEYGVMVGINTGLISNEAAPFGVKRSGLRGEGSKYGADEYLEKLYL  
CIDAG

## SEQ ID 6159

TTGCTTCTATATATTTGATCCCTATCAAAGGGCTGCATTACTTTCTTTCTAAAGATTACTATCGCATAAAAGTATTTTTCTTAAACGACAGGGATGCCCGCTGCCATATTCAAACACC  
GCCCGGATGTTGCGCTGCCGATCGGATGCTTCAGACGGCATCGGAAGGTTTGCACTTTTGGAAATATGAAGATGATAATGTCCGCGAGATTGACGGCATT

## SEQ ID 6160

LLIYCTLSKGCITFLSKDYIRIKSIFLKRQGCARALFKHRPDVALPDRMLQTASEGFVLEEDNVREIDGI

## SEQ ID 6161

TTGTCAAGAAAGTGTGGGAAACGCAAGATTTTAATACSGATGGCGGGATGTGCAAAATCTCGCCGACCGGGCGGGATCGGTAAGGTTTTCGCGGCAAGATATGGGGTGGTCCGGG  
GGATTTCCGTTAAATAACGCTTCTTTTATTTTTCGACCATATGCGCCTGAOCCACATCAAACTCTCCGGCTTCAATCTTTTACCGACCGGACCCAGGATTCATGTTCCGGGGCAGC  
TTGTCCGGTATCGGGCCGAACGGCTGCGCAAGTCGAATGTGAT

## SEQ ID 6162

LSGKCGKRRDFNTDRDVQNPAAPRDAVRFCRQDMGCGISVKIRFFFIIPSDHYAPDPHQTLRLQIFYPDPDHSCSGAACRGYRAERLRQVECD

## SEQ ID 6163

TTGGCGCTCGGCTGGTTCCGCGGTTTCGCGCGTGGCGGATTATTTTCGTTCTGTTCTGCGTTATCTCTGCGCAGCGCTCAATGCCAATCT

## SEQ ID 6164

LAVGWRFRFSGVADYFSFRSGFILSAAACQQL

## SEQ ID 6165

ATGTTTCAAGTTTGGGTTTAAACGGCAATAGACCACTATATCCCCCATATCTCGCCATTGGATACCGACAATGAACTTTAGGCACGAGCGTCTTCAAGCGTTGGCAACAGCAGGACTT  
TCGTTTATGACAGTTTCGGAGACCAAGATTTTGTATACCGAAAAATTTCCGCAACGCTATGAGGATTGGGTTGCCAACCCTATGCGGAACTTGGGCTATAAAACAGACGCGCCCTATT  
TAAAAACATGATGAGCGGGGATATTTGGCTGCACAACGGCTGCCGAAATCAGCCGAGCGCCATGTCAAGCCGGAAGCGTGGGATGCCATTGATGCAGAGATGTAAATTTTATCATTT  
GATAACAGCCCTGAAGAAATCGGAGCAGGTTTAAAGTTGGCATTGAGCCGCTGCCGACAGGATAAAACCGAAGCAACGAAAAATAATCCGCCAGCGCCGAAACCGCGGAACCGCCG  
ACGGCCAAAACAAAACCGGCATAAAAAACCGCCGAAAAATCCGACGCGGGTTCAACAGGCTGCCCGGTTTAAACGGCGCGCGCAGGAAGTTTCGACCGAATTCGCGTAGGCATCGGTAA  
AGCGAAAAAGGCTTCGCCGCTTTCTGTGCTCACTCGGTTCCGTTTCCGAACAAACCGGTTTCGCGCGGTATAGCGTTTCGCCGATGCGGCAACGTCGGAAGAGAGGACGGCAGCGCTGCC  
GTCCAGCCCAACCGGATTTTCCGCCCGCTCCAAATTCGCGACGCGCACAGACAAACCGTTCTCGCA

## SEQ ID 6166

MFRFGVNGRNPPIPHILPLDNDNETLGTTLVQALANSRTFYDSSDQDFDTEKFRQRYEDWVANLCNGLYKTRRALFKNNMSGDIWLHNGCLKISPSRHKVPEANDAIDADDVLSL  
DNSPEEIGAGLKLALSRCDKPRTKRKILIRHARKPEPADGQNKTKIKRPNKPDGSGNRLPRLTGAAGSFDRILAVGIGKAEGFAFLVPLGVSVEQTVFGGIAFAGCGNVGREDGTPA  
VQPPQDFAAVQIADAHQTVLA

## SEQ ID 6167

ATGCCGCTCTTCAAAACCAAGCGGCGGACGAGATTTTCGAGCGTTTTCATCGGAGAACGGTTTGTCTGTGCGCGCTCCGCAATTTGGACGCGGCAAAATCGGTTTCGCGCTGGACGCA  
GGCGTGGCTCTCTCTTCGACGTTTCGCGCATCCGCGCAACGCTATACCGCCGAACCGGTTTGTTCGGAACGGAACCGAGTGGCACCAGAAAGCGGCGGAGGCTTTTTCGCGCTTATC  
CGATGCTTACGCGCAATTCGTTGAAACTTCTCCGCGCGCGCT

## SEQ ID 6168

NPPVQNDQAGPDDFRAPSCENGLSVZVRNLDGGKIALRLDGRRAVLSSDVAASGERYTAEHGLFNGTENGHQKGEAFFGFTDAYGNSVETSCRAB

## SEQ ID 6169

TTGAACAGCGGCGCATATACCGCGCTCCGCCCATCATACGCTTCGCGCACGGCACAGGCCCAAGACAAAACCGATACGCTCAGCGCGAAAAACCTGATATTCATAAAAGCTCCCCAA  
TAAAAAGAAATATGTTTCAACACACAGACGACACAT

## SEQ ID 6170

LNRRHIPASAAIIRFRHGTGRQRQNRVQGREKPDHKSPIKRYVSTHRTTH

## SEQ ID 6171

TTGATTTATCGTTTCTTCTTTTCGTTGAACCTCAGCCCTTTGGGCGGTAAATCAGACTTTATTTGGGAGGGGCGCAACCCCTTCGAATCAGGACGCGACATAGGGCGGTCTT

## SEQ ID 6172

LIYRVSFVPEQPFQAVKSDFIWEGRNPPRIRTAHRVLI

## SEQ ID 6173

GTGACGGAATGTACGCGCACAAACGTTAAACGCCGANTAGGATTTTAAACGAAATTAGCACACTGATATCGGTTTTCATTTGGAATTTGGAATAATTTACATTTCTCCGGGCGGGCAGGC  
AGGTTTCAGACGGCATCTCGCAGCAAAAGCGGTGTGCGAAGACGGGTAAAGAAGGGCGCGCAATTCGGAATTAT

## SEQ ID 6174

VDECTRTNVKRPNRILITQISTLI SVPTWNLKFTFLRAGRQVQTASSGKRRCKTKGEGARNPDY

## SEQ ID 6175

ATGAAATCACTCAAAACCTTCTCATTTGGGCGATAGTGGTACTGGTTCGGCTTAGCATCTTTACCACTCTGGCCCTCAGCGAGGCGAACAGGTCAGCGCGGTATGGATGGTTACCGCG  
CCATATCGGTTTACTGTATCGCTTACCGTTTTCAGCGCTTACATCGCCAAACCGGTGATCGGCTCGATCCGAACCGTCTCAGCGCGCGGACGACACGACGCGCTTGGACTACGT  
TCCGACGCAAAAGCGGTATTTGTTTCGACACCACTTTTCGCGGATTCGCGCGCGGGCCCTTTGTCGCTCGGTTTTCGCGCGCGCAATGGGTTTATCTACCGGTTACTTTTGGGATTATC  
TTCGCGTGGTATTTTCGCGCGCGGTACAGGATATGACGGTCTTGTTCGCTCTATGCGCGCGACGGTAAGTCTTTGCGCGATATTTGTAACAGGAACTCGGCATCTGCCCCGCGGTGA  
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TGCCTGTTTATGGGATTTTACAGCGCCATATCGGTCGCGCAAAATCGGCGAGATTTCCATCGTCCGCTTATTTTTCGCTGATTTGGCGGTAAATTTACGCGCGAAGATGTGGCGAAAGC  
TCCATCGGCGATTTGTTGACCTTGACGGCATCCAGCTCACTTGGCGGATATGATTTACGGTTTTCGCGCTTCGGTTTTCGCGCTTGGCTCTGCTGACCCCGCGGACTATCTCTCCA  
CTTCTCTGAAATCGGTACGATTGCGGCTTGGCTTTCGGTATCGTCATCTGTAATCCGCTTTGCAAAAGCTTCGCGTTACCCACTTTATCGACGCTTCGGGCGGTTTCGGGCGGTATTTCTCAGGCAC  
ATGTTTCCCGTTCTTGTTCATATCCATCGCTTCGGTTCGGTTTCGGCTTCCAGCACTGATTTCTTCGCGCACCGCGCAAAATGCTGGAAGAACGAAACCCAGCTCGGTATGATCGGT  
TACGCGCGGTATGTTGATGGAAAGTTTCGCGCGATATGCGCTTCGCGCTTCCAGCACTGATTTCTTCGCGCACCGCGCAAAATGCTGGAAGAACGAAACCCAGCTCGGTATGATCGGT  
ACACCGCGCGCGAAGTAATTAACCAAGCTGAACCTTCCCTGTCGATGCGCAACCCCTGTTGCACACCGCTAAGGAAGTGGGCGAAACACCATCTTGTTCGCGCACAGGCGGTTCGCGCTAC  
CCTCGCAGTGGGTATGCGCGCATATGAGCGCTCTGATTCGCGCGGAGGCGATGATGCGCATCTGCTGATCACTTCGCGCTGTTGTTTGAAGCCCTTGTTCATCTGACCGCGCTGATGCG  
GGTACCGCGCTGCGACGCTTTATGATTTAGACTTTGGGCGACATCTTCTACAAACCTTCGCGCAACCGGACTCCATCCCGCAACCTGATTGCGACCTTCTTCGCGCGGTGCGATTGTTGG  
GCTACTTCTCTACACCGCGTAACCGACCGCTGGGCGCATCACTCGCTTGGCTTTATTCGCGCATCGCAACCAATGCTGCGAGGCTAGCCTTGATTTGTTGCGCGGTGCTGCT



GATTAAGATGAACCGGACCGTTATGTCGGGTGGCACTCGTTCCTGCCGTGGCGTACTGCTTGAACCTGCTACGCCGTCTGCAAAACCTGTTCCACAACGACCCGCGCGGACGTTT  
CTTGCCACCGCAGGCAAAATACAGCGACACATTGGCTAAAAACGAAGTCTTGGCGCCGCTAAAGACATCGCGGAAATGGCGCAAAATCATCTTCAACGACAGATTAAATGCGCGGTGACCA  
TCCTCTCTTGTGCGGTGTCGTGCTGTCGCCGTACGCTTGGCTACCGCCCTCAAAAGCAGCAAAAGTGGCTGGCGGACCGCAAAAGAAATCCCGCGGTGTACCGCGACGCAAAACA  
ACCGGAGGAACAAAGTGAAGCA

## SEQ ID 6176

MKSLKTFLLWIGIVLVGLASPTTLLALSRGEQVSAVMVTAASVYCIAYFYSLYIANKVMRLDPNRLTPAERHNDGLDYPVTHKGVLPFHHFAAAGAGPLVGPVLAAGNYLPGLMTI  
FGVVPAGAVQDMFVLFVSMRRDGLSDIVKQELSTVPGVIAISIGIMIHVIMAVLALIVKALVHSPGTTTAAHMPIALFMGIYTRHIRPCKIGEISIVGFLILMLAVITYGEVAKS  
SIHWFDDLGITLQWIMYGVFVASVLPVWLLTPROYLSTFLKIGTIAALALGIVINPALQMPAVTHFDGSGFVPSGTLFPFLFTIACGAVSGFHALISSGTPKMLENETHVRHIG  
YGMLESFVAHALAAAAASLDPGVYFAMNSPAALIGTDANTAAEVITTKLNFVDAATLLHTAKEVGENTILSRGTGAPTLAVGMHIMSRILPEGAMMAFWYHFAALLFALFILTAVIDA  
GTRVARFMIQDLGSIFYPFGNFDISIPANLIATFFAVALANGYFLYTGVTDPLOGINSINPLFGIANQLAGVALIMCAVVLTKMKRDYVWVALVPAVGVLVITCYAGLQKLFHNDPRASF  
LAHAGKYSITLAKNEVLAPAKDIGEMAQIIFNDKINAGLTFLFSVVVTAAYGLRTALKARKVGHPTAKEIPAVYRDGKQPREQSEA

## SEQ ID 6177

GTGAAGCATAAGCTCGCGCTTGTGGAAAAACATCAAGCTGACGGCAAACTTGTGCGAGCGTGGCCGATTATGAAAACTACGTTGCACAACACGTAACATAATCCAAAGCCCCCG  
TGATGAACAGCTGCAATTTCAAGACTATGCGGCAACGCCGCTGCGGCGCAAAAGCGGACGCTGCTGT

## SEQ ID 6178

VKHLASWNTIKL/FANLMAGVPDYENYVAQQRKHNPAPVNMKLPQDYCRKRRGANGERRC

## SEQ ID 6179

ATGACCCCTCATCCACCCGACCGCGCTCATGACCCCAAGCCGAACCTGACCTCCGCGCTCAAGCTCGCGGTACACCCCTCATCGGCCCAACGTCGAATCGGTGGGAATACAGAAATCG  
GTCCGACCGCGCTCATCAACGGCCACACCATCGCGGAAAACACCGCATTTTCCAAITTCGCGCTCGGCGAAATTCGCGAGGACAAAANTACCGGACGAGCCGACCAAGCTGAT  
TATCGGCAACCGCAACACCATTCGCGAAATTCACCACTTTAATTTAGGCACGGTAACCGCATCGCGGAAACCGTATCGCGACGACAACTGGATTATGCGGTACTCCCACTCGCGCAC  
GACTCGGTGCTCGGCAACCAACCATTTTCCCAACAACGCTCGCTTGGCGGACAGCTTACCGTGGCGGACTACGCTGCTTTGGCGGCTACACGCTGCTTCCAAATTCGCGCGCATCG  
GCGACTACGCGATGACCGCTTTCGCGCGGCGGTACACAAAGAGCTGCGCGCTACTTTATGGCATCGCGGTACCGCGCGAACCAGCGCGCTTAAACAGCGAAGGTATGCGCGCAACCG  
TTTTACCGCAGAACAGATTTCGCGCGTCAAAGAGCTATACAAAACCTCTACCATCGCGCATTCGCTTTGAAGAGCAAGCGGACATTCTCCGCGCGCGCAACCAAGCCGAGCTT  
GCGGTATTTCAAGACTTCTTCGCAACATCGACGCGCGCATCATCGC

## SEQ ID 6180

MTLIHPTAVIDPFAELDSGVKVGAYTVIGPNVIRIGANTFIPHAVINGHTTIGENNRIPQFASIGEIPQDKYRDEPKLIIGNGNTIREPTTFNLGTVTIGETRIDNWHAYCHLH  
DCVVGNHITFANNASLAGHVTVGDYVVLGGYTLVFPQCRIGDYAMTAFAAGVHDDVPPFMAAGYRAEPAGLNSGEMRRNGPTABQISAVKDVYRTLYHRGIPFEAKADILRAETQAE  
AVFQDFPAQSTRGIR

## SEQ ID 6181

TTGGGGTGGAGCAAAAGCTCAGGGGTAATACCAAACTTAGCAACCTCAATCGGCACATCTGCCGAAGCAATGCAACCGGGGCGATTGGCTTTAGGGGGAAGTTCTGAAGCATCGAAAA  
AATTTAGTATAGCAGAAAGCTATCTGGCATCTAGTGATGGCTATGGTGAATAGCATGGTTCTGCCGCCAAGATAAGCAATTTGGAAAAAGGCACATAAATCATATTGTGGGAACGA  
TAATAAAGGCTTTATGTCGATGACAGCGCAATGTAAACAAGATAACCGTAAGGACTGAGTCGGAAGAAATATTTCTCAAGATACGGTCAAACTTACGGTGGGTGGCACTAGGGTTT  
AGATCTTCTTACATATCTTTTGGCAGTTCATTTGGAGCGTTTCTACAGCCACAGCTATTGAAAGCTTGGCAGTGGCGAGCAGCAGCAATCAACGGGCTACCGCAGTGTACTTTTG  
CGAGTCACAGCAGCGCTTGGCAGAAAGAAAGTTTGGCATTAGGTTATGAACTCGGCAATGCTTATGGTCTGTGCTTTAGTGCAGATCTGTGGCGAATGAAGAAATACCGTATC  
AGTGAGTTCCGATACATTGAAACGAAATCGTTAATGTCGCGGATGGCAGCAAGATTTA

## SEQ ID 6182

LGLRQKLRGII PNLAISIGTSABANAPGALALGSSSASKFSLAEGYLASSDGYGAIAIGSAKIKQLEKGTINHIVGNDNKLIVDADGNVITIVRTSEKDIILSRVGYTGAVALGF  
RSSSHNLFASSFGAFSTATAIESLAVGDSSTGYSRATPFSHSLAELALGYSFTRANAYGSVALGAESVANEENTVSVSOTLKRKIVNVDGTELL

## SEQ ID 6183

ATGCCGCTGAAGCCGCTTCCCGCTCAGACGCCATTTGTACGGATGACCAATATCTCCGTTTTTTTACTTTCAATAATCAGATATGCCCGAACCCGCTCGCAACAGTATCCGTA  
CCGATCCCGCAATGT

## SEQ ID 6184

MPSEARFPLQTPFCTDDPSSVFLLSIIIRYARTTVRQRYRTASACQ

## SEQ ID 6185

ATGAGAAAAAGCCGCTTAAGCCGCTATAAACAATAAATCATTTGAAGCTTTTGTGCGAGCGTAACGCAAGAACAGCAACAGGCTGACAGCATTTGTATACGGAATGTTATCGTC  
GCTATGATGATTGGATGCGAGCGAATTTAGCCATTTCCGTATCAATCACAGCACATTTTCCGCAAGCAGCAAAACCATATTAATGGAATTGGAACTTTTGAACCGGGCAAAAGCTCA  
TTACGCAAGTTTGACGCAATTTCCAAAGAGCATTTTGAGCGTATTTAAAGAGTGGCAACCGGCTTTT

## SEQ ID 6186

MRKSLRSRYQNKILFVAGVTARTATEPDSIVTDCYRRYDVLDAFESHFRINHSTHFAERQNHINGIGNFWNRAKRHLRKFDPKHEFEPYLKECEREP

## SEQ ID 6187

ATGCGGCGACGCTGCTGATACCTATTCTTTTTCAGTTTTTATTTTATCCGCTGCGGGACACTGACAGTATTTCCATCGCATGGCGGAGGCAACGCTTCGCGGTGCAACAGAACTTG  
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CTACTCCATTGATGACGTGATTCGCGGCGAATACATAACAGCCCTGCGGTGCGCACCGATTACACTATCCGCTTACGAAACCAACCGCTGAAACACATCAGCGGTTTGACGGGTTA  
ACCACTTCTTTATACACTTAATGCCCTGCACTCTCGCGCACCAATCAGAGGTAGCGGAAGTAGGAGCAGTCTGGGCTTAAATATTGGCGGGATGGGGATTATCGAAATGAAACCT  
TGACGACCAACCCGCGGACACTGCTTTCTTCCCACTTGGTGCAGACCGTATTTTCTGCGCGGATAGACGTTGTTCTCTCCCAATGCCGATACAGATGTGTTTATTAACATCGA  
CGTATTCGGAACGATACGCAACAGAACCGAAATGCACCTATACAAATGCCGAACACTGAAAGCCCAACAACTGGAATATTTCGAGTAGACAGAACCAATAAAAAATGCTCATCAAA  
CCCAAAACCAATGCGGTTGAAGCTGCTATAAAGAAATACGCCATTTGGATGGGCGCGTA

## SEQ ID 6188

MRARLLIPLFVPILSACGTLTGIPSHGGKRFVPEQELVAASARAARKMDLQALHGRKVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTGL  
TTSLSLTINAPALSRQSDGSGSSSLGLNIGMGDYRNETLATNPEDTAFSLHVLQVTFPLRGIDVVSANADTVFINIDVFGTIRNRYEMHLYNAETLKAQTKLEYFAVDRTNKLLIK  
PKTNAFEAAKYENYAVDGA

## SEQ ID 6189

TTGATTCACACTGCCATAACCGCTTGTGCGCAAGGAAACAAATGAATTTGCCATTCAAAAATTCATGATGCTGTTTGCAGCGGCAATATCGTTGCTGCAAAATCCCAT

## SEQ ID 6190

LIRTAITACCGKQNEFAYSKIHDVCSGNIVAANPH

## SEQ ID 6191

ATGGATATGACGGGCTCAAGCGCGGCTTATCCGCCGCCGAGGGGCAAGGATATATACAGCTACCATATCAAGGAACCTCAACCAAAACAAAGA

## SEQ ID 6192

MDRTGLKAAVIRPPEGQGIYATFISKELQPKQR

## SEQ ID 6193

TTGCTGCAAAATCCCATTTAGTCATGCGAACGGTTTGGATGCCGTTTGGCGGATGATATGCAGGCAAAACACTACGAACGGGTGGCAAAATACCATCTGTTTGGTAATGCTCGGGCAGTG  
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ACACGGACACGAAGTACACAGTCCGTTTCGATAATCATGATTCAAAAGACACTTCTGATTTCAGCGCGCGGTAGACGCGGTTTACCGTTTACCACTTCATCGGACAGGGTCGGAATC  
CATCCGGAGGATGATATGACGGGCTCAAGGCGCGGTTATCCGCCCCCGGAGGGGCAAGGATATATACAGCTACCATATCAAGGAACCTTCAACCAAAACAAAGATAAACACTGTTTC  
CGCAAGCCCCTTTTTCAGACGCGTGGCTAAAGAAAATGCCGGTCCGCTTCCGGTTTTCTCAGCGGTGCGGATGAAGCAGGAAACTGATATGGGAAAACGACCCCGATAAAATTTGGCG  
GGCTAACCGTATGATGATATTTCCGGCATCGTCCAAGGTGCGGTTAATCTTTTTTAACGGGTTTTCAGGGATTGGGAGTTGGGCAATTACAGACAGTGCCTTAAGCCCGTAACTAT  
GCGGACGACGGAACCTTTACAGGGTATTACAAATTTAGGAAATTTAAGTCCGGAAGCAACACTGCGCTTACAGGCGCAACCGCATTACAGACAGTGCCTTTGCGGTAAAGACAGTATCACT  
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AATTTTTTTGAAATACCGGTTATACAGAGAAAGTATTAAGCAAGCATCGAATGCTGATTATCATGTTTCCGCAATCAGTAGATGCTTTTTCTGAAATGGAACAGTAATCAAAATAG  
TTGCGGAGATAATATTGTAAGGCATAAATCTTATATCCCTGGATCTTATAAGGAAAGATGGAATTTTGAATATATCAGAGAAGCAGATGGAATAATTAATCATAGATTATTGTGCC  
TAACCAACAACTCTCTGAAAAA

## SEQ ID 6194

LLQIPISHANGIDARLDMDQAKHYEPGGKYHLFGNARGSVKNRVCVQTFDATAVGPILPITHERTGFEVGIYETHFSGHGHVHSPFDNHSKSTSDPSGVDGGFTVYQLHRTGSEI  
HPEDGVDGPQGGYTPPGGARDIYSYHIKGTSTKTKINTVPQAPFSDRLWKENAGASGFLSRADEAGKLIWENDPKNWRANRMDIRGIVQAVNFTGTGQGLVGATITDSAVSPVTV  
AAARKTLQGIHNLNLSPQAALAAALQDSAPAVKDSINSARQWADAHNPITATATQALAVTEAATFVWGGKJVELNPAKMDWVKNVTGKYPAAHMQTVDDGEMAGGNKPLESKNVTNTN  
NFFENTGYTEKVLRLQASNGDYGHPQSVDAFSENGTVIQTIVGGDNIHVKLYIPGSGKGDGNFEYIREADGKLNHRLFPVFNQQLPEK

## SEQ ID 6195

ATGGAAATTTTGAATATATCAGAGAAGCAGATGGAATAATCATAGATTATTGTCCCTAACCAACAACTTCTGAAAAATAGTAGA

## SEQ ID 6196

MEILNISEKMEKLIIDYLSLNNFLKNSR

## SEQ ID 6197

ATGTCCCGATGGCAGCGAAGATTATGATGCGAGTAATGTCCGCCAGTTGAACCGCTTAAGCAACAGTACAAACCGGTGCGCGCAAGTGTGCGCGCTTGGCTTCGTTAAAACTGCAC  
AATTAGGCAAAACGACAAATTCGCTTTTCTTTGGGCTTTGGAAGCTATAAAAAATGCCAAGCGGTGCAATGGGGCGGTGTTTAAAGCCCGTGAAATGTGTTTAAATGTGGCGGG  
CAGTTTTGCGCGGACCGGACCGGCTTTCCGCGCGGGGTTTGGGAAATTCGCGCGGCAAAACCGCAACCTCGCGTTGCGCGCAAAACCGCGGCGATCTTCAAAAGTTTTCGCAATGGCGG  
CAGGAAGTGGCGCGCTTCCGCGCGCGGCGAGCAAAACCGCGCAAACTGCACAAACAGCGCGAAATGGAAGAGCTGCAACAGTTGCGCGCGCGCTTGTCCGAATGAAAAACAT

## SEQ ID 6198

MSPHARKIYDAVNVRLNRLSKRTNVRGASAAALSLKPAQLKNDKFAFSLFGFSYKNAQAVAMGAVFKPAENVILNVAGSFAGPDRAGAGVFMKFGKPTPAVAAQNAHPAKVLQLR  
QEVAAALRAQAEIDRLKHKQAEENELQQLRRALSELKHH

## SEQ ID 6199

ATGCTCACGATTTAGAAAAAACGCCATCCGCGACCATTTACCAAAATATCGGCAAAACCTGCCCGTTCCGTCGCGGTCTTCGACGCGGAAATGATTGCGCGGTGCCAACGCTT  
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CATCATGCGCGCAACACGCGCGCAAGCGGTGATGAGCAGCGGACGCTTTCGCTTCGAGGAGCAGTTGTTAGACCGCGACCTGCGCTTCTGTCGAAAAAGCGGTTCGGAAGTACG  
TTCCACTTTCGCAAGGCGCGCGCGCTATCTCTGCCCTTACAACTCTATCACTGACGCAAGCAAGCGCCAGCAAAACCTGCTCGGCTTTGAAGCCCCCGCTTGTGGGACAGCA  
AACCAAGCGCGAAGAAATTGAAGCTGCTGCGGACATCGCGGACAAATTTCCGCGCGAGGTTCAACGGCGGACCGGCGGCAAAATCGATGACCGGATTTGGCTCAAAAGT  
GACCAACGACCGCGCGCTGCTGAAAGCGGCTGTCACACCGTCCGGAATGCCCTTTTACCTGGCAGCGATATGTTGGAACCGTGCATGCTGTTGTCGAACCAACGATCTCTG  
CTTCCGACATCAGCATGGGCGCGCGGTGATCTGCTGCGCGCGGAAACAGTTTCTATTGCATAGACGAAGCGCACCACTGCCCAAAAAAGCGCTCAGCGCTTTTCCGCGGAAACAT  
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GAAGGCTCGAAACACCGCTTCAATACGCGCATGCTGACAGCGAGCTGCTCAACACGTTGCTGGGCTGAACGATGCGCTTTCCGCGCGCAACCGCGGCAAAACAGCAACGCGTGGC  
TCATCGACCGCTGACCGGAGTTCGCGCTTTTATCGCCGATATCGAACAAATCAAGTACGCGGTTTGGGATTTGCTCTCCACTGTTTCCATTTAGGGGCGAGGAGCGGTTCGCGAATGGAT  
AGCCCGCGCTGCGGAGCAAAAAACGACTATATTTCATGCGAGCCCATCAGCAGCGGCTCCCACTTGGCAACAGCTGTCGCGCGCGCGCGGAGCGCGGTGCTGACTTCGCGCAC  
CTGCAATGCTGCGGAGCTTCACTTGATTGTCGCGCAAAACCGGCTGCTGCTGCTGCGGAAACCAACCTTCCGCTCAAAAGCGCTTTGACTTTGAAAAACAGGCGCACTTAC  
TCCCTTCAATATACGCGAGCCCCAAGAGCCCCAAGCCCCAAGCGCGCGCTCATGGAATGCTGCCCAAGCTGATTTGCCCAACCGAAGCATCGGCACACTGCTCTGTTTCTTGGG  
CAACAAATGACGAGTGTGCGCTGCACTGCGCGGAGACTACCTGCGCTCTGCTGCTACAGGCGAATTAACCAAGCGCTTCTCTGCAAAACACCAAGCATAGAGAGCGG  
AAAGCAGCATCATCTTCGAGCTGCAGAGCTTCCGCGAAGGCGTCACTGCGCGGCAACCGCTTCAATCGAAATCAACAGCGCGCATCAAACTCATCCAGGCGGTGCGCGGCTCATCCGCAACAGACTA  
AAACCAAAACCGTTGGATAGAACACGCGCGCAACCGCTTCAATCGAAATCAACAGCGCGCATCAAACTCATCCAGGCGGTGCGCGGCTCATCCGCAACAGACTA  
CGCGCGCTAACCATCTCGACCAACCGCATCAAAACGAGCGGTACGGCAACAAATTTTGGCGCGCTGCCACCGTTTAAAGGATAGG

## SEQ ID 6200

MLTDLEKNAIRDHYQNIQKNLPGFRPRASQREMIAAVANAFSRTLTREEGGEPKREGESIAVIEGPTGVGKSLAYLLAGGIMAQTRGKRLIVSSATVALQELVDRDLPLFVKSGLLEI  
FALARGRYLCPYKLYQLTQSNQONLLGFEAPAVLWDSKPKPEELKLRLDIADEF SARRPFGDRDAMPEKIDDAIWLKVTNDRHCLKAACFNRPBPFYLARDMLFTVDVVVANHDL  
LADISMGGVILPAPENSPYCIDAEHLPLKALSRAARHSNIAVWLEKLPLQTKIAL/TKAEALNLADEAAASLLDSLHEWQPHLEBEPSSLXGSENDRTINSEPTWLMEDGKIP  
EGLETTVSNIAARSLKHVVLNDLALSARREKEQDGLIDRLTGEPLFIARIEQISAVDILLSTVSEIEGEPLAKWIRARRDDKNDIYNASPISSASHANSLMRRAGAVLTSAT  
LQSLGPNLILRQTLGLWLPETITLALKSPFFDEFQGLYIPSTIYASPKDPEAHTAAVIEWLPLKLSPTAIGTLVLFSRQKQDVALHLPDYLPLLLVQGLPKAVLLQKHQAIEEG  
KASIIPLGDSFAEGLDLPGTACVQVILAKLPFAMPIDNFIETQNRWIEQRGNPFIETVPEAGIKLQAVGRLLIRTEQDYGRTITLDRIKTQRYQQLLAGLPFFKRIG

## SEQ ID 6201

ATGTTAAATGAAATTTTGAAATTTATTCGAGACAAGGGGAATTTTGATAGGAATTGGAATTAGAGAAGCGCATTACCGTCCCACTGCAATAGATATATTAATTTATTTATAAATG  
AAAGAAATCTTGTATTTGGGGGAGATATTATATCAAGAAAGATAATTTATTTTCAACAAATATGATAATTGTTTACGAGGGAAGTAATTTATTTAACAGTATCAACAAAGCAATGCA  
TTATTTATCTCAAAATAAATAGAGAATGCATACGTGCTTTTGTGTTTGAATTTATC

## SEQ ID 6202

MLNFIETYSRQGESLIGIGIREAALPVPTAIDILNLPINERILVLGGDIYIKKNYFYQTYDNWYEGSNLNFNSINKAMHYLSQIKLENAYVSFVLFPI

## SEQ ID 6203

ATGACAGCTGTAGATGGGAGATGGCAGGAGAAACAGCCAGTTGTTAAATCTATTAGACCACTACGCGAGATGAATTACGTCAAGCATTCGCAAGAACAGGTTTACAGCTACTGGTT  
CAGATGCGGCTCAATATGAACATGGAAAGTCTGATGCGGTGAAAAATAGATATTGCTCCAAATGGAGAGGTTATAAGAACCCAAAGAGTCCCGGCAACCGCATGGTGTACAGGAAAAA  
TCCGCAACGACAAGATTATGAAGCAATCCATTGCCAAATAATCATCATCTTCCGATTTTGTCAAA

## SEQ ID 6204

MQTVDEMGAGNKFVVKSRPTTRDELQALQEQGFRRTGSDAAQYETWKGPDGVKIDIRPGEVIRTPRVPRFDGVQGYKYPQDYEGNPLNNHHSYFVK

## SEQ ID 6205

ATGGGTGACAGGAAAAATATCCGCAACGACAAGATTATGAAGGCAATCCATTGCCAAATAATCATCATCTCGGATATTTTGTCAAATGAAAAAAATATTTTTCACAAATGTAAGCCTTA

## SEQ ID 6206

MVYRENIRNDKIMKAIHQIIILIDILSNEKKYFSQCKPL

## SEQ ID 6207

TTGAATTTTAAATTAGATACAAATAATTTCTGTAGATTATGAGGATAAGGAAGATAGCTTGTTTCCCTTGTTTATACCCGAAATAGAGCTATATAAATACCAATTTTATAGTGAAATATATTA  
TTGATGTAGGGATTATATAAAAAATATCTGCTGAAACAATTAATTTTGAGCCACTGGGAAAA

## SEQ ID 6208

LNFKLDVNNFVYEDKEDSLFPLFIPEIKLYKYQYSEIILDVGLIILKISAEITNFEPLGK

## SEQ ID 6209

GTGAGCCTATTACAGGACAGTCTTTTCCGGTAAAGACGGTATCAACTCTGCCAGACAATGGGCTGATGCCATCCGAACATTACAGCTACTGCCCAAACTGCCCTTGCCGTAGCAGAGG  
CCGCAGGTACGGTTTGGAGAGGTAAAAAGTAGAACTTAACCCGACTAAATGGGAT

## SEQ ID 6210

VSLIQDSAPAVKDGINSARQWADARPHITATAQTALAVAEAAGTVHGGKVELNPTKND

## SEQ ID 6211

ATGCAGACTGTAGACAGGGAATGGCTGGGGGAAACAAATCAATTAATAAGGGACAACTCTGTTGAAAAATCAACCGGTCTGACAATACCTAATAATTTAAAGGAACAATTAGCAATGG  
AAGAAGTTAAGGCAAAACCCACAGGCAAACTCTCGGAGAACTACCTCTTATGTCCGACTACTAAAAATGGTTGGTTGGCAAAAGACGGCTGGGTTAAGCGGTTCAAAATATAAACAAAGT  
TGAGATACATTACATTGAAAAATACAAGAACCGGTGAGAAAAACAGATTCAAGTTAAAGGAT

## SEQ ID 6212

MQTVDEMGAGNKSILKIGTQSVKSTGRTPNNLKEQLAMEEVKANPQGTTPARIPPHSDTKNGHLAKDGVKRVQNKVKELHYIENTRTGERTDFKFD

## SEQ ID 6213

ATGTTTTAGATGATGTAATGTTTTTTAGATGATTTAAATACCAATCCAATCACTGACGAATGGTATATGTCCAATTTTGGCGATAAACAATTTAAATTTTGGAAAGTTACGAAGCCT  
TTGATATCTTAAACAATTTGTTGATTACATGATTGAAGAACAATGATGAAAAATCAGAAATGAAATCATGGAAATATTGAGACAAATTAATATCAAGCAGATACCAACGAAAAATTTTA  
TACAAATACACAGAAACAGAAAAATGTAGAATATATAAACAAGAAATTAGTCAGGATATTTTAAATGAAATCTTTAGA

## SEQ ID 6214

MFLDDVNVFLDULWNPITDEMYNSNFKHRIKILSYEAFDILKQFVDMIESEHDERSEYELMELRLQKYQADTNEKFTNTQKQKIVELYKQELSDILNELFR

## SEQ ID 6215

ATGAGAAAAAGCGCTCTAAGCCGGTATAAACAAAAATAACTCATGAACTGTTTGTCCGAGCGTAACGCAAGAACAGCAACAGAGCCTGACAGCATTGTTTATACCGATTGTTATCGTC  
GCTATGATGATTGGATGCGGGCAATTTAGCCATTTCCTGATCAATCAAGCAGACATATTTGCCGAACGACAAAACCATATTAAATGGAATTTGGGAACCTTTGGAAACCGGGCAAAACGTCA  
TTTACGCAAGTTTGACGGCATTCCAAAGAGCATTTTGAGCCGATTATAAGAGAGTGCGAACGGCGTTTAAACAACAGTGAGATAAAAGTTCTTGTTCACATT

## SEQ ID 6216

MRKSRLSRYKQNKILFVAGVTARTATEPDSIVTDCYRRYDVLDAGEFSHFRINHSTHFAERQNHINGIGNFWNRAKRHLKFDGIPKEHFEPLYKCEBRRFNNSEIKVLVFF

## SEQ ID 6217

ATGGCGTTAGCTGTGCAACAACACTTTCTGCTGCTTAGCGCGGCGGAGGCGGCCTTCTGCTCCGACTTTAATGACAGGCGGCACCGGTATCGGCAGCAACAGCAGGCAACGATAG  
CGGAATCAGCAGCAGTATCTTACCGCGGTATAAAAAAGCAATGTGCAAGACAGAGCATGCTCTGTGCGCGGTGCGGATGACGTTCGCGGTACAGCAGGAGTCCCAAAATCAAGGCC  
CCGAATCTGCATACCGGAGACTTTTCAAACCCAAATGACCAATATTAAGAATATGATCAACCTCAAACCTGCAATTTGAAGCAGGCTATACAGGACCGGGGTAGAGGTAGGTATCGTCGAT  
ACAGCGGAATCCGTCGCGCAGCATATCTTTCCCGAAGTGTATGCGAGAAAGAACCGGCTATAACGAAAAATTACAAAAACAAATTACAAAACTATACCGCGTATATGCGGAAGGAAGCG  
CC

## SEQ ID 6218

MALAVATTLASACLGCGGGTSAPDFNAGGTGIGSNRATLAESAASVYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKIKAPRICIPEFTQTQMTNIKMINLKAIEAGTITGRGVEVGI  
TGESVGSISFPPELYGRKEHGYNENYKMKLQKLYGVYAEGBA

## SEQ ID 6219

ATGCGGAAGGAAGCGCCTGAAGACAGAGCGGTAAAGACATTGAAGCTTCTTTGGACAATGAGGCCCTTATAGAGACTGAAGCAAGCCGACGGATATCCGCATGTAAAGAAATCGGAC  
ACATCGATGTGCTCTCCATATTATTTGGCGGGCGTTCCGTGGACGGCAGACCTGACGGCGGTATTGCGCCGATGCGAGCTACACATAATGAATACGCATGATGAACCAAGAACGAGAA  
A

## SEQ ID 6220

MRKEAPEDRGKDIASLDNEALISTEAKPTDIRHVKEIGHIDVSHIIGGRSVDGRPAGGIAPDATLHIMNTHDGTNKEK

## SEQ ID 6221

ATGAACCTTCAACCGGTGCTCAACCAAGCTTTAAGCAGCGTTCAAAAAAAGGCAACACATTTCTCCGCGAGCCCGCTCAATTCATTGCGCGGAGGCGCGCTGGTTGCCGCTGTCGCCCTCA  
TGCTGCTGAACGGTAAAAACCGCAAAACCATCAACAAAAATCGGTTGACCGCGCGCTTTGGGCTACCTCGCTACCGGGCTATCAGATGTGGCAGCAAAACAAAGGGCGGGCAACCGTAAC  
ACAAAGCGATTTCACCTCGCGGAAAACTGAAGAAACATACAGCCGACCGTATTCGCTACCATGATAGCCCGCGCGCTTCAGACGGCATGATAGCAAGCCGAACCGCGGACTATC  
GAACAGGAAAGCGGCACAGACCCCGAACTGCGCGCATGGCTGCGCCGCAATACCGCTGCGCCGAAGCATCGGGGACATCGCCCGCGCTCGGCAACGATGAGGCGCTTGGCGCGCGAGA  
CCTATCTGGCGCAAGGTTGGTCTGTCGCCGATTGTCGCGGAAGAAACCGTCTTCTCGCCCGCTGTCGCGAGCTTTGAAACTGGATGACAATCTGGTGGAGAGTTTGGAAAGGCAACT  
AGGGATT

## SEQ ID 6222

MNFRLILNQVLSIVQKGNFTSGSPLNSFGGALVAGVASHMLNGKNRKTITKIGSTAAALGYLARGYQMWQNKGRATVTQSDFPQAGKTEETYSTFVLRTHIAAASDGHIDEAERTTI  
EQESGTDFTAAWLAAEYRLPASIGDIAAVGNDEALAAATYLAARLVADLSRKEVFLARLSQALKLDDNLVESLERQLGI

## SEQ ID 6223

ATGCTGCGACCATCCGCAATGCATGGGTCAAGCTGGGCGAACGTGGCGTCCGCTCATCAATAACAGTTTGGAAACAACATCGAGGGCAGGCACTGCCGACCAATTCACAAATAGCCAAAT  
CGGAGGAGCAGTACCGCCAAACGTTGCTCGACTATTCGCGCGGTGATAAAACAGATGAGGGTATCCGCTGATGCAACAGAGCGAT

## SEQ ID 6224

MSAAILRNWVKLGERGVIRVNNFSGTTSRAGTADHFQIANSEBQYRQTLFLDYSGGDKTDEGIRLMQSD

## SEQ ID 6225

TTGTGTCTCATTCGCTGCGAAAGATGAAAGAGATGTTTTTATTACGGATGTGGTAGGACAGGTTGCCCTAATCGCTCTGTTGCATCAGCGGATACCCCTCATCTGTTTATCACCGCGG  
GAATAGTCCGACCAACGTTTGGCGGTACTGCTCTCCGAATGGCTATTGGAAATGGTCCGCGAGTGCCTGCCCTCGATGTTGTTCCAAAACCTGTTATTGACGATGCGCAGCCACGCTTCGC

CCAGCTTGACCCATGCATTGCGGATGGCTGCAGACATTATTTCCTGTTCTTGGTTCCATCATCGGTATTCATTATGTGTAGCGTCGCATCGGGCGCAATACCGCTCGAGGTCTGCGCTCC  
ACGGAACGCGCCCGCAATATATGGGAGACACATCATGTGTCCGATTTCTTTTACATGGCGGATATCCGTGCGCTTTCAGTCTCTATAGGCGCTCATTTGTCAAAGAGCTTCA  
TGTCTTTACCGCTCTGTCTTCAGGCGCTTCCCTCCGCATATACCGCTA

## SEQ ID 6226

LCVIAKRDKEIDVFTFDVVGQVALIHLHQADTLICFITAGIVEQRLAVLLLRIGYLEMVGSAFPRCCSKTVIDDHAHTFAQLDPCIADGCRHYFSFLVPSCVFIMCSVASGAIPPAGLPS  
TERPFIINWETTSMPISFTWRISVGFASVSIRASLSKEASMSLPLSSGASFRITAV

## SEQ ID 6227

TTGTCTATCTGCGCAGATACGACCAATCCGGCGCAACGAAACCGTACACATCAAAAGCGCGTCTGCAGCTGGGCGCAAAAGGTACGCTGTACACAGCTTTGGGCAAACTGCTGAAAGTGG  
ACGGTACGGCGATTTACCGACGGCAAGCTGTACATGTGCGCACCGGCAAGGGGCGAGGCTATCTCAACAGTACCGGACGACATGTTCCCTTCCTGAGTCCGCCCAAAATCGGGCAGGATTA  
TTCTTTCTTCAAAANTATCAAAACCGACGGCGGTCTGTCTGCTTCCCTCGACAGCGCTCGAAAAACAGCGGGCAGTGAAGGCGACACGCGCTCTATTATGTCCGTCCGGCAATGCGGCA  
CGGACTGCTTCCGCGAGCGGCACATTCGCGCGCCCGCGGTCTGAAACAGCGCGTAGAACAGGGCGCGCAGCAATCTGAAACAACTGATGTGAGTGGTGGCTCCGGAATCATCCGCAACAC  
CCGAGACGGTTGAAGTCCGGTCCGCGACCGCACAGATATGCGGGCATCCGCTACGGCGCACAACTTTCCGCAACGCGCGGTACAGCATGCGAATACCGCGACGGCGTACGCAAT  
CTTCAACAGTCTCGCGCTACCGCTCTATGCGGACAGTGGCGGCGCATGCGGATATGCAAGCGGCTGAAAGCGGTATCGGACGGTTGGACCAACAGGTACGGGTCTGCGCTC  
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CCACACTGGGCTAGGACGACGACATGAGGCGAAAAACAGTGAATGCAAAACCGACAGCATTAGTCTGTTTGCAGGCATACCGGACGATGTGGCGGATATCGGCTATCTCAAGGCGCT  
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TTTCCGCGCAACGGGAGATTGTACGGTTGAAGGCGGTCTGCGCCACGACCTGCTCAACAGGATGATTCGCGGAAAAAGGCGAGTCTTTGGGCTGGAGCGGCAACAGCCTCACTGAAGGCA  
CACTGGTCCGACTCGCGGGTCTGAACTGTGCAACCTTTCAGCGATAAGCGCTCTCTGTCTGCGACGCGCGGCTGGAACCGGACCTGAACGCGGCGGACTACCGGTAAACGGCGGCTT  
TACCGCGCGGCTGCGACCAACCGGCAAGACGGGTGCACGCAATATGCGCGCACACCGCGGTTCGCGCTCTGGGGGTGGATGTCGAATTCGCGCAACGCTGGAACGGCTTGGCAGCTTAC  
AGCTACACCGGTTCCAAACAGTACGCGCAACACAGCGGCAAAATCGCGGTAGGCTACCGGTTT

## SEQ ID 6228

LSIWQIPTNPAQTKPYTSKGLQLGDKGTLYTRLGKLLKVDGTAITDGLKLYMSARGKAGYLNSTGRHVPFLSAAKIGQDYSFFKNIKTGGLLASLDSVEKTAGSEGDTPSYVRRGNAA  
RTASAAAHSAFAGLKHAVEQGGSNLENLMVELDASESSATPBTVEVADRTIMPGRILRRITPTTAAAVQHANTADGVRIFNLSLAATVYADSAHAADMDQRRRLKAVSDGLDHNGTGLRV  
IAQTQDDGGTWEQGGVEGKMRSTQTTIGLAATGENTTAAATLIGRSTWSENANAKTDSISLPAIRHVDVIGYLGKLSYGRYKNSISRSTGADEYAEBSVNGTLMQLGALGVNVP  
FAATGDLTVEGGLRDLKQDAPAEKGSALWGSNSLTETGLVGLAGLKLSQLPSDKAVLSATAGVERDLNDRUYAVTGFTGAAAAATGKTGARNMPHTREVAGLVDFBFGNGWNLARY  
SYTGSKQYGNHSGQIGVGYRF

## SEQ ID 6229

TTGCGGCTGTTCTTATGAAAAAGAAACCCCTATTCCAAATGCGCTCTTATTGTTTCAAGACTTCTTCCAAAGATTTCGGCATCAATCAGACGTATACGGGATTAACAAAAANTCAGGACAA  
GGCGCGGGCGCCAGACGGTACAAATGGTACGGAACCGATCCGCGCGTCTTGGCGCTCTTAGGACCGCTTCCCTTTGAGCGGGGCGGGGCAACCGGTACCGGTTTTTGTTCATCCGC  
CATATTGTGT

## SEQ ID 6230

LRLFLMKRKYNSCLLLLQDFDQRFQINQYISGLTKLRTRRAADGTNGTEPIRPVLGRLEFPFLSRGGATRTGFCSSAILC

## SEQ ID 6231

ATGGCGGATGAACAAAAACCGGTACGGGTGCCCCCGCCCGGCTCAAAAGGAACGGTTCCCTAAGACGCCCAAGCACCGGGCGGATCGGTTCCGTACCATTTGTACCGCTCTGCGGCGCGCC  
GCCTTGCTGATTTTGTGTAATCCGCTATACGT

## SEQ ID 6232

MADEQKPVVAPRLKNGSLRRPSTGRIGSVFPVPSAARLVLIFVNLVIV

## SEQ ID 6233

TTGTTATCCGCCATATTGTGTGAAACACCGCCCGGAACCGGATATAATCCGCCCTTCAACATCAGTGAATCTTTTTTTTAAACGGT

## SEQ ID 6234

LFIRHVLKHPPEPIIRPSTSVKIFFLTC

## SEQ ID 6235

TTGCTTCACTTGCCTGCGCTGCGGAGAGAGAGAGAGGTTTTTTCGGGCTGGATTCAATTTTCGGCTCCTTATTCGGTTTAAACCGGTTAAAAAAGATTTCCTGATGTTGAAG  
CGGATTATATCGGTTCCGGCGGTGTTCAACACATATGCGGA

## SEQ ID 6236

LPSLAACAAEKRFFAGWIHFRLLIRPNRLKRFSLMLKGLYRVPGVSTQYGG

## SEQ ID 6237

GTGACGGCGGATTTAGCCTACGCGCGCAACGCATTACCCACGATTATCCGGAACCAACCGGTACAAAAAAGACAAAATAAGCACGGTAAGCGATTATTCAGAAACATCCGTACGCAAT  
CCATCCACCCAGGGTGTGCTGCGGTACGACTTCGGCGGCTGAGGATAGCGGCAGATTATGCCCGTTACAGAAAGTGAACACAGTAATATTCGCTCAACAAAAAGGTGAACGA  
AAACAGGGCGAAAGATAAAGCTGACGCAATATCTGAAGCGGAAATCAGAAAAACGGTACGTTCCACGCGGTTTCTTCTCTCGGCTTGTTCGCGGTTTACGATTTCAAACTCAACGAC  
AAATTCAAACCTATATCGGTGCGCGCTGCGCTACGGACAGCTCAGACACAGCATCGATTGACCAAAAAAACAACAGAGTTTCTTACCGCGCGGTGAGGATGGCGGAGCGCTACGG  
TTTATAATAACGGAAGTACGCAAGACGCCATCAAGAAAGCGACAGCATCCGCGCGTGGGCTCGGCGGTATCGACATCACGCCCAACCTGACCTTGAACGCGCG  
GTACCGCTACCAACATGGGACGCTTGAACCAACCGCTTCAAAACCCAGAACCGCTCGTTGGGCTATCGCTACCGCTTC

## SEQ ID 6238

VQADLAYAERITHDYPTGKDKISTVSDYFRNIRTHSIHPRVSVGYDFGGWRIAADYARYRWNNISKYSVMNKKVNEKGEKINVTQYLKAENQENGTFHAVSSLGLSAVYDFKLND  
KFKPYIGARVAYGHRHSIDSTFKTTEFLTAAGQDGGAPTYYNNGSTQDAHQESDSIRRVGLVIAGVGFDTFNLTLDAGYRYHNNWGLENTREKTHEASLGRHYF

## SEQ ID 6239

ATGCGGCTGAAACCCGAAAGCGTTTCAGACGGCATCGGTTTTTTTTTAAAGCGGTATGTTGTTGATCGATGCATCAATTTGTATAGTGTT

## SEQ ID 6240

MPSETPKAFQTASVFFKAVCLLDASFCTIV

## SEQ ID 6241

ATGTCGTGGCGGATTATAACGCGCCCGCGCGGGGCAATACGGCAAAATGCGCGCAAGCATCGGCGATGGCGGAACCGGGTTCCGGCGGTAAAAATGCCGTC

## SEQ ID 6242

MSWRIITRPAAGYKCRAKHRLAEPGFGRVKNV

## SEQ ID 6243

ATGAACAAACACCCCTTTCCCTCGCGCTGCTGGGACACACCAACACCGGCAAAACCTCGCTCTCGGCAACCTGTTGCGGACAGCGGCTTCGGCGAAGTCAGAAACGCAACCGTCCACCA  
CAGCGCATGTCGAAGAAGCGCCATCAGCGACGGCGGACATGTTGGTTTTCTGTATGACACGCGCGGCTCGAAGACGCGGGCGGTGTTTTGGAATGGCTGGAACCATACGAGCA  
TCGTTACAGCGCATCGAGCGGTGCAACAGTTTCTCGGACGCCAGCGCGCATCAGATTTCACCAAGAACGCCAAGTCTCGCGGAGGTTTTGCAAGCGATATGCGCAATGTACGTC

GTGCGGCACATCGCTTCGCGCGAAGCCGTGCCGAAGCACCCGGTAATTAACACAGCCATTGTTTTCCTTTCTTCTTCGTTTCCCAACCCGTTCACGATATCATACACCCCTTCAGAGCGGCAT  
CGCGCGCGCTGAAAAAGCACACACCGTACCACCACGACAGGACACATTCACATGAGAAACCCAAATCAGCCTTCGCGCAACCGCCCTCGCCCTATTCTCTTCGCGCTCGGAAACGGCGG  
CGCGCCCGCACAGCCCAAAGGGGAAATTTCCGAAAAACCGCACCGCGCGGTTCAAAATCTATGATGCCCGACTTCTCGCGTATGGGCAAAATGGTCAAAAGGCGAAGAGCCCTACGATGTGCGAA  
AAATTCAAACAGGCGGGCGCGCGCTTTCGCGAAGGACGCAAAAAACCGTTACACTTTTTGAGTCCGATCCGAAGGCAACGGCGCGCCCTGCTCGCGTTTGGTCGGATGGTGCAGAAAT



TTGAGCCGAAAAACAATAATCGCCGCGCCGTCGAAAACTCAACGCCGCCGCCAAACCGGCAAACTGGACGAATCAAGCCGCTTACGGCGAACC GGCGCAAGCTGCAAAATCTG  
CCACGACAGTTTCGGCGGCCCGAA

**SEQ ID 6256**

SEQ ID 6256  
VRHLASPKFAEAPVIRKTAIVPFFFLVSQTCFRVHNTLQTASRLKTTTTVPFRQDTFMKQTQISLAATALALFLSACGNGGAPQPKGEISENRTAAFKSMMPDFSRMGKMKVGEEFYDVE  
KFKQAAAAFAESSKKPPTFLFESDPQNGRALPAVWSGAKFPAEKTKPAAAVEKLNAAAQTGKLDEIKAAAYGETGASCKSCHDSFRAPE

**SEQ ID 6257**

SEQ ID 6257  
TTGTATAGTGGTTTAAATTTAAATCAGGACAAGCGCAGAACCGCCAGACAGTACAAAGAAGTACGGCAAGGCGAGGCAACGCTGTACCGGTTTAAATTTAAACCACTA

**SEQ ID 6258**

LYSGLNINQDKATKPQTVQEVROGEATLYRFFKFKPL

SEQ ID 6259

SEQ ID 6259

TTGATGTCAGAGCTGTCCGATACAGGCCCTGAAATTGACGGATTGCGGGCCGTGCGCGTGCTATTCGCTCATTTATTTCCACCTGAATAACCGCTGGCTGCCCGAGGATTCTCTGGGGGTGGACA  
TTTTCTTTGTCTATCTCGGGATCTCTCATTTACCAACATCATTTCTTTCTGAAATACAGACGGTTCTTTTCTTTCCGGGATTTTTATACCCGAGGATTAAGCGGATTTATCCTGCTTTTAT  
TGCAGGCGCTGCTCTGCTCTCGGTGATTTGCTCTTCCAATCTCTCTTTACGAAGATTTCAACCAATGAGGAAAAACCATAGAGCTTTCTACGGTTTTTTTGTCCAAATATTTATTTGGGGTTC  
TGATTTGGGGTATTTTCGATTTGAGTGCCGACGAGAACCCCGTACTGCATATCTGGTCTTTGGCGGTAGAGGAACAGTATTACCTCCTGTATCTCTTTTGTCTGATATTCTGTACAAAAAA  
CCAAATCACTACGGGTGCTGCGTAATATCAGCATCATCTCTTTCTGATTTTGAACGCGATCATCGTTTGTGCGGCCGGGTTTTATACCGACATCTTCAACCAACCCCAATCATTTATGCTT  
TTTCAGACTGAGGTTTCCCGAGCTGTGTGTGGTCTGCTGCTGTGGCGGTTTACGGGCCAAACGCAAAACGGCAGACGGCGCAACAGAAATAGGAAACCGGCACTGTCTTTCACTCATCTGCTT  
GGCGCATTTGCTGTCTGCTGCTGTGTGTGATGCACAAACAGATCCGTTTATCCCGGGAATAACCTTGCTCTCTCCGCTGCTGCTGAGCGGCTGTATTCGGAAGTATGCAATACGGGCAC  
TTCCGACCCCGCATCTGTCTGCGCAAGCCCCATCGTATTTGTTCGGCAAAATCTATTTCCCTATACCTTGTCTATGCTTACCATTTGGATTTTTATTGCTTTGCGCCATTACATTTACAGGCACAAACAGCT  
CGGATCGCTTCCGCTATCGCGGTATCGCGGTGTCGCGGTGACGGCGCGGAATTTTCCCTGTTGAGCTATTATTTGATTGAACAGCGCTTTAGAAAACGGAAGATGACCTTCAAAAAGGCATTTTCTCTG  
CTTTATCTTGCGCCCGCTCCCTGATGCTTTGTCTGGTTACAACCTGTATTCAAGAGGGATATTGAACAGGAAACCTCCGCCGCTGCCCGGACGCGCGTGTCTGCGGAAATAATTTTCCGG  
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GGTGGATGAGAAGCTGGCAGACAAACCGTTGTGCGCAAAATACCGGGATGAAGTTGAAAAAGCCGAAGCTGCTTTTCATTTGCCAATTCTATGATTTTAGGATGGGGCGGCACCGCGCGG  
AGATTTGAAGCGCAATCTCTTCTGATACCCGGGTTCAAAGCCCGGATTCAGGGAACCGTCAGAGGATATCGGCTGCTCAAACTGTATATGTTTGTGCAAAACATATCATCAATCAGCGGTT  
CTCCCTTGAGGGAGGAAAAATTTGAAAAGATTTTCTATAAACCAATACCTCCGGCTATCTCGGCTATTTCGGGATTTGGGCGACATTCGGCAAGAGCAATCAGGCGGCTTTGATTTGGTTAAAGATATTCC  
CAATGTGCATTGGGTGGACGCACAAAAATACCTGCCCAAAACACGGTGCATATACGAGCGCTATCTTTACGGCGACCAAGACCACCTGACCTATTTCGTTCTTATATATGCGGGCGG  
GAAATTTTCAAAACACGAACCGCTGCTCAAGCATTCGCGAGGCGGCGCATTTGCAG

**SEQ ID 6260**

SEQ ID 6260  
LMQAVRYRPEIDGLRAVAVLSVIFPHLNNRWLPGGFLGVDIFFVISGFLITNIIILSEIQNGSFSFRDFFYTRRIKRIYAPAFIAAVSLASVIA SQIPLYEDFNQMRKTIELSTVPLSNITYLGF  
RLGYFDLSADENPVLIHWISLAVEBQQYILLYPLLIFCYKTKSLRLVLRNISIIPLLIITASSFLPAGFYTDILNQPNITYLSTLRFPPELLVGSLLAVSGYQQTNGRRQITENGKRQLLSLCLCP  
GALLVCLFVIDKHDPFIPGITLIIPLCILLTALLIRSMYGYTLPTRIILSASPIFVGKISYSYLILYHWIPIAFAHYITGDKQLGLPAKSAVAALTAGFSLLSYTILEBQLRKRMTFKKAFPC  
LYLAPSLMLVGYNIIYSRGLIKQEHRLPLPQTPVAAENNPETVPLTLGDSHAGHLRGFLDYVGGREGWKAKIILSDSECLVWVDEKLVNADPLCRKYRDEKAEAVFIAGPYDLRMGGQPVV  
RFEAQSLPIPGFKARPEFRVTKRIIAVKFVYVFANDTISIRSPLRBEKKRPAINDQYLRLPRAMGDIGKSNQAVFDLVKDIPNVHWVDAQYLPKNTVEIHGRYLYGDQDHLTFPGSYHGR  
EFHKHERLILKHSRGGAQ

SEQ ID 6261

SEQ ID 6261  
TTGCCGAATATTAAAATCAATTTTACCGAAATGTGCGCGCCGCACATCAGGCACAACGCCGCGCGCGCCAAACGCCGGAAGCCATTTCCTCCCTTTCCTTTCCCGCGCGCGGTTA  
TTTCCCTTTTCCTTTCCCGCGCGCGGTTCAAAACACGCCAAGATCGAACAAAGCGCGGAACAAAGCGCCAAAATATGCCA

SEQ ID 6262

SEQ ID 6262  
LPNIKINFTEVVPFHIRHNAADAAAKRGKAI SPFLSRRRVISPFLSRRRVQTRQDRTKREQSRQNP

## SEQ ID 6263

SEQ ID 6263

TTGCGCGGGGAATGTGCGCGGCTATTATGGCATATTTTGGCGGCTTTGTGTCGCGTTTGTTCGATCTTGGCGTGTTTGAACGCGGCGCGGGGAAAGGAAGGCGGAAATAACGCGGCGCGG  
GAAAGGAGGCGGAAATGCGCTTTCCCGGTTTGGCGGCGCGCTCGCGCGCGTTTGTGCGCTGATGTGCGGCGGCACATTTTCGTTAAATTTGATTTTAATATTCGGCAACTGTGCGGAATATCT  
CTCTAAATTTCCGCATTTTTCGCAACCGGGTTTCCGCACCGGGACACTCGGGCGGTATGTTCAATTTGTGCGAATGGAGTTTATAGGAGATATGGGGTTGAAAAAAGTCTGTTTGACCGTGTTG  
TGCCGTGATTTGTTTTTGCTTCGGGATATTTTATACGTTTGACCGGGTAAATCAGGGGGAAAGGAACGCGGTTTCCCTGCTGAAGGACAAACTCTTCAATGAAGAGGGGAAACCGTCAATC  
TGATTTTCTGCTATACCATATTCGAGATGAAGGTGGCAGAAAGGATTTATGSGCAGCATCCGGGGGAGCGGTTTATGTGSGTGTGATGCTGAAAAACAGGAATGAAAAATACGATTATTA  
TTTCAATCAGATAAAGGATAAGCGGAGCGCGCGGATTTTCTTACTGCGCTACGGTTTGAACAAATCGTTTAAATTTCAATTCGACGATGGCGGAGCTGAAGGTGAAGTCGATGCTGCTG  
CCGAAGGTCAAGCGAGTTTATTTTGGCGAGTTTGAAAAAGTCAGTATTGCCGCGCTTTTGTAGCACTTTACCCGGATGCGGAAATCAAACCTTTGACGACGGCACAAACAACCTGATACCGG  
AGACGACGATTTTGGGCGCGAGTTTGCCTAAACGGGGCGATTAAAGCGGAATTTTGCCCGAATGATGTGTCGGGGATTGGAGCATCGCCAAACCCGCAATGCTTCCGACGAGCATATAC  
GATATTCAGGGTTTGA AAAACATTTATGGATGACGCGCGCGCAAGATGACTTACTGCGCGTGTTCGATGCGTCCGAATGAAGCGCGGAGCAAAACCGCGGCGGATCTT  
TTGGGTCGCGCGACAAGAGATGAAGGAAATTTGGA AAAAGCGCGCAAAAATTTCAACATACAATATGTGCGCGCGCATCCCGCGGAGACTACGGGCTTTCGGCGCAACCGCGTTAA  
ATTGCGCCCTATGTCATCGAAGACTATATTTTGGCGGAAATTAAGAAAAACCCCATCGAGGATGAATAATTTATCATCTTTTACGCGGTGCGGCGTTGACGATGAAGGATTTTCCCAATGT  
GCGATTTTACGATATGAACCGCGCTTCCTTCGGAAGATTATTTGGCTCAAGCCCGTTTATGCGCTGTTCCTGCAGCGCGACATTCGATTTTGGCAATTTGACGATAAAAAATCAATCGCAT  
GTCAATACAAA

**SEQ ID 6264**

SEQ ID 62664  
LRGECARLLMHILAALFALCSTILACINAAAGKERGNNAAGKEGGNGFPAPGGGVGVVDPVRHRHIFGKIDFNIRQLSEYLLKFRIPRTGFPHRDTRGVCSICRNGVFRDAGLKKVCLTVL  
CLIVFCFGIPIYTPDRVNGGERNAVSLILDKLFLNEEGKPVNLIFCYTILQMKVAERIMAQHPGERPVPVLMSENKNEYDYFNQIKDKAEATYFFLYPLVGNLKNSPNFIPTMAELKVKSNML  
PKVKRIYILASLEKVSIAAFLSTYPDAEIKTFPDGNTNLLIRESSYLGGGFVANGAIRNFARFMVGDWSIAKTRNASDEHYTFYKGLKNIMDDGRKKMTYLPFLDASELKGADGETGTGVT  
LGSPDKMEMKEISEKAAKNFNIQYVAPHRQTYGLSGVTALNSPYVIEDYILREIKKNPHTRYELYTFYFSGAALTMKDFPNHVHTALPKASLPEDYWLKPVYALFRQADIPILAFDDKNQSH  
GSKD

SEQ ID 6265

SEQ ID 6285  
ATGACTCAAAAATCCACCATTTGTTTATACCATACACGAGAAGCCGCCGCGTGGCGACCCAAATCGCTGCTGCGGATTTGCGAGGCGTTTGCCCGCAGCCGGATATTGATGTCAAACCTG  
CCGCAATTTCCCTGTCCGCCCGCATTTTGGCGGCATTTCCCGAATATCTGACCGAAGCGCAGCGGTACCCGACGCGCTTGCCGAATTGGCGCAACTGGTGAAACAACCCGGTGCAAACTG  
AATCAAACTGCGCAATCAACGCGCATTCGTACCTCAACTGACCCGCGGATTAAGAAATTGCAGTCTAAAGGCTTTGCGGTTCGCCACTATCTCTGCGGACCTCAAAACCGATGAAGAAAA  
CGCGTACGCGAAGCTACGACCGCATCAAAGCAGCGCGGTAAACCTGTCTCTGCGGAAGCGAACATCGACACCGCGCGCGCTTAAAGCGGTGAAAAAATTTGCCAAAAAAATTCGCGCA  
GCAATGGGCGCGTGGGCGAAAGACTCCAAAACCCACGCTGGCCACCATGCAAAAGCGCGCACTTTTCCATAACGAACAATCGTTTACCGTACCCGATGGAGACTTCGATATCATCTGCTGTAC  
CGACAAACAAAGGCAATAAAAAAGAGCTGCGCGACGCTGTTGCCCTGAAAGCCGCGCAATCTGACGCGACCGATTAATGAGCAAAAAGCCCTGCTCGCTCTTCGCGCAACAAAGTGAA  
GACGCAAAAGCTAAAGCGTATTGTTCTGCTGTCATATGAGAACCGCATGATGAAGATGTTCGACCCGATGTTCTTCGGACACGCGCTCAAAGTGTTCTTCGGCGCTGTATTGAAAAAT  
TCGCGCGCAACTAGGCTGCGCGCAGCGCTCAACGCTCAACAACGGCTTCGGCAACCTGATTGCCAATCTGGACAAGCTGGATGGGACACCCGCGCGCGCTGGAAGCTGAATGCGCGCGT  
TTCGCGCGCAACCTGATTGGCGATGTTGCGATTCGCAAAAAGGCATCACAACCTGCACGTTCCAGCGATGTCATGCTGTATGCTTCTATGCTCGGATGATCCGCAATTCCGCGCGT

ATGTGGGACAAAACGGCAAGCGCAAGACCAAAGCCGTGATTCCGACAGCAGCTATGCCGGTGTTTACCAAGCAACCATCGATTCTGCCGGAAACAGGGCGCAATTCGATCCGCACAAATGCGGTACTGTGCCCAACGTCGGACTGATGGCGCAAGCGCGGAAGAATACGGCTCACAACAACAAACCTTTGAAATCGAAGCCGACGCGTCAGGTTCAAGTGATTGATCGGGCGGGCAATGTCTGATFAGCAGCAGCGTGTAGGCAGCGCGGCATCTGCGCGATGTGCCAAACCAAGACGCTCCCGCTCAAAGACTGGGTACAACCTCGCCGTCAACCGCGCCCGCTGAGCAACACGCCC GCCGTGTTCTGGCTCGACGAAAAACCGTCGCGCAGCAGAGAGTCTGCTCGCCAAAGTCAAAGGCTTACCTTTGCCGAATTTGGATACCAACGGCCCTCTACATCCGGTGCTCTCGCGCCGGAAGAAG CCGCTAAATTCAGCTTGGGCCGCTGTGAAAAACGGCGAAGACACCAATTTCCGTAAACGGCAACGCTCTCGCGGATTTATCTGACCGCACTTGTTCGCCGATTTTGGAACTGGGTACAGCGCGAA AATGCTGTGCCATCGTTCCATTGATGAACGGCGGGCGGTATGTTTGAACCCGGCGGGCGGTTCTGCACCGAAACAGCTCCAACAGTTCTCTGAAGAAAAACCACTGCGTGGGACTCATTTG GCGGAATCTCTCGCGCTTCGCGTATCGTTTGAAACATCTGGCGCAAAAAACCGGCACCGCAAGCCCAAGTCTCTCGCGACACTTTGGATGCGGCCACCGAAAAACTGCTGTTGAACGACA AATPCGCCCAACCAAGCGGGCGGAATCTGCACACCGCGCGACCAATTTTACCTTCAACCTCTACTGGCGCAAGAAATGGCGGCGCAAGACAAGATGCCGAACCTGAAAGCCGCAATTTGC TCATTGGCAGCGCTTTGACTGCGCAGCAAGCCAAATCGTTTGAAGAACTCTCTGCGCTACAAGCCAAAGCGGTGCACATCGCGCGCTACTACCGACGCAATCTTGAAGAACGCCGCACAA GCGATGCGTCCGAGCGCAACCTTTAATCAAGTACTAAACGCCCTTA

**SEQ ID 6266**

MTQKSTIVTYHTDEAPALATQSLLPVQAFARHADIVKTKADISLSGRILAAFPYLLTEAQRPVDALAEGLGVKQPGANVILPNISASVPQLTAAIKELGSKGFVFPDYPADPQDTEEX  
AVRERYDRIKGSAVNPVLEAGNSDRRAPKAVKNFAKKNPHSMGAMAKDSKTEHVATMQSGDFPHNQSVTVVPDATSVSIVFTDKQGNKKELREPVALKAGEI IDATVM SKKALLAFIABQVK  
DARAKGVFLSLHMKATMMKVS DPIIFGHAVKVFPAFVFEKFGKLAAGVNVNNGFNGNLIANLDKLDADTRAAVEARIEA VYAANPOLAHVSDSKGITYNLHVPSDVTVDASMPAMTRNSGR  
MWDKNGKAQDTKAVIPDSSYAGVYQATIDFCREHGAFDPTTMTVPNVGLMAQAAEYEGSHNKTFKELIADGQQVQIDAAGVILMQHVDVAGGIWKNQTKDAPVKDWQOLAVNRARLSHTP  
AVFVLADENRPHSKSLAKVKAYLAELDTNGLYIRVLAPEEAAKPSIGRLKNGEDTISVTGNVLRDYLTDLPPILELGTSAKMLSTIVPLMNGGGMFETGAGGSAPKHVQQPFIENHLKWDNL  
GEPFLALVSPFHLAKQTKGNAKAQLVADTIDATTEKLLINDKSPKRRKAGELDNRGSHPTLYTYAQELAAQDKDAELKAAPFLAALATDAEAKIVKELSAVQKAVDIGGYAANPEKAAQ  
AMRPSATPNQVILNAK

SEQ ID 6267

ATGAAACCTGTTCCAACCATCTGACCGGCATCTCTTTGGCAACCGCCCTTCCCGCATCGCACACGGTATGCATAAGAGCAAAACCCCTGGCTATGGACGAGCTGCCCGCGATTGCCCAAC  
AATATTTCAAACGCGCGGAAACCTGTTACAACAAGCGCGAAACAAGCAGATTTCGCACGCAACAACACCAAAATTCCTAFTCCAAGCCCTACCTGCGCGGATTGGGACAGCGTAAGCA  
AATGTGCCAAATCGCTATGGATTGTTTGCAAAAAAACC CGCAATCTGAATTGCGAATAAAGCGCATCAGCAA

**SEQ ID 6268**

MKTVP TILTGILLATALPASAEHGMHKS KPLAMDELPPICQYFKRAETCYNKAGNKADFARNNTFKFLFQALPAADLGQRKQMCQIAMD SFAEKNPOSELRIKPHOO

**SEQ ID 6269**

TTGTTCCAGGTTGTGTCAAATACTATATAAAAAATCATCGGTTTACGATGATTTCGGTAAACGCCCTGCAACAAACCGCAATCGGCAGACGCTTTTATCAATGTTTTATGGTATTAATTAT  
ATGGTCATTTTTGGGATGGGGACTTGCCA

**SEQ ID 6270**

LFRLCOLLYKNHRFTMIFRNALQOTAIGRRFLSMFYGINLYGHFWDGDLP

**SEQ ID 6271**

TTGACACAACCTGAACAAAAAGAACCGCCCTGAATCAGGGCGGTTTGTCTTTCGGGGGAAACGGCGGGATTCGACTAAATTTTATTTTATTTGATTAAATACATTTATTTCTTATAAAA  
ATTTAAATTTACCATAAAAAACGCCATATACAAAAATCTTGGAGTAACTACTGCATTACACTATTAGAAGGATGCAGGGTCATG

**SEQ ID 6272**

LTQPEQKRTALNQGGFALRRKRDSTKFFIDLNTFISYKNLIYHKNSHIQKSWSNYCITLLEGCRVH

**SEQ ID 6273**

TTGTTCTTTAAACCCATTGGGAAAAAAGTAATTTTATTTCACCTTATTTCACCTTTTTTTATAAAATAATTCAAATATTTAATTTTATATATTAAATTTAATTAAATATTACATGACCCCTGC  
ATCCTTCTAATAGTGTAAATGCAG

SEQ ID 6274

LFFNPLGKTNFICTLFAPFFINIIQIFNLYINLIKYYMTLHPSNSVMO

**SEQ ID 6275**

ATGCGACCCCTCTATTTCATTTCCGACCTGCATTTGAGCGAAAAACCCCGGAATGACGGAATCGTGTCTGCTTTTACGTTCTGCGCGCGCGGGCAGCGCGGGCGGTTTATATTT  
TGGGGCGATTGTGTGATTTTTGGGTGGGCGATGACGAAGTTTCCGAGTTGAATACTTCGGTTGCGCGGGAAATCAGGAAATGTGCCGACAAAGCGGTGCGCGTGTCTTTGTTCAGGGGCAA  
CCGCGATTTCCTAATCGGTCCGGATTTTTCCGCGCAGCGGGGTATGACGCTCTGCGCGGATTACTCGGTTTGGAGCTGTTGCGAGCAGCAACACCTGATTGTGCCACGGCGACACATATGTGC  
ACCGACGACAAAGCATACCTTCGCTTTCCCGCGCATTCGTGCATTGTCAGGCGCGCTCAAAAAACGTTCTCTGATGCTGCCCTGAGATGGCGCAGCGCGCTTCCGCCAAAAATCAGGCGGTGCA  
GCAAAATGCGAAAAACAGTGCAGCCCGCGCATATTATGAGATGCTCAAFGCGCGCTTATCCGCGCGCGAGGTTTCGCGCTTTAAACGCGGAAAGCGTGATACAGCGACACACCCACCGCGAGCA  
TATCCATCAGCAAAACGGCTTTACCCGCATCGTTTGGGCGACTGGCATAACGACTATGCTTCAATCTCCGCGTGGACGGGACGGCGCGGTAATCGTCCGCGCGGAAAGAAATGC

**SEQ ID 6276**

MRPSYFISDLHLSEKHPELTELLELFLRLSAAAGQARAVYILGDLFDHWGDEVSELATSVAREIRKLSDKGVAVFVVRGNRDFLIGRDFCRQAGMTLLPDYSVLDFPGSNTLICHEDTLC  
TDDKAYLAFRRIVHCRRLQKLFLMLPLKHWRLTAAKIRRVSKMKQVKPADIMDVNAAPTAROVRAFNAERLHGTHREHITHENGPTRIVLGDHNDYASTILVDGDAVAVVPPRC

**SEQ ID 6277**

GGACAAGCGCAGCAAGCCGCGCAGACAGTACAAGAAGTACGGCAAGGCGAGGCAACGCTGTACCGGTTTAAATTTAAACCACTATAGATTTCAGAAGTATGCGACTCGGCAGCATTGATGATTCTGCGCCCGCCACATCCCCAT

**SEQ ID 6278**

GQGDEAADSTRSTARRGNAV\* I\*TTIDFRSMAVGSIDDFCRPPH

SEQ ID 6279

TTGTCAATTTTGTAGTCTTTTCGAACAGGATGCCGATATGATCAACCCCATCGCCTCGCTTTTCCCCCTAGACGGCGGTTATGCCCAATCCGTTGAAGCATTCGCCCGGATTTTTCAG  
AGTACGGACTGATGAAGGCGCGCTCAAAGTCGAATTAATCGGCTCAAAGCCCTGGCCGCGAGATTCGCCAAGTGC CGCCCTTCAGTGC CGAAACCGCTTGCCGAAATCGACAA  
AGTCATCGAAAACCTTTTCATAGAGAAGCGCGGCGCGCTCAAAGCCATCGAAGCCAGACCAATCATGATGTCAAAGCCATCGAATATTGGCTGAAAAACGTTTTCGCCAAGTGC CGGAA  
GTCGCCCGCTGAGCGAGTTTCACTCCACTTGCCCTGCACCGAGCAAGACATCAACAACCTGTGCCCGCCCTGATGCTCGAAGAGGCGCGCGAAACCGTCACTCTGCCCAAACCTTGCCGAAA  
TCATCGCGCAAACTCACCGCTATGGCGCAGCACTTTGCCCGCTCCGATGATGAGCGGACGCGCACCCAGCGCGAGCCGCCACCGACCATTTGGGCAAGAAACGCCCAATGCTGTGTACCG  
CTCGCAAGCCCGAGTTCAAATATCTTCAGCGCGCAAGAATTTCTCGGCAAAATCAAGCGCGCGGTTCGGCAATCAACAGCCCGCATATGGCCGCGCTATCCCGATGTGGATTTGGGAAACACATCG  
CGCAACTTCTGCGAAATCAGCCTCGGTCTGACCTTCAACCCCTACACCATCAAAATCGAGCCGCGACGACTATATGGCGGAGTTTTCACAAACCTTCAGCGCGCATCAACACGAGTTTCTCATCG  
ACTTCAGCCGCGAGCTTTGGGGTTATATTTTCAATGCGGTATTTTCAAACAAAAGTCAAAGCGGGCGAAGTCGGCTCTTCCACCATGCCGACAAAGTCAACCCCATCGACTTTGAAACCTC  
CGAGGGCAACCTCGCATGCGCAACCGCGTATTTGGGCTTTTTCGCCGAAAAATCTGCCCGTCTCAGCTGCGCAGCGGATTTGACCGCAGACACGTAATGCGCAATATGGCGGCTGGGCGTG  
GGCTATGCCGTGTGGGTTTTCGCCGCCCATCTTGC CGCGCTCTGAACAAGCTCGAGCGGAACCTTGCCCGCTTTCGCCCGGATTTGGATGTCACTTGGGAGCTGCTCGCGAGCCGAGTTCAA  
CGAATGAGCGCGCTTACGGTGTGCCAATCTTCAAGAAAATCTGACGCGGTTAAAGCGCGCATCACACCGAAGTCTGAAAGGCTTTATCGGATCGCTGGAATTTCCCG  
CGAAGCCAAAGCCAAATTTGCTTGAAGTACCCCGCGCTGTATGTTGGGCAAGCTGAAGCGTTTGGCGAAACCGAAT

## SEQ ID 6280

LSIFDVPSEQDADMINPIASLSPLDGRYAQSVEALRPITSEYGLMKARVKVELNWLKALAAEPPIAEVPPPSAETLAETDKVIENFSLDAAAVKAEATTNHDVKAEITWLNKKRFAEVPPE  
VAVSEFTHFACTSEDIINMLSHALMLQEAETVILPKLAETIGKLTAMAHDLAAVPMNSRTHGQPATPTTLGKETANVYRLQRQKILQAQEFGLKINGAVGNYNHMAAYPDVDMETHC  
RNPVEISLGLTFNPPYTIQIEPHDYMAEFQTLRSRINTILIDPSRDVWGYISLGYFKQKVKAGEVGSSTMPHKVNPIDFENSEGNLGMANAVIGFLAEKLPVSRWQRLDSTVLRNMGVGV  
GYAVLGPAHLRGLNKLFPNPAALADLDVTWELLAEPIQTVMRRYGVANPYEKLKDLTRGKGITPEVLKGPISLEIPAEAKAKLLELPALYVGRKABALAKRI

## SEQ ID 6281

TTGATTTTGTGGGGGAATGGTTGACTTTGAACGTGTCCACGTTTATAATTCAATTCATCGCGCATCGGGTCCGATACGGGAAAAGCCCCACCGAAGCGGGGCTGTACAGGGAG

## SEQ ID 6282

LILLGEMLTANVSTFIIQFIGASGADTGKAPPKRGLYRE

## SEQ ID 6283

TTGGCGGCTCTTTATGCCGTCCGAAAGCCCTTCAGACGGCATTTTCTTTGATTTTGTGGGGGAATGGTTGACTTTGAACGTGTCCACGTTTATAATTCAATTCATCGCGCATCGGGT  
CCGATACGGGAAAAGCCCCACCGAAGCGGGGCTGTACAGGGAGTAGGAAA

## SEQ ID 6284

LAASLCRPAKALQTAFPFDFVGGMVDFPERVHVNSIHRRIKRYGKSPTEAGLVQGVGK

## SEQ ID 6285

ATGAGCTTCATTTTCCTACTCCCTGTACAAGCCCGCTTCGGTGGGGCTTTCCCGTATCGGACCCGATGCGCGATGAATTGAATTATAAACGTGGACACGTTCAAAGTCAACCATTC  
CCCAACAAATCAAGAAAAATGCCGTCTGAAGGGCTTTCCGACGGCATAAAGAACGCCAAGTTTCCGGCTTGGCGCGGTGGGGCTATTTTAAGAACTCTTTTCGGATTGTTCTT

## SEQ ID 6286

MSFIFLLPVQAPLWGFSTRIGRCADELNYKRGHVQSPPFQONQRKMPSEGLSDGKIKPPSLRLGGGAILRLTLFGFVL

## SEQ ID 6287

TTGCCATGGTTAATGAAAACTGGCAGAAAACCGAAGCGTTACGAGCAAAAACGAGTCATAAAAAGTCTCGTTTAATGCGGAAACAGAAAAAGAGCTTTTGAATATGCCAAAAATC  
TCGATTTTCCCAATGGGTAAATCAATCATAAAAGAAAAATCAAAAAG

## SEQ ID 6288

LPWNEKLAENRKRYEQKRVIKKVSFNAETEKELLEYAQNLDPSQWVKSIIKEKIK

## SEQ ID 6289

TTGGTTCCGTTTTCATTAACGGCTGTGCCGTTGTAAGAATAATAACGTTGACACGTTCAAAGTCAATTACTTTTGGATTTTCTTTTATGATTGATTTAACCCATTGGGAAAAATCGA  
GATTTTGGGCATATTTCCAAAAGCTCTTTTCTGTCTCCGATTAACGAGACTTTTAAATGACTCGTTTTCGCTCG

## SEQ ID 6290

LVRFSINGCAVVRILNVDFKVNLYLIFSMIDLFEWEKSRFWAYSKSSPSVSNLSTFLMTRPCS

## SEQ ID 6291

ATGAATGCTGTCCAAGTTTAAACTTTCAACAAAACCTCCGTCCGTACTGTGCGGATAACAAAGCGAGTTGTGGTTTGGCAAAACGATGTTGCGAGATTTAGGCTACACCAACCCCTC  
GCCGAACGGTTGACCTGCACTGCAAAAACGAGGGCGTAACAAAACGGTACACCCCCACACAGCGGGAACAGGAGATGACCTATATTAACGAGCCGAATCTCTACCGCTTGATTTATCAA  
ATCCCGCAAGCTTCGCGCAGAAGCGTTTGAAGAATGGGTAAATGGAACCCGTCTCTCCCGCATCCGCAAAAACAGGCGGCTGCCAAGTCGAGACCAAAAACACCGCCGACGACCGTACCGGA  
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CCGAACCGCTGCGCTACGCTCCACGATGACACTGCACACGGGCTTGACAGCGCAAGTGTGAGACGACCCGCCAAAGCCGAGCCGAACATGCCCATCGACGGCAACTCTTTAGCCGACAT  
TCCCGCTATGGTTTATTACGCGACATGGATGATTGAATCGGGCAAGACATCTCCCGCCGCTGAAGCAGCTCGGCTGCAGGACGGCGTTACGATGTGAGCGGTTTGGCAGCAAAACCGT  
CCAATCTGAAAGATCCGCGCGGCCCTCGAAGTGTGCGGGGATATGCGGACAAAGACGCTCCGACCCGATAGCCGATGTCCTGAAGGCATTACGCAAGGCTACGGTAAGG

## SEQ ID 6292

MNAVQVLNFPQNSVRTVADNKGELWFLANDVCEILGYTNPRRTVDLHCKSRGVTKRYPTTSGEQEMTYINEPNLYRLIISRKPAAPAEFEWVMTVLPAIRKTTGGCQVGPKTITADRTG  
LRQVAVALVGRKIDYSSAYSMIHQRFNVESEDLPAGKLEPAVAYVHALTLHTGLTGEVLDAAPPKAEPLPIDGNSLADIAAMVYGTWNTIESGKDISAPLKQLGCRQAVTWVTHBTR  
PILKRSAAALEVLRYADKDAADRIAACLBGIYKATFR

## SEQ ID 6293

TTGGAITTGACGATGAGTGTGAAGAGTTTTCAGGAAACAGATCGCCTATTGGCTGAACGAGAGCCGCAAGGCATCAGATAACGCGATTTGAAGGCTTTGAGTTGCCCGACCGGAAC  
CGCGGATATATCGGAAATGTTGAAACGCTATGCCCGCGTGA AAAATGCCGTCGGAAGATTCGGCGCGCATTTTCGTTTACCTTACCG

## SEQ ID 6294

LDLMSAERFCKQIAYWLNSRKASDNADLKAFEPAGREPADYREMLKRYARVKNVRRFRHFPTLP

## SEQ ID 6295

TTGGTTTATTGGGCTTTGGCGGAGGCTTTCCGATCCCGGATCGCGAGACTTTGACCCCGCAGCGTTCCGAATCGGCAAGGAGGCGTTTCGAGCTGTATTTCGGCTGCCGCCGACAGTG  
ATTTCGGCGGTATCACGCGTGAGGATCGCGGCACCTGAACAGGCATTTTGGATT

## SEQ ID 6296

LVTWALAEAFGIPDAETFDPPQRESARRRPFELYFGLPADSLRLITREDAPHLNRHFWI

## SEQ ID 6297

ATGATGTATGGAATTGATTTCCGGCTCGTCCCGTCCCGCCGCAATATCCCGCGCAGGCAATACCCCGCGCAACAACTGCCGTACGGTCCGGCGCAGGCGCAAGCGTCAGCTTCCCG  
TCGCCCTGCACCGCATAAACCGGAGCCCGTTTGGCGCCCGTGGCGCAACCGGCGCGCAACATCCCGCGCTCCCGCGAAACCACTTCAGGCACACCGGTGAGCGGTCCGACACAA  
AACGGATACGTGCGATTTCATACGCATAACCCGCGCAACCCGCGCGCATAGCATAAAGCGGCGCGCTTTTCCACATCCGTTACAAACGCATCGTCCGAAATGCAGCAGCGCGCC  
CGCAGGCACGCTCGTGAACCGCATCGTTCAACCATCCGACACCTCTCTCGCTCCAAAATACGGCTCGGCTTATCATTTGGCAAGCACGCGGAAACGCGCAATCAAAGCCTTCAAA  
TTCATTGCACGATACCGAAC

## SEQ ID 6298

MMYGIDPRLVPPRHIPRAQIIPGKQPAVTVRRRRKRLPVALHRIHQPRLPVAPTGANIRRLRRNLQAHRSVGHKTDVDFIRITRRKPARRISIKRPPFFHIRYKRIVRMQQPA  
AQARLVNRIVQPSRHLVPAFKIRLGLIIGKHAETRNQSLQIHCTIPN

## SEQ ID 6299

ATGTTACGCTTACCGAAACCGACTTCCCGGCAACCGCGCCCTTGTTCGCGCTCCATAATCCCGCGCGCGCGCGGAAATGACGGCAATACCGGAATCCGACAGCCCGCGCGCAGAC  
GCGAGGCAACGCA

## SEQ ID 6300

MFSPTETDFPANAPLFAASIIIPGPPPEMTAIPESDSRRARRQANA

## SEQ ID 6301

ATGAATTTGAAGGCTTTGATTGCGCGTTTCCGCGTTCGCAATGATAAGGCCGAGCCGATATTTTGGAGCGACGAAGAGGTGTCGGGATGTTGAACGATCGGTTACAGGGCGTGGC  
TCCGCGCGCGCGTGCATTCGCGGATGCGGTTGTAACGGATGTGGAAGGCGCGCGCTTTATGCTTATCGCGCGCGCGGTTTCCGCGGTTATCGGTATGAATCGACAGTAT  
CCGTTTGTGTCGCGCGC

## SEQ ID 6302

MNLKALIRFRVLANDKAEYFWSDEEVSGNLNDVHEACLRGRLLHSDDAFVTVVEKGRPLAYAAAGGFAAGYAYEIDSIRFVSDG

## SEQ ID 6303

ATGATAGATACGGTCGCCACACGCGACGCCCGCGATATCTTGATAAAACCTTATCCATCCAAACCCCGCGCGGATCGTCAAAATACAGCAACGCCGCAAGGCCAA  
ATCCCCCGCGCGGTTTTCATTCGCGTTACAACTGCGCGAATCTCTCGCG

## SEQ ID 6304

MIDTVAPHGTPADILDKNLHPTPRRRPDGIVKYSNAAKANPRAAPHSAYNHNPFS

## SEQ ID 6305

TTGGTTTTCGAAGACGCGCAGGTGCGCGAGGTGTCGGCGCGGCTCGCGCAAGTTGTTGCGCCACGCGGATGTTTTCGCGCGTCCCGGCAACCGGTGAAAAGCGGATGATACGG  
AGGCTTTGGAAGAGCGCGCGCTTCGGAATCGAACGGAAGCGCGCGCTTTCAGCGCGTGCAGGATGTGATCCTGCAAAATCAACCGGATGGGCAAGGACGAGCTTGAACTGTATCGGAA  
GGCGAATTACGCGCAGGTTTGGATAAGCGCAAAATCGCGGAGAAATTTGCGTGAGGCTGTGGTTCGGATGTTTCGTCAGTTTCGGTATCGTGCA

## SEQ ID 6306

LVPEDQVREVSAGAAKLLRHGDVFAAVPGKRVEKADDTALEKAGASELEREAAAFDAVDVILQINRMKGDELELYAKANYGQGLDKRKSANLREAVVRMVRQFGIVQ

## SEQ ID 6307

TTGTCGAGTTGGGGGGTTTATGGCTCGGATTCATGTGAGAAACAATGGCGGCAACCGTTTCGGCGCGTGCCTTACGCGCAATCTGCGCGCGGAGCATTACTGTATCGTTCCGAAGCAGG  
ACGGTCAATCTTGGGGCGGATGCTACGGCGCGCCCAAGGATGGCGATGTTTGGCGCTGGGTGTCTTGGAAACAGGTTTCCGTTTGGATGACCGCGCAGATTATGTGAAGACGGCGAT  
GTCTTCGCGTATCACTCGCGATGTCGCTTTGCGTATCGGACGGTCCGATGATGCCACGTGCTCAGGATGCGCGCTTATTTGCTTCGCGCGCGGACTTTGCGTCTCGCGCGGCTATC  
CGCTGCCAGTCTGCCAAATCGGTTACGCTGCCCAAGCAGGCTTTGCTGACGGTTACGCTTAAAGGGCGGAAATAAGAAGGCCCGGATATCGATATTTGATTACGCGCAGAAAGTTCC  
GCCAGTTG

## SEQ ID 6308

LSSWGGFMARHVRNNGNRFGVPGYGNLAAEHYCIIVAKQDAILGADAYGPKDGDVLLALGVLEQGFRLDDAQIIVKTAMSSGITADVGFAYADGADDAHVQDAAYFASGADFASAGRI  
RCQSAKLVLPQALITVTLKGAENKKAADIDILYGEKPGQL

## SEQ ID 6309

ATGGCAAAAAGACGAATACGGCGTACGGCGACCCGAGCGGATGATGAAGCAGCGCGCGGGCTGTTTCCGATGCATATGCAGCGCAACAGTACGCTGAACCGTTTGGCGGGCAAGATGC  
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CCCTGTTTTCGCGCTCGCGATTATGGCGGACAAACAGCGCGGAAGCGAGGCGGTGGGATGAGCCTGTGCGAGGCGGGTTTGGCTGTAATCAGGCGCGTTTCCCGTTGACGCGCGCGCG  
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AACGGCGCTTGGGACACAGCGCGCGAGTTGAAGATTGCTTACCGATTGTTTACGATGGATACGCTGGACAGTATGCGTACCGTCTCGACAGATTCCGCTGCGCGCGCGGATTTG  
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CGCGCGCTCCCGAGCAAAATCAAATCCGCTGTTTGGCGGATGCGGGTTTGGGAACCGCTTATTCCTGCTGAAATGCCGCGCCCATCCGTTTCTATCGCGCGGATGAGATGAAGTA  
TTGCGCGGATAAGTTTACGCGAGCGCGAATCGGGCTTGAAATCCCGCTTCTGTTGCGGACAAAGTTTTCGCGTACCGCTTCGCTTATTTGGCGCGCGAGCGGTTTGGAGCGGTTTGGC  
AATACCGGCAACACGCGGATGCGCTTTCTTTGGTCTGAGAAGGAGCTTGACACGCGCAACCGTGTGGAACCGCTCGTTCGCTGCGGATACGCGGTTGTCGCGAAACCGCGCTTTGCGGTG  
ATGTCGCGCGGGGTGCGAAGGAAATACCGACTACCGGTAACCGTTGTGATACCGGTGCTTCTTTGACACGCGGATATCCCG

## SEQ ID 6310

MAQKTNPAYGDQAMMQAAGLPAHMQNRNSTLNLAKMPAGTAGAEATLRKQTTQHPMPVVRQDLTRGMDEIRFNLVNPVSALPDMGDNATBGRGVGMSLSEAGLRVNOARFPVDDGG  
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KFEGDKAAGDSPLRVLLSPAQYNRFADPKFRLQASAIARASQANQNLPLFDAGLWNGFILVKMPRIPIFYAGDEMRYCADKFSAESEGLKIPASPADKFAVDRSVILGGQAVLEAFA  
NTGKHGMPFPFWESEKLDHGNRVETLVGTIRGVAETRFPAVDVGGGAKETIDYGVTVVDTVVPLHGGIR

## SEQ ID 6311

TTGAGGGAGCGCATCGAGGAGCTTGAGAAGGGGGCGGAAAAACCGGAGTGGAACCGCTGACGGTTCCGATAATTCGTGTTTCGGGATTTTTCGAGCAGGATGTGAAAAAGGCGGTGG  
AAAAGCTGATTAGGAGAAGCTGCGCGGTATGAGCGGACATGAAGCGGAGGCGGCAAGGCGCATTACCGCGAATCTATACGCGCGACCCGATCGGGAATTCGATTGTGGAAG  
CCGCGAGCTGAGGAGTGGCTGCGCGGCGAGAACCGCTTTCGCGAAGCGCTTAAATGACGCGCTTAAAGACGGGACTCCGCGGAGGTATCGGGCGGTTCGATATGTTTAAAGCGGCA  
AAATCCGCGCGCAACCGGAAAGCCCGCGAAAGCGCGCTCCGCGGAGAAATACGCGCAATACCGCTTCGCGGATATTCGCGGGGCGCGACCATCGGCTTCGAGCGCGCGCGGATT  
ATTTGAGCGGCAACGCGCTGCGGAAACTGCGTTCCATGACGGAAGAGCAGGTTGAGAAGTTTAAATCT

## SEQ ID 6312

LRRIEKELEKGAEPGVETADGSDNSLFGDFSDDEVKKGVEKLIQEKLAGYEADMKRQBAKAHYREIYTAHPDADSIVESRELEWLAGQNLVRKAFNDALKDGTAAEVIQAFDMFKAA  
KSAABPEKPAEPKPAKNTPWTLSDIPAGRDHTASDGPPDYLGNALAEKLAHTEQEVEKFLNS

## SEQ ID 6313

TTGGCTTACCAATTTATCTTTTAAACAAAATATCGGGTGTGCGGATTTGAACGCTCTTTCCAAACCTCGACGCGCTTATGATGCAAAATGCC

## SEQ ID 6314

LVLPIYLLTKISGVRLNVPFNLDAFYDANA

## SEQ ID 6315

GAGTATGCGAGTCCGCGAGCTTATGATTCTGCGCGCGCGCACATCCCATTCGGACATTTTATGTGACCTCCGCGCTCTGCTTTTAAATAATTTGCAAAACATTTCCGCGAGCTTGAACC  
GGCTGTCTTCGGTGAAAAACCAAAAGTATTTTCAA

## SEQ ID 6316

EWQSAALMISAARHIPRTFHCRLRCP\*IIANNFRSLNRPVFGKTKSIPQ

## SEQ ID 6317

ATGGAGATGTAAACCGGTCGCCGAGCAGGCAGCTTATGATGCCGAATCGAGCGAGCGACGAGCAATGGCGGACGTTTTCGCGAGTCAGTATTTTGGCAGCGCGCGCACGCGCG  
AGGATCATGCGGATTTATGCTTTTCCCTGCGCTGTCGCGCGCGCGCTGTGCGGATTCGGGTATTTGCCCTCATTTTCGCGCGCGCGCGCGGATTTATGAGGCGCGCAACAGGCGCGGTTTGC  
CGGAAAGTCGGTTTCGGTAGGCTGAACATTTGCCCTGCGCGAGCAGAGCAAGCAATCCGATTCAGGACATCGCTTTCGCGTTTTCGCGTTTTCGCGAAGCGAAGGAGCTGTTTTCGCG  
TATTCOCAGCATATGCTGTATGTCGCGCGCGCTTCGCGAGCTGAGCAAGTATTTTGAATCTTGACCTTGGTGACAGCGGCAAGGTCGCGCGCGCTCGGTCTGTTGGTGGAAAG  
CGTTTGGTGGCGCTTGGCGAGTGGAATAACGCGCAGCTTTTGGCGCGGATGATTTTCCGAAGGGCGCGCTTCTTTGTTCTCATATCGGACGAGCAAGCAAGCAATATTCGCTATCT  
GTGGAACACGCGCTTCAGACGCA



**SEQ ID 6318**

MENVNRVPEQARYDAECROADEALAVFPVAVSIFGSARTPDQHADYAFACRLARRLSDSGIAVSGGGPGTMEANKGAFAGKSVSVGLNIALPHEQKPNPYQDIALFRSFAERKAVFFR  
 YSOAYVVMPPGGPGTLDLFEILTLVOTGVKPPRPVVLVKGAPWSGLAEWINDAQLLARGMISEGASLFSISDDDEEILAYLSEHGLQTA

**SEQ ID 6319**

TTGCCGACGGCGCGGCGCATTTGCGGACGCAACGGCGGACCCCTGGCAAACCTTGCAAGGCAGCCGCATTTCATCCGCCGCCCGCATCAGGGGTCAAACCCCTGCCGCCCTTGGGTCAAACCC  
TGCCGCACATCTCTGCCGCACATCTCTGCCGCAAACCTTTATCTTCCTGGTGGG

**SEQ ID 6320**

LPTGRRIAGRNGGPWOTLQSRICIRPRIRGOTPAALGOTLPHILPHILRQTLIFRG

**SEQ ID 6321**

[illegible]

SEQ ID 6322

SEQ ID NO: 6322

LARGTEKQPDVSGIPSGDEAGFELDTGVMPDGLARQYADMAKYRAKPSSEAVGIDPDDGAVSAAAAAADSGAAVPSAVSDMEARSVADDAPSGRSADADRGVPSAYGVNVRPGGAPGAA  
SVAPGGSAAAAAGGIARVAPLPAGQYFDGLDTRGRKALAKEAGLDIKGVADPGQIAAPVRRKIQQATHARIADYQAASEAQGYLPPPPVRMDADVPPKKFQSVPADALDKESRRFPDAL  
FENVRRHQTVADYTDAGIMRREAGMAMRGHYTEGLAESAGAVRAYRAQHPESADVLDRLNRAVGYCYRRNNGNSVPLLRSERGERLQGVRTALPDGDASAVVGGGRGLTRALPTEDKGLA  
QDVQRQDVRQGLTYQGGRLTFDAGADANAALQGLPGSIVASGNAIPARRQNLQVRARAEAGAPGLSASENLACTDGGKRAFPVAGKKPDTVPLVPLNPQVASEAGRVSPKKRMADAAADFTREL  
AADRRRPEKAGVPLGGGYYRFEHTDRRHIDALAGVPGRPGKGMPEEFADMAGPNSNDGLVSDGRRLYKLGREAETLRAGGLSEAVPSEPGRDYRPTQEARAKVMQFPRADAAADGKPAGR  
AQPARAKDTPVAGKAAAAAKNAATEKPPSSDKVRNIEAGKSRVPPDGKGKSAQAQAAATEKPSKTKGKRPADTKASNDPEARRKARVGLQGGPVTVYQKROAQVQKPKFKAALHDEASIKKRLA  
ESTIGLAEKVDVAAVSETPADPKAKMLQSRQVNGFDGRTGKTLVLENTLPERAVAAWHELGHRRGPAFTKAYKSELREARLDGCHGLLRITADVQTEGREGTGDAAAASVRPAAVEBAVEL  
YAEORTGGVAGYENRYGVKVGNGLRKGLTAGLARIALLRRVLORLAGKAGGASDADVFMALADLHGNVEGARDAPWGGNHRAVMFARAEDGAAERKSSESLEKLRAETIRISGREVPB



GNNLREYKRNALLEYGKSLRGFPVYNKDTGRELSLGRSGITEILRH DYKDAEHLQSIAPQI IENAVYIDTLPNEDLAKNGDIQGYEYVVSGLNVGGADYTVRAAAVAVSRNGNRYYDHKLTK  
TEKGNLLSLLRJVSTTGASESKSPISGIDDKRLQLQLQDKDAGKGIADPFTAVRFSRAANTI EAAIGRITGKKSIDLNRALKDREWDASKGIQLQFLGRQRJEDITYGGVL DGLKEYGRLSL  
FGADANKAVTEADKVVREWRGLKEEDAKALADLMHDAFLAKVDADPLMRKDAQKRLDGIPTALDIADGKIEKAAVAVSAGARIARADAAYNKAQRAADKAAYALEKAQEKHGREILADEA  
DMRLRLFLFYADSEAKRALRRAGADVAAESRAKTDVAVMLBQARADV KRLKEDVGAQKALEGLLALNRRFAGLEPDAQRVTVRKARDYDRAHPGQVRDALAE LRLARAGQDAETVRRLKERPD  
NELGGVYFPLARGDYLVVVKDADGNSANVSRAETLSEAERLKDALKADPGAGFKVSPVMKSRDYIRSRAVVGSGFMRELGEAVGMLDLDPQARARLADTLTQLYLNSLPDTSWAKHIGR  
KGPVGFSDDARAGYALQNMGSGANYLAKLRYLNRMAEQLDVHKGQFVDVRKJZEGFLDQROLQVADHEMRKHEAVMNPNSKLAQALTGFGFLMMMGSPASAVVNL SQTAMVAVPVMAAKWC  
YAGAARELRLASKQIGLRFGEKPTNIEDSLNGDKAAFPKADYGVILDSQAGDLAVANGVDEPLGASAWQVMMDKAAWLFHAEKFNQVTVVAA YRLAKRAGADSEAFQOAKKATYDG  
HFDYAAQNRPRFMGNAAKVVFLFKQYSONLLYALGRNAYLAFKGDKEARKTLAGILLVSHAMASGLILFLPVVSTLLAVASMLGSDDDDFDWAERALRMLADAFGDKAGEVLAKGFSRLTP  
LDVSGRLGLNQLVFPDIQDGLGKKWAE SLVVGSTGAVVGAGIADGVRTSSVPRTANTLSIMKSH

**SEQ ID 6323**

[illegible]

**SEQ ID 6324**

MSDLVRYDPLEHGRVLGGLEKFGYGTQKDRAAAADDTALTRGFKNSMRSARMGNALTGDCHEELGLRLKAEDMDYRKIQBGRKSQARRELGEAWKGGVGGGLSNVWGLKKDWREKGLDG  
ALEVDVGEMAGAVLBPAPNALVPLATATAGGILGALAGGNAAGVAYAGATLGNFLMEYGGQLDRAAEAGVDPADKDAVMAPIGRGAPGALKNAAVKGAVVGADRAAMKLGSLAHGKKA  
AGKAALEKMGVAADKAAVAANKGTPPEFAALAKESARGGLGGAARHAAAYATESAGEFAGYILGTGLANGWEZKGAALFAPSLGHSVAGFAGTKYAAVTDPLRPGRTEGGCAGGYRG  
QQEGGQAGPGRGAGVACGGTGGCGRRHRLRTEARNRAARVSIIRITISIRILCGSLRTVRSRRRRGGFSAALPTAIRTRTRNRWRAGKNSRNFVSRRTGRNFWTRA

**SEQ ID 6325**

TTGTTTCGGAAGGGTTTCGCGATGCGGTTTGTTTGAGCCGCTCTCCGGGGGATTTTGGGAGATGAAAGGAAAAGGAGGAAAAAGAGAAGGCCCGGAAGGGGGCGGAGGAGCGGGAGCGGGCGCGCG  
CACAGCGCACCGTCCGCGATGCGGTGCGGGCTACCGTTGCGAAATTATGAGCGCCGGCCGCGCGTTATCGGAATGTGATGGATTTCGAGCCGTAACAATATTGAGGATGGGGCGCGCGGGTT  
GCGCCGGCGCGGTGCTTTGCAACGGGGTGCAGATCCGGCTTTGGGGTTTCGGGCGCGGATAAGCGCTTTCGCCCGATGCGCGGGCCGGGGCGGATTTTCGCGCGCGCGGATACGCGCCCG  
ACGGAATCGCGGCGAGCGGACGCCGCCCGCTTTGGGATTTGACGGGAATGTGTATCGGGGCGGCAAGCCGGTGCCTGATTTTGACGCGCGAGCGTCCCTTTGGTGTCTGCGCGGGCGGATTCGC  
TGCGCTTGAGGACGCGGAGCTTTATAAGAGGGCGACTACGCGCTTCGCGGGCGGCTTGAAACGGCTGATGTCAGCGCGGCACAGCTTAATCGCGGGCGCGGGATTTGCGCGGAACAATAA  
AAATGCGCGCGTACGGGAATTGCGCAGGGAAGGCTGCGGGCGGATTCGCGCGGAGAAATCGGCGGCAAGCTGAGCGCGGTTCGAGAAGGGGCGCTTGATGTGCGGCTTTAAGCGCAAGCAG  
GGTGCCTTGAAACCGCAGATGCGCGCAGAGGAATGCGGACAGGGCGTTTGATGTGCAGCAGGCCGAGCTGGGGATGAAGCGGCAGGGGTTTGAGATGAAGCGTGAGGCGGATTCGCTGCGGAGC  
TTGAGGATAGGAAGCGCATTCGCCGATTTGACCGGGCTTTATGTTTTCGGAAGTGGAGCGGCGAGCGCGGGGAGATTGCGCGCGAGATTGATGCGCTTAACGGGAAGTTTGAGCGGCAAGG  
GGAGAAGGGCTTTGACCCGAATGTGTTCAAGACTGTCAAGTTATGAGGTTGCCGACCCGGATACGGGCTTGACGCGGAGCGCGGAGGGGATTTGCGATTTCGCGACGGGCAAGCCTTTGGAT  
TGAGATTTCGCGGAGAGCGCGGAGAAGCGTTATGCGCGCTTGGCGTTTAAGCCGAACGGTTCAGAAAAAGCGCGCGGTAAATCATTTATGAGAATGAGAAGGCTGAGAAGAGGGTTGAGC  
AA

SEQ ID 6326

LFGGFMGLFEPSAGDFWEMKEKEKEKARKGAEEERAAAQHRADAVRRTVANYEAGPARYRNVDLSRNNIEDGARRLRACAFERGADAGLGFSGGDKALSPDARAGADFARRDTRP  
TDAGGRTPPPLGFDGNVYRGKKPVRDFDAQRPVLSAGFDALSPEERELYKRAFTPYAGALNGQLTAAQLNARGIVAETHNKMAAVRELGRERLAAAAEAANREAVLQXGRFDAAVKANE  
GALNREMAQRNADRAFDVQOAEELMKRQGFEMKREADALEDEKRIADLTRAYGFAKSDGQRGRIARQIDALNGKFERQGEKGFDPNVFKTVSYEVADPDTGLTAKREGIVDLRTGKPLD  
VEFAGEREKRYAALGFKPNQKTAGGKIIYENKEGKRVBO

**SEQ ID 6327**

[illegible]

**SEQ ID 6328**

LNLPILTLILINDFTAGRFLTVRLKAQRRTLLALSRLKHQRLARPQIDNPLALRRQARIRVGNLITDSLEHIIHVKALLPLPLKLFVKRINLPRNLPALVRLAKTISPRQIGDALPIL  
KLQIRLTLHLKPLHLPOLGLLHKRPVRIPLRLHAVQRTLVRNLRRIKKPLLQHRILTVRILRRSRQPPPAQPFDRRIIFIMFRHNPARRIKLCRQRTVQGGPRIRRSRPLIKLPLLR  
QRIRGRHQRTLKVKITHRLAAPITHIPVKSQRRRRPSAIRRRARIAPRETRPGPRIGGKRLIAARKPGTGIRTPESTRPAQPPRPLINIVTAQIHHIPITRRPGLIIRNGTPHRIGTVEL  
CRRLPLPLRLPLGLLFFILLHLHPKIPGRRLKQTHRPSEQKSKLSKNPSPIKRLKRLTNKNRNPFGPINQQVTKKHTDGGPPGANKKPLCKAVAFONSLGLCLRSGL

**SEQ ID 6329**

ATGGCGGGGCGGGTACGTGTGTAGCAACCGCGTATCCGGCCCTTTGCGCATATATACAAGTCAAACAAGGCAAAATCAGGCACGGCAAAAGGCTGCAATCGGCTGCCTGTTCCGGCG  
CGCGCAACCCGCATTACAGACAACGACGCGGGGTATGTCTCAATATGCGCGCAATAGGAAAACCTTCACATCTTGGCGTGCAAAATTCAGAAAAAAGCGCAACACGAAAGCAAGATCC  
GGTGTGTTCCGATGTATTGAATGCCATAGGATTTACAGCCGTGGCATTAAAGGAGGCATATCCGGCGAATCTGTTTACAGGAGAAATGGCGCGGGCGTATTGGCGGACCGGAAACGCTT  
AAACCTTATATCATGGAACCTCGCCGCCCTCAACAATAACACAGATGTGTTTGTGAATTTGACGGCTTGCGCAGCGGGGAAACAACCCGTCAAGACCGGACCG



TAAAGAGGACTACGGGAATATTGGGAAGGAGGCGCGCATGGTATCGGAGGGGGCGGTTTACGGCATGAAATACAGGACGCTTTTCATCCGACGCGTTACGCTCGTCCCTTATGAT  
TCTTCTTTGCCCGTGCATACGCTTTGGGATTGGGCTGGGAACGATGCCATGACCATCGGGCTGGTGCAGCGCGATTGACGAGCGTGGCATCATAGGCTACATCGAAGACACGACCGGA  
CGTTGGAGCTGGTATGTTCGCGAATGGAAAAGCTGCCCTACGGTGGGGGACGGACTTCCGCGCAGCAGCGCAGGACGCGCAACTTCCAAACAGGCAAAAGTACGATGGAGATTTTGAC  
CGAATGGGGCGCAGTCCGCTTTCTGTCGAAAACGCGACCGGTATCGAAGAGCGCATCAGGGCGGGCGGATGCTGTTTCCAAAGTGTACTTCGATAAAGACAAAACAGCGCGCTTTTG  
GAATGCTGAAACGGTACGGCCGCCAAATACATCGGAAAACAGCGGTGGCAATGGGGCGGCTGCAGCAGCAATATTCGACGCGCGGATATGTTCCGCTACCTGGCGCAGCGGTTGATT  
TAATGGATACAGCAGCAATACGGGATACAGGAAACGCGGTATCGGATTGGAGGCTTTAT

## SEQ ID 6344

HTGKTVDLKLPAKLDGLFKPCRYKVMYGGGGKSHGAASALLALGAQRPLRLCAREIQKSMRDSVHRLKDKVAQILGLHFYEITDFRIRGANGTLPVPSGLQSHFVDSIKSFEGIDIV  
WVEBHGVSKKSDVLPPTIRKEGSEIWIITLNPOMETDETYRRFIAMPSEDWLCIEINRDNPNPPEALNRERLKAQRSMKEDYGNITWGRPRHVSGBAVYRHEIQDAFHSGRVTLVPYD  
SSLPVHTVDLGNWDAMTIGLVQRDLTSVRIIGYIEDTHTRLDWTVALEKLPYRWGDFLFDHGRTRNPQTGKSTMEILPLGLGRKSVFVNQATGIEEIRAAARMLPKVYFDKDKTARLL  
ECLKRYGRQIHAKTGVAMGPLHDEYSHGADMPFLYAQAVLDIMDTGSNTGYTETFPVSDWRLY

## SEQ ID 6345

TTGGCGGAAACCTGTCCAAAAGCGCGAGCAGATTGTGCGGAATTGTACGGAAGCCCGGAGGACACATTCACAAAAGCGCGTATGTCCAAAAGCGTGGCGCGGGGTTAAGGTTTGG  
TGGAAATCGAGCGTAAATCATACGCTATGGATACCGCGAATCGAGATTTCGGAATCCGCCAAGACGGCGGGCATCCGTATCGAATTGTAGGCGCTGAAGATGACGGGAAGACGGT

## SEQ ID 6346

LAENLSKSAEQIVAELYGSPEDTPTKARMPQTVAGFKVLVEIERKSYGMDTAEKLSIESARTAGIRIEFVGPEDDGKDQ

## SEQ ID 6347

TTGGCGGATTCGGAATCTTCGATTTCGGCGGTATCCATACCGTATGATTACGCTCGATTTCACCAAAACCTTAAACCCCGCCGCCACCGTTTGAACATACCGCCCTTTGTGAATGTGT  
CTCCCGGCTTCCGTACAAATCCGCGCAATCTGCTCCGCGCTTTTGACAGGTTTTCGCCCAAAATTCGATGCTCGCTGTACGGCGCAACCCGTTTCGCTTCCCGCTCCGTACTTAA  
TTAAGGTTGAATCCCA

## SEQ ID 6348

LADSEIFDSAVSIPIYDLRSISTKTLNPAATVMNIRAFVNVSSGLPNSATICSALLDRPSAKFRCLRCTAATRFASASVTYLRKSA

## SEQ ID 6349

ATGCGTGGCTGTACGGCGGCAACCCGTTTCGCTCCGCGTCCGTTACTTATTTAAGGTTGAAATCCGCATAATCCGGCGCATTCGCGTTTGTTCGCGGACAGCACCATCGCCCGCGC  
TTTGCTGTACCTCGTCATCAATTCGCGGCTCCACGCGTCTTTCGCAACCCGTCGCGAGCTGTTCGCGGCAACATTTGATTTTCGCGCGATTTTCGCAATGCTCAAAACCCCGCGC  
GGTAATCCAGCTCGACTTTCCGCCAATCCTCATC

## SEQ ID 6350

MPALYGNPFRFRVRYLPKVEIRIIRRIAVFVRQHRPRLCLYLVIIQIARPHAFPGNPADVLRENIVFAPDFGNAQNPAPVFIQDFAPILI

## SEQ ID 6351

ATGCAAGTATTTTAGCAATCTCAAAGCCTTTTCGAAACCGTCAGCAGCTGGGTTTGGGGATCGTTATGTTGATGCTGCTGGTCGCCACCGCATTTGCTGACCGTTATGCTGAAAG  
GCTTGCAGTTCATATGTTGGGCTATGCGCTGAACACGGCGTTTGTCCCGTCAAAGAAATATGAAGGCGCGCAGGCCACGAAGGCGATATTTCCCATTTTTCGCGGCTTGTATGACCGCGT  
GTCCGCCACCATCGGTACGGGTAACTCGCGCGGTGGCGAGTCAGTGGTAACCGCGCGCGCGCGCGGTATTTGGATGTGGATGACCGCTATTTTCGGCATGGCCACAAATACGGC  
GAAGCGGTGTTCGCGGTGAAATACCGCGTCAACAATTCGAAAGCGGAAATGTCGCGCGCGCGCATGTTATACATCGAAAAAGGCTTGGCCAAAACTGGAATGATGCGCGTTCATTTG  
CGCTGTTCCGCACATTCGCTTCGTTTCGTTATCGGCGAGCTCGGTGCGAGTCCCACTCGGTGTCACAGGCTGTGCAAAACAGCTTCGCTATCGAACTGCTATACCGCATTCGTTGACCGT  
TCTGACTGCCGTTGCGTTTATAGGTGTTATTAAGGCATCGCCAAAGCGCTTCTTTCATCGTGCCTGTATGGCGGTGTTTATATGTTGGCGGTCTTTCATATTCGTCATTAATTC  
GATGCACTGATGCTGCGCTCAAGCTGATTTCCTCGATGCGTTCAGCGCGCAGCGGTAGCAGCGCGCGCTATCGGTACGCTACCGCTACCGGTGCGCGGTGCTTCCAAATG  
AGCGCGGTATGCGGTCTCGCGCTTATTCGCGCGCAGCGCGGAAAAACCGAACCCCGTTCGTCAGGCTTTGGTTTCCATGACCGGTACTTTTTCGACACCATTTGTTGCTGCTGCTGATTAC  
CGGTATCGTGTGCTCATGGTCTGCTCGCGCAGCGCGGAGTTTGTGAAACCTGAATTGAGCGCGCGCGCTGACAAACCGTCACTTTCAAAAAATGCTGCCCGGCATCGCGCGCTGG  
ATTGNGACCATCGGCTGATTTCCTTTCCTACTCAACCATTCCTCGCTGCTGTTATACGCGGAGAAATGCGCGGTTCAGCTTTCGCGCGAGAGTTTCGCGCTTTGACCGCGTGGGT  
ATGTTTCTTCGCTATGCGCGGTACCGTGTGAGCTTGATTGCTATGCTGCTTCGGATACATTAACCGCTTGATGCGATTGCCAACCTGACTCGCGCTTTGTTGATGCGGAAAT  
CATCGTCAATGAACACCGGACTTCAAAACAAAAATCACAACCGCGAATTGCGCAT

## SEQ ID 6352

MQVFLDNLKAFPEIVSSNVWGSVLMMLLVGTGIVLTVMLKGLQFTMLGYALKQAFVPSKYYEGGAGHEGDISHPAALMTPALSNTITGNIAGVATAVVTGGPGAVFHRMTAIFGMATKYG  
EGLVAVKYRVNNSKMGSGGPMYYIEKGLKMKWMAVAFALPGTASPFGIGSSVQNSVAQVQTSFGIEPAYTGTITLTVLTAVVVLGGIKGIAKAAFIIPMAVAVFVLGGLSIIIVRS  
DALMPAVKLIFSDAFSAQAVAGGAIQTVIRYGVARGVFSNEAGMGSAPLAAAKTDPVRQALVSMGTGFLDTIVVCSITGIVLVMGLLAGGEFVKPELSGAALITVTFQKMLPGIGW  
IVTIGLIFAYSTILGWYCYEKCAYVYFGEKPAALYRVGVSSVMPGTVLSLDLWLASDTFNGLMALPNL/TALLMAKVIVNETRDFKQKITNGELPH

## SEQ ID 6353

ATGGCACTTTTCCTCAGCATATTCGCCATCTGCTGCTGATTGGCTGATGTTGAAAAAAGCATGAGCTTCTTACGTCGCACTGCGGATTACCGCAGTCTGATTACGCCATCAAAC  
TTTTCCTACTTCGCGGATGCGGGAATGCTGCTCAACGCCACCGCGCTTCGCGCTCGTCAAAGCTCAGCGCGATTACCGTGAATTTTCGCGCGGATATGTTCAACCGTATGATGGAAC  
CAGCGGCTGCATCGATGTCATCCGCAATGGCTGGGACCATCAGCCGCAACCCGCTAGCGCACTGATGATTATCGGCTGGGCTTTTGCTTTATGATGAAGCGCATTCGCGCTTCGGC  
ACGCTTCGCGGATTCGCGCGGATTCGATGAGCTTGGCTTCAATCCGTTGAAAGTGGCGATTTCCTACTTTGGTGAATGAATTCGCTGCGGATGCTGTCGCGCGGTTCGCTACCGCA  
CTTGGTTCGCTTCGCAACCGCTGAACCTGAGTCCGGAAGACATCTCGCCATCGGCGAGGAGACGCGGCGGTGATGCACTTCTTCGCAAGTTTCGCTATCCCTGTCATCGTTTGGGCTTCAT  
CGTGCTTGGCTGAAATCCGCAAAACTTGGGCTTCGTCGCAATTCGCGCTTCTCTCTGCAACCACTTCATGACCGCATTCGCGATGGTCAACGAAGAAATTCGCGTCTGCTGCGCGC  
GCAATCGCGCTGATGGTGTGCTGATTTCGCGCGCAACCAAGCTGGGCTTGAAGCAAGACCGCAAGAACGCGAATGCGGAAAGTGGCGTTTCGCGCAAGTTCGCGCAAGCACTTCGCGC  
CTTGGGTATGCTGATTCGCGCATGCTGGTGTACCGCATCAAACAGCTTCGGAATCAAAGGCAATTTGACAGCAAGAAAGATGGTTCAGCTTCCAACTGCGGCTTGTATTTGCCAAAT  
TACCGTCAGCGACTCCCTGACGATTACCTTCGCAATATTTTCGCAAGATGTCAGCGGCTTACCAAAACGCTGACGTCGCGCTTGGATTCCGCTGCTGCTGACCGTTTGGATTTC  
ATCTGCTGTATAAAACCAATTCAGAGATGCTGACGATTTATGCGGTAACTTCAATCAAACCAAAACCGCTGCTGCGCTGATGGGTGCGCTGATTATGCTGCTGATGCTGCTG  
TCGCGCGGCAATTCGATGCTGAAATCATCGGTAAAGAAATTTGCGCGCAATGCGCGGCGAACACTGGGTTTATTTTCGCGCTATTCGCGCGGATCGGTGCTTCTTCGCGCTCAA  
CAGCGTTCACCTGACCTTCGCTCGGATTCAGCAGCAATTCGCGCTTGATACCGGCTGCTGCTGACCTGATTCTGCGCTGCTGCTGCGCGGATGCGCAATATGCTGCTG  
CTCAACCAATCATTCGCGGTATGATCGGTATGAGCTGAAAAATTCGGAAGTGGCATTTATCAAGAAACCGTTATCCCGATGCGGATTTACGCGGCTGATTGCGCTGCTGCGCGCAATGA  
TTTCTCTCTC

## SEQ ID 6354

HALFLSITPPIVLLIIMLVKKNMPSYVALPITAVLIYAIKLFYPGDAGMLLNATAASGLVKTL/PTITVIFGAIMFNRMETPGCIDVIRKMLATISPNVPAQIMIIGWAPFPMIEGASGFG  
TPAATAAPILMSLGFNPLKVALFTLVNNSVPSVPGAVGTPTWFGAPILNLSAEDILAIQRQTVGMHFPAGFVPIVIGLGFIVPWEIRKILGFLVAVPSCPIPYAALAHVNEEFPSLVAG  
AIGLMVSFAANQWGLSKDHAKDPNAEKVPFAQVAKALAPLGLMLGMLVWTRIKQLGIGKILTSKEEWSFQLPFDLSKITVSDSLTITFGNIFGQDVSASYQTLVPAHIPFLVWIC  
ILLYKTKPKDWTIYAVTFNYTKKPLALMGALIMVQLMLVGDNSMKVLIIGKEFAAMAGHNVVPSYPLGAIGAFPSGNTVSNLTPGPIQQQIALDTGLSVTLILALQSVGGAAGHNV  
LNNLIACVTFLVDKNSGEGAIKKTVIPHAIVGYIAVVAHIFFL

## SEQ ID 6355

ATGCCGAGATTGTGATGAGGATTGGCGCAAAGTCGAGCTGGATTACCGGCGCGGGGTTTGGAGCATTCGCCAAATCGGGCGCAATACAAATGTTTCGGCGCAACAGCTGGCGAGGGTTG  
CCAAAGAACCGCTGTGGACGCGGATTGTAATGACGAGGTACAGGCAAAAGCGCGCGGATGGTGTCTTCGCGGACAAAAACGGCAATGCGCGGATTAAGCGGATTTCAACCTTAAA

## SEQ ID 6356

MPRLSEDEMRKVELDYRRGLSIAIRIGRYNVSQAHVGRVAKERVWTRDLNDEVQAKARAMVLSADKNGNAPDYADFNLK

## SEQ ID 6357

ATGTCGGGATTGTGCGGATTTGACAGGTGTACAGGGGGTTGTGGATTGACAAACGCGGAGCAGGTGGTCAGCCGCGAGGCTTTGGCGGAAACGACAGGCTGAAAAATGTCGGAATCA  
CTAAATTTACCAAGCTGCTGGTCGACGACGCAAAATCTACCGCTGACAAAGGGGATTTTCAAGCCCGCATAGGGTTTGGCGAGACGCGCCCGTCAGCGTATCGGTATTGGATTGCGG  
GATGGCGGTATTGGAATAGGCGATACGATTTGCACTCAACCGCAGGAAATGCGCTGTTGGGGGCTTTGATGTCGGGGTTCGGACAGCAGTTTCCAGTATTGATGGGGCGCGAG  
TTTTGAGTGTTCGGGAATTATCTGGAATGTTCCGCCAAAAACGGGAGGTTCGATT

## SEQ ID 6358

MSGLSIDDKVYQGVVDLHNAEQVVSREALAETTLGLKMEITKPTKILLVEHGKIYVRVTRGIFKPAIGFGETRPFVSFVLDGNGVLEIGDVLHLNPEMRSLGALMSGFGQFSSIQMGRE  
FSVLRNLYLECSAKNRLDF

## SEQ ID 6359

TTGGGCATCTATGGAGCATGGTGTATTATGGGATTAAACACAAGAGGTTTAAAGAAATATTAAAGATATGATGACAATACGGGAAAGTTATTTGGCGGAGCGTCCAAAGAAATATTTCA  
ATAGCGGTTCGATTAACAAATCTTGAATACCGGATTTCGCGCAAGGAGGTTTCTTATACAAAGCGAGGTTCGGGTATTGAAGTTAAAAATATTAAAGAAACATTAATGCACATAG  
ATTAATTTGGCTTTTGTATTATGGGAAACACGCTTCTCAATAGGCCATATCAATAGGGATAAGACAGATAATAGAATATCTAATTTGAGAGATGTTACACATGCTGAAAAATATGAAAAAT  
AGAGGGAAGTTTAAAAATAATACTAGCGGCATCTAGGGGTTTATTTCCATAAGCGCTTAAGAAATGGCAAGCTAGGATTATGGTTAATAGAAAAATAAAATATTAGGTTTATTGTAAC  
ATATTGAAGATGACGCGAAAGCGAGAGAGGACGATCTAAAGATTTTGGCTTTGTAGTG

## SEQ ID 6360

LGIYGAWCFMGLTQFVLKELLRYDDMTGKLYWAERPRKYFNSGLHYKSWNTGFSQKEVFLYKRLGLKLFKQYNAHRLIWLFPVYKHAASSIGHINRDKTINRISNLRDVTHAENMK  
RGKPKNNTSGHTGVYFHKPSKKWQARIMVNRKNKILGLFEHIEDAAKAREASKDFGVV

## SEQ ID 6361

ATGAACGGGGCGGAATTTACTGACGCCCAAAACAAAAAGCAGGTTATGCGGTGCGATTGGGACAGCCCGGAGCGGTGGTTGAAAAACGGCAACCTTGAAATCACAATCCGCCCGCGCA  
AGTCAAAACGGAGCGTCGAGCAGAACAGCGCGGTATGGTTTGTATCGTGAATTTTCAAGAAAGTTTATCGATGGGAGAGGTTTACTCAAGATGATGCGATGAATTTTAAAAAG  
AAAAATTTATGGATGATTGAAATGCCTAACGGCAATTAATGGGTATATCAACGACAAAATTTACAGTTCCGGAAATGCTGAATATCAAGAAAGATTTATCTTGGGCATCTATGGAG  
CATGGTGTATTATGGGAT

## SEQ ID 6362

MNGARETITPQNKQVMRSIWSDPDGWFENGLEITIRPKSKRSVEQNRLWFLYREISEKVFIDGRRFSQDVWHEFLKRFICGIEPNGQLMISTTKLSVREMSYQEKIISWASHE  
HGVLMD

## SEQ ID 6363

TTGCGCGGGCGGATTTGATTTCAAGGTTCGCGTTTTCAAACACCGGTCCGGGCTGTCCAAATCGACCGCATACCTGCTTTTGTGTTTGGGGCGTCAGTGTAATTCGCCCGCGTTCA  
TTTCAGAGCGGCTTTTCAACCGGACACCCCAATGCTTCAAGGCGCGGTATCGTGCGCAATTCGCAACGCGCATATAAACTCTTTGTCTTCGCGGCTTAGGCTTCGCCCGCTGCCGTG  
ATCGCGCGCGCGCGGCAACCGCACCGAAACCGCGCCCAACCGCGCTTTTCAATCCCGCGGCTGCTGCTCGCGCGGAAACGGCAACACGACGCGTTTCAGGTTGTCTATGCACA  
CGCCCGCGATGTTCCGGGTGATGCGCGCTTTGGCGGCTTTGCGTATCGCGC

## SEQ ID 6364

LRGRIVISRLPFSNHPSGLSIDRITCFLFWGVSVNSAPFISDGLSRRQPPMLQGGVSCAIANGAYKTLCLRLGLRPCRSSRRGGNRTNPRNRRFSIPPRASRPNGTTRPFQGHCT  
RPRCSACIARLWRLCVSR

## SEQ ID 6365

ATGTCAGCGCGATACGCAAGCGCCAAAGCGCGGCAATGCAACCGCAACATCGCGGCGGTGTGCAATGACAACCGTGAACCGTCTGTTGTGCGGTTTCCCGGGCGAGACGACGCGG  
CGGAGTTGAAAAGCGCGGCTTTGGCGCGGTTTCGGGTGCGGTTCGCGCGCGCGATCGACGGCAGGGCGCGAGCCCTAAGCGCGAAGACAAAGAGTTTATATGCGCGCTTCGCA  
ATTCGCGCAGATACGCGCTTGAAGCATTTGGGGTGTGTCGCGGTGAAGCGCGCTGAA

## SEQ ID 6366

MSSAIRKAAGGQCTPNIAVCNDNPETVVLRCRPFETHAGLKSGLGAGFGCGCRRGAIDGRGAGLSREDKEFYMRSLRTIRRLALGVVGVKRLK

## SEQ ID 6367

TTGGCGGCTTTGCGTATCGCGTAGACATCCCAACCTCTCTGTCGATGAAATCCCAACCTCTGTCGCGCATCCGCTCTGTTCCATCTCCAATTCGCCCACTCCACCGCAACCGCGG  
CCGCTTACCGGTTCGCGCGCATATTCGCGCGCAATGCGCGCACTGCTGCTGTTGATAGGCAACCGCTTGAAGCGCGTCCAGAGTAACCTTCAGGGCGTTGTCCAAATCGATCACCG  
TCTGTTTTCGCGCGGCTCTTTGTTGCTTTGGGTATCAGCGGCATATACGGCAACCGCGCTTCGAGACGCGATCGCGCGCGGCTTCGCGCATACGGCGGACGCTTTCCTTATAGCG  
CGCGCGCTCCGCGCTCTGACCGCGCTGTTGCGCAATCCGCAATATCGGTTCGCGATACGGGTGAAGCAGGATAAGGCGCGTCACGCGCATTCCTTCCGCTGCGCTTCACAGCG  
CGCGCGCAATATCGGGCAGGCGCGTTCGCGCGCGGATGATTCGTCGAGCTTTCGCGCGCTATCGCGCGGCTCCCGCGCGCGCGCTTTTTCGCGACTGCTTGTTCGCGCAGGT  
TTTGCACGATTG

## SEQ ID 6368

LAALRIALDIPLLSDEIPTLVCRIRLPHLQFPHLHRQTAAATYRFAAIFGGNAPHLFVVVIGNALKRVQSNLQGVVQIDHRLVCAAVFVRFYQPHIYGNRAPGRHRARPLEDTADGFLIR  
RRLRAPRDPVAPNPFISVCRYGVRQDKARHAHSPAGCVHRPAPNIGQAACAAARNYPCSLAAVIAAPAPAAARFCRTALLRQVLHDL

## SEQ ID 6369

ATGACGGCGCAAGGCTGCACGGATACATCCGCGCGCGCACGCGCGCTGCGCGATATTGGGCGCGCGCTGTGGACGAACCGCGAGGGAAATGCGCG

## SEQ ID 6370

MTAARLHGYIRAAHAACPIIGAGLWTPAGECA

## SEQ ID 6371

ATGCCGTCCGCGCAAGGAAGGGGGTCTATTATACAAATCGTCAAAACCTGCGCAACAGGCAAGTCCGCGCAAAAGCGCGCGCGCGGAGCGCGGATGACGGCGGCAAGGCTG  
CACGGATACATCCGCGCGCGCACCGCGCTGCGGATATTGGGCGCGCGCTGTGGACGCAACCGCGAGGGAATGCGGTGACGCGCTTATCTGCTTACCCCGTATCGGCAAAACCG  
ATATTGGCGGATTGGCGCAACAGGCGGTGAGGAGCGCGGAGGCGCGGCTATAGGAAACCGTCCGCGTATCGCGCAAGGGGCGCGCGATGCGCTCCGAAGGCGCGGTTCGCGTA  
TATGTGCGGTGATACCAAAGCGCAACAGACGCGCGCAACAGAGCGGTGATCGATTGGACAAACCGCTGAAGGTTACTCTGGACGCGCTTCAAGCGGTTCCTATCACACGACA  
GGCAGGTGCGGCGCATTCGCGCGCAATATGGCGCGCAACCGGTAAACGCGCGCGGTTCGCGGTGAGGTGGGGAAATGGAGATGGAACAGCAGGATCGCGCAGACGAGGGTTGGGATT  
CATCGGACAGGAGGTTGGGATGTC

## SEQ ID 6372

MPSRARKGGLLQIVQNLPOQSPAKARGGSRDDGKAAIRHPRARRLPDIGRRPVDATGRGMRVTRLILPYPVSANRYWRIWRNRAVSAEAAAYKETVRRIAQAGAMPSEGAVAL  
YVRLIPKANIKDGANKTVILDLNALKVLFDALQGVAYHNDQVRRIAAEYGGEEPTVGGGLAVEGKLEMBQTDAADEBDFIQBGHNV



**SEQ ID 6373**

TTGAGTTTCCACAGAAAAATCGAAAAATGAATATTTTTTACGAAGAGTCGCGCCAGTTCAAAGTTGCGGTGTCGTGTCACAAAAAACGACGCCTACCTACCAAGTCGATACCCAACACGGCA  
AACGCACCAAAGTGAAGGCAAAACAATGCTCTTGCAGAGTTTGACGGCGATATGGCGGGGTTTGTGAAAAACGCTCAGGGCGAGCGCGCGGCACATCGACACCGGATTATTTGTGGGAAGTATG  
CGCGAAGAGGAGTTTACCGCGAAGGCCATCGCCGAGAATATTACGGCCATCGCCGACCAAAACCGAGCTGGCGGGCAGCTTGTATTGTCGCTGTAGCGCCGCGCGGTGTATTTCTACAAA  
AAAGCCAAAGGGCTGTTCAAAGCCGCGCCCGAAGAACTTTGAAACAAGCGCTTCCGCCATCGAACGCAAAAAACGACCAAGCAGCAAACTGCAAGCTTGGGCGGAAGCTTGAAACGG  
CGAGAGTACCCGCTGAAATCGCGCGCGATTGAGAACCACTTGACCGCGCCGACGAGCTGCACTGACCTACAAAGCTTTTACAAAGCCGCGAGCAGTCAGAAACCTCGCGCTACGA  
CTGGGCGAAAAACCGGGCGGCATGTAGTCCATCTCCGCAATACCTGCAAGACGGCTTTGAAATCAAATACTTCCCCAAAGGAACAGGTTTCCCCGAAGCTCTCCCTTCGGAATGCCCGAC  
CTGCCAAAGGCGCAGCTTACCGCCCTTTCCATTGACGACGAATCGACCAACCGAAGTGGACGATGCCTTGAGCCTGACCGAATTTGGGCAACGCGCAGGAAGCGCGTGGCATCCACATCGCGG  
CGCGCTGCTTGGCGTCCGACAAAGCGCGCGAATGGACAAATCAATTATGCAAGCGGTGTAGTACCGTTTATTTCCCCGGCGGCAAAATCAGCATGCTGCCCGAAAAACTGGATTACCGCGGT  
CAGCCTCGATCGCAGGCGCATACCGCCCTGCCGTCAGCATTTATTTCAGATGTGACGAGCGAGTTCAAAGCTGCGCGAGCGAGCTTGCAAAATCGAAGCGGTCAACATCGCGCGCAAACTGGT  
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ATCGGCATGGCGGTGACGATTACGGCTGCTTTACCTCGCGGTGCGCGCGCGCGCGCATACATCAACCAAAACCACTCTCAGCGTGATAGAGACACCGCGGAGCGCGCTCTTCCAGC  
AAAGCGATGCCGAATCTTCGCGCGCCCTGCGCGATTGTGACAGCCTAGCGCGCTACGCGGACTTCCAAAGCGCAGATGGAAGCCTACTGGAGGCTCTGTGTACCTGCAACAAAGGCAT  
CAGCGAACTGACCGCGACGATTTGAAAGGAAGACTCTGCCGATCGAAGCTTGCACATGCAAGCGAGCGCGCGCGGGGCAAAACGCGAGCGCAATGCCGTC  
ATCAGCGAATTGGATGCGGAGAGCAGTTGTCTCGCTCAACTACATCAAGGCGAGCGCGCGCGGGGGCAAAACGCGAGCGCAATGCCGTC

**SEQ ID 6374**

LSPHKIRKIRNFIYEESSGQFKVAVVQKNDATYQVDTQHGRKTKVKANNVFAEFDGDMAAFLENAQAQADIDTDLLEWCVGEEEFATAELAEYYGHAPTKTELAATLIALYAAPVVFYTK  
 KAKGVFKAAPETLKLQALAAIERKQQDAQIDANABALKRGMPSLEAIDLRTILHAPDKQSLTYKTAFTKAADALKTSAYELAKTKGGITSIPQYLDQGFELKYFPKGTGFPDLSLFPMPD  
 LPKADVTFASIDDESTTFEVDLALSITLGLNGTKRVGIIHAAPSLAVRQGGGHEQIIMQLRSLTVTFPGGKITMLPENWITAFSLDAGAYRPAVSIYTFVDGFEFNVGEPTCKIEAVNTAANLR  
 IQATEPHFNAETGLDQAGEMMPAHHQDLITWIFYQFATALQKARGKYEPDRAPQYDYSELDEEGNVSVVRRERGSPIDITLVSEMHILANSTWAOHLDENGLPGLFRVQPAQKVMKSTQSEPH  
 IGMGVQHYGWSFSLPRAADYINQKQLSLIDDTAEPLFQQSDAELFAALRDFDTAXAAYADPQRQMEAYWSLVTYLQQQGISELTATILKEDLVRLEGLPLTRATGIPFDALPKSQALFK  
 ITLDEADQGVNLTALAAAPGGTLAGNAV

**SEQ ID 6375**

TTGTTTGGCGGGGGCGGGCTGTTCCGGCACCGGGATTTCGCCGACGCGCGCGCCGAGCAGCGCGGGTTTCCGTTCCCGCGTGCTGCCGCTATGGATGGCGGGCGTTTCGCCCTAGAGGAAG  
AAAATCATTTGCCCGCAGCAGCGCAATCAGCCGCTAAATCGCCATCGGGATAACGGTTTTCCTTGATAATCGCACTTCGGAATTTTTCACGTCCAATACGGTACATPACGGCGATGATGTTGT  
TGAGGCACACCAATATTGCCCATCGCGCCGCGCAGCGACTGCAACGCGAGAATCAGGGTCACGAGACGGCGCGTATCAAGGCGCATTTGCTGCTGAATCGGACCGAAGGTCAGGTTGGACAG  
GGTGTTCGAGCCCGGAAGAAGAACCGACCTGACGCGCCACAGCAGCGCAAAATAAACCAGATGTTTCGCGCCGATTCGCGGCAAAATCTCTTACCGATGATTTTCCACATCGAAATTTGTCGCG  
CGACACCAATCATCGCTGAACCAATATACGCGACCACTTCAGGACAAGCAGCGGTTTTCGTTTGATTCGAAGGTTACGCGCAATAATCTCCAGGACCATCTTTGAATTCGAGGATTCGCGG  
CGTACGAATTCACAACTCGCAGCAGAACCGGAATCCAAGCCGGACGTACAGCGTTTGGTAAAGACGCGCTGACATCTTTGTTCGAAAAATATTGCCGAAGGTAACTGTCAGGAGTTCGCTGAC  
GGTAAFTTTGGACAAATCAAAACGGCAGTTGGAAGCTGAACCAATCTCTTTGCTGTGTCAAAATGCTTTTGATTCGAGCTGTTCGATCGGGGTAAACACAGCATCGCGATCAGCATACCC  
AAAGGGCGCAGTCTTTTGGCGACTTGGCGCAACGGCAGCTTTTTCGCAATTCGGGCTTTTGGCGTGGTCTTTGCTCAAGCCCCAGCCCTTGGTTGGCGCGGAATACGGGACCACTCAGGCGGA  
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CAGCATGAAGCGCCAAACAGTATGACGAGGTACGAAACCTCGCAAGAAGTGTCATCAGCGCGCTCTCGCTCGGATGCGAGCGAGATGTCCTTCGCGCACTCAGGTTTTCAGCGGTGCGAAACCGAAC  
CAGGTTGGCGCTACCGACCGCGCCGAACGATACCGGCACGGAAATTCATACCAAAGTGAATAATCGCCACTTTTCAACGGATTTGAAGCCCAAGCTTCATCAGAATCGGCGCGGCAATCGCGGAG  
CGTGCCGAAGCCGATGCGCTTCAATCATAAAGGCAAAAGCCGACGATATCATAGTTGCGTACGCGGGTTCGGGCTGATGTGGTCCGACGCCATTTCGGGATGACATCGATCGATCGAGC  
CGTGCTTCATCATPACGGTTGAACATATTCGCCCGCAAAATCAGCGTATTCGCGCTGAGCGTTTTCGATTCAGCCAGGACGCGGGGTGGCGTTTGAACGCAATTCGCCGATCGCGAAGTATG  
AAAGTCTTGATGCGCTAAATCAGCATCGGCTAATCGCGCATCGGACGTAGGAAGGCATCTGTTTTCCTACCATCAGCCAAATCAGCAGGACGATGGGGAATATGCTGAGGAAAGTG  
CTATCAACGAACTTTTTCGAGCACTTTTCGATCAAGGCGCGTCGAGGTTTGGAAAGACGTCCTAAATCCCGCACACCCGATATTTCGGT

SEQ ID 6376

LFFGAGCSGSGIGLIPDAPPGRGAASVVRVLP.LPWWAARPLEEENHCRDDGNHAVNRHRDNGFLDNRTFGIPFHVQYGYGDDVVAEHHAHRAADGLQRQNGHGQAGIKGDLILNRTBGQVGH  
 GVGAGEERTDRAQIRRKINPVFARHCCKFLTDOPHHRIVAADQHQLNHNQRTHQGKQRFGLIGSYGNRPGIFEGFIIQDDANPNQGHERNSRDVQLVRRADILSENTAECNRQGVAD  
 GNFQGIKQKLEASFPFFAGQNAFDSELFDAGNHQHADQHTQGRSGPGLDGRHHRFGFIIYVFGVVPVAAQALVGGEGYGHQADACAGDERREFPVDRHQCGIRNGAGGADGDEAQVFDPRPR  
 HDEAQITDTRDDETCEEVHHAGLPADGEDVFGTVQRCETEPGRKTDRAERYGRIHHQSENHRFHPIEAQHQNRRNGNRRAAGCAFNHKGKSPADNHQLRYGVYVGNRQCGFPADDIDNA  
 RGHPTTHVHNRAENNRREKFTPEAGSGGQVBOHSRLAEVEKFGDGVNQHCGNRQCGDVGHRTHFQHQENQDDGGEYAEKKNHESFLGICILRRVEWVKDVQIIPHYRYFG

SEQ ID 6377

TTGCGCGGGACGGCATTAAACCCCTTCTCCACACGGCTGGTCCGCGCGCAGGCGCTTCAGGTGGCAATTTCCTCCGCCATTGTGATTTTTCCTTTTGTTTATGTGTGTTTAATATCCGAAG  
CCCTCGAAGTCGTCTTCGCCCTTTGCCCTCGCGCTTCGCGCGCAAAACCGCGTCCGCGGGCTTCACCAAAAAGCCATACCGCCACAGTTCGCGCGCGCGCGAAGACAGCGCGGTGATGATGC

**SEQ ID 6378**

IRGTAINPFSNGI VPPQALOVRISSAILIFFPVTMCLISEAVEVVPFAFAVALAAONRVGGFHQKPYRORRRRAERORGDDA

SEQ ID 6379

SEQ ID 6379  
ATGGAATACCCCTGTTAAGCATCATCAACCGCGCTGTCGTTTCGGCGGCGCGCGACGTTGGCGGTATGGCTTTTGGTGAAGCCGCCGACGCGGTTTTGCGCCGCAAGCGCGACGGCAAAAGCG  
AAGACGACTTCGACGGCTTCGGATAT

**SEQ ID 6380**

MDTLLSIITALSEGGAATLAVWLLVEAADAVLRRKRDGKGEDDFDGFQY

SEQ ID 6381

ATGTTGGAAATTTCGGGAAACTGATGAACCGTCAATTCGCGCGAATTCGCGTCAATTCGCGCGAAAGCGGGAATTCGGAAACCGCGAACGCGGCAGGAATTTATCGGAAACGGC

SEQ ID 6382

MIKRFETDEPSEPPISVIPAKAGIRKPRTROEFIGNG

SEQ ID 6383

GTGATGATGCTTAAACAGGGTATCCATTGTTTATTTCTTTCGGTCGGTTTTATGGGTCGGGGTCGGATTCGCCCGCCTCCGTCAFTCCCGCGCAGGGGGGAATCCGGAACCCCGAACG  
CGGCAGGAATCTATCGGAACGGCTGAAACCGGACGGACCGGATTCGCCGCTGCGCGGGAATGACGGTTTCGGTTCTACGGTACTGTGTCAGGTTTCGGTCAATGTTGGAATTCGGGAACCT  
GATGAACCGTCAFTCCCGCGGATTTCCGTCAFTCCCGCGAAAGCGGGAATCCGGAACCCCGAACGCGGCAGGAATTTATCGGAACCGGCTGAAACCGGACGGACCGGATTCGCCGCTGCG  
CGGGA



## SEQ ID 6384

VMLNRVSVLPFGRFYGSGDSRRLRHSRAGGNPETPNAAGIYRRLKPDGPDRLRGNDGVSATVTVFRSCWNFGKLMNRHSRRFPSPFRKRESGNPERGRNLSETAETGRTGFPFPA  
RE

## SEQ ID 6385

GTGATTCGCGACGCTTTCGTCAATTCGCGCGCAGCGGGAATCCGGTCCGTCCGGTTTCAGCCGTTTCGATAAATTCCTGCCCGGTTCGGGGTTTCGGGATTCGCCCTTTCGCGGGAATGA  
CGGAANTCGCGCGGAATGACGGTTCATCAGTTTCCCGAAATTCACATGACCGAAACC

## SEQ ID 6386

VIPDAFVIPAGAGIRSVRFQPPFINSRVRFRIPAFAGMTIEGNDGSSVSRNSNMET

## SEQ ID 6387

GTGCGGGGCGCCCGCTTCAGCGGCAATTTTTTCCAAACAATCTGACACAGCGCGCGCCCAACGAAAATTTGCTTCGCGGTTCGGGATGTAATAAGCGCGGAGATGACGCGAAGC  
AGCGCGGCTTCGTCGCGCGCTGGAACCGCAATCTTCAGACCGCGGTACATTTTTTCATAGCGCGGTGTTTGAATTTCTTGAACCTTCGCGCGCGCGCGGTTCGCGTTCCAGTACC  
GCAAGGCTTTTTCAAGTCTTCGCGCGCGCTTTTTCTTGTGCGCGCAGATGTAATTTGAAGCGGTTCGCGAGGTGAAGTTGAGGTATTCGCGAAACCCGACGCACTCGAAGCGCGGT  
TTTGTAAAGCCCGGTTGATTTGCCGCTTGTTCGCGCGCGCTTCGCTCCGACGCTTTCGGTTTTCGCTTTCGGAATTCCTTTTCAAAATTTGCGTTT

## SEQ ID 6388

VRGPPFRFRHFFQJIFDTGGRPRKIVFAVDVLSGGDQKQRLRAAVEPAIPQTGVHFFIAAVFEFLRLRAGALAFQVPGFTQVFAPAFTLVPPDVFEVAVEVEVLRKPDLEGA  
FVIAIRVGIALLRRGRPRDGFGLRVSDCHSVFPKFAF

## SEQ ID 6389

ATGACAGTCCGAACACGCAAAACCGTCCGAGCGGAAGCGCGCGCAACAAGCGGCAATACCAACCGGGCTATTACAAAAACCGCGCTTCGAGTCCGTCCGGTTTCGCAAT  
ACCTCAACTTCAACTCGGCAACCGCTTCAATACATCTGCGCGCACAGAAAAAGCGCGCGCAAGACTTGAAGAAAGCCCTGCGGTACTTGAACGCCAACCGCGCGCGCGCGAA  
GTTCAAGAACTCAAAACACCGCGCTATGAAAAATGTACGCGGTCTGAAAGATTGCGGGTTTCGACGCGGACGAGGCGCGGTGCTTGCCTCATCTCCGCGCTTATTTACATCCGC  
GACGCGAAGACAAATTTGCGTGGCGCGCGCTGTGTCGAAGATTGTTGAAAAAATGCCGCTGAAGCGGGCGGGCCCGCACCTGAAAGCCGATGCCGCTGAAACGCGCGCG  
GAGGCATT

## SEQ ID 6390

MTVVRNTQTVRTTAAPOQGGNTNPGYKNRAFCVGFQYLNFNHGNAPFYIWRHKEKGGREDLEKALRYLERQAGAPFKKLKHRRYKMYAGLKDCGFDGTEAALLAVISAAYIR  
DGEDNFAMAAACVEDLLEKMPPEAGRAPHPESPMPETAGGGI

## SEQ ID 6391

TTGCGTTTAAACCGGTTTTTAAATCTCGGTAAGCTGGGATATTCCTAAAGCGTTTACCGCCCTTCCCGCTCAAATTCGGCGATTGCGGGGGGATATTCCCAAGCACCGCGCTCT  
TTTTCGAGCTGCGGCCCGCGATGCGCTCTGAACCGCGCGCGCGCACGATTTGGTTTCGCGGTAGTACGTCGCTTTTCTCTCCGATTTCGCGCTTCGCGATTTCGCAAAACCGCG  
ACCGCGTCCCGGTGTGGTTT

## SEQ ID 6392

LRFNAPFKSRVWDIPKAFYPPSRNSAHCGDIPQAPPFLRLPPMPSETRRRRTDWFAGSTSLPPHSAPSRISQNRAPACRCWF

## SEQ ID 6393

ATGCGTGAACCTGTCTTATTTGCAACCATGCCGACTTCAAAACCAACACCGGACCGCGGTGCGCGGTTTTCGAAATGCGCGAAGCGCGGAATCGCGAGGAAAAAGCGAGCTACTACC  
CGCGAACCAATCCGTGCGCGCGCGCGCTTTCAGACGCGATCGGGGCGCGCAGTCGCAAAAGGACGCGGTGCTTGGGAATATCCCCCGCAATGCGCGCAATTTGAGCGGGAAGC  
GGTAAACCGCTTGGGAATATCCAGCTTACCGGAGATT

## SEQ ID 6394

MRETCFYCNHADFNTWTGTVPVRGFAKCAKARNAREKATYYPRTNPCAAGAFQTASGAAVAKRTAVLGBYPFRNAPNLSKAGKTLMEYPSLPEI

## SEQ ID 6395

ATGAAAGTCTGTGTTTAGGTGCGGTGTTCGCGCGGTATCTCCGTGTGATATCTGCGAGAGCGCGGACATGAAGTAACGGTCATCGACCGCACCGAGGGTGTGGCGATGGAACCAAGT  
TTGCGAATGACAGGCGAGCTTCTTACGGCTATACACGCTTGGGCTGCAACCGGTATTTCGACCAAAAGCACTGAAACGCGTGTATAAAGCCATCCGCTTTACTGTTCGCCCTGACCG  
CGGCTGTATCAATCGAATGGCTGTGGCGGATGCTGCAAACTGCAACGCAACCGCTATCAATCAATAAGAGCGCATGGTCAGGATTTCCGAATACAGCGGTGAAATGTTCGCCCT  
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CGGTTTGAACAGATGCGGTGTGTGCGCGCTGCGCTGCTTCAAGAGCATGTGTGCGCGAGTTGGATCTCAATCTGCCATTTATCCCGTCAAGGCTATTCTTGACCTGCGCGTCA  
CAATTTCCGACGCGCACCGGTTGCACTGTTTAGTGAAGCTACAAAGTCGCGCATCAGCGGTTTGAACAACAGAAATCCGCGTCCGCGGAATGCGCGGAATTTGCGGCTACGAAACAA  
ACTGCCCGAAAACCGCGCGCAACCTTGCGCTTGTGCTGCAACGACTTGTTCGCGAAGCGCGGATTTGAGCCAAAGCATTTGCTTGGAGCGCGCTCAGGCGGATGACCGCGACAGTACG  
CGGTTAATCGCGCGCACCGCTTTGAAACCTGTTCTGAATACCGGCGCAGCTACTTTGGGCTGAGCAATGTCGCGGGTTCGCAAAATGACCGCGGATATGTCGAGCGGCAAGACA  
CGAAATCCGCGAGCGAGATTGAGCTGTGCGCTATCAAAACTG

## SEQ ID 6396

MKVLVLGAGVAGVSSVWYLAEAGHEVTVIDRTEGVAMETSFANAGQLSYGYTPWAAPGIPTKALKRLFKSHPLLFRPDGGLYQIEWLWRMLQNTATRYQINKERMVRISEYSREMPFR  
FEAQTDNMFEGRRKGTQLFRQTEVEEAQDIADVLERVGVPPYRLKPEBCAEFEPALARVTAIVGGHLPLADATGDCRLFTENLYKLQEKGVRFYPNQTIIRIDHNGLRKAVETETG  
RFETDAVVCALGCPSTVLAQLDLALPIYPVKYSLTLPVINSDGAPVSTVLDESXKVAITFRDNRIRVGGMAELSGYETKLPKRRETLALVVNDLFPEDGDLSQLSWSGLRPMTPDST  
PLIGTRFENLPLANTGHTLGTWSPGSAKLADIVSGKDTFIRSDLSLSRQKL

## SEQ ID 6397

GTGCGGAACAGCGCGCGCGCGCAAAACAAATGCCGTCTGAAACCGGAAAGGCTTCAGACGCAATTTTATCGCGCTTTCGATTACGGCG

## SEQ ID 6398

VPEQPAPPNPKRLKPEKASDGIFIAVCIAQ

## SEQ ID 6399

ATGAACCGAATCGAGGAAACGGAAGCCGTCCAATCACTGGCCAGCGTAGGGCGGAACAGAACATTTTGGCGGCATCTTGATTGAACCGACGCGGATTCGCGGTGCGCAATCTTGACCC  
CTGAAAAGTTTACCAGCGCGCAACACAGGATTATTTTCCGCGCTGCTGGATATGGCGCGGCAACAGAGCTATCGACATCATCAAGCAGCAAGCTGGAAGCGCGCGCGAGGC  
GGAAACCGCGGTGCGCTTGCTTACTGTAGACCTGAACCAAAACACCCCAAGCGGAGAAATATCAGCCGCTACGTTGGGATTGTGAACGACAGGTTTGTGAGCGCGGCTTGTGAAG  
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AGACATTCGCGCAGACCGTTGAGGATTGATTGCGCGTTTGGACAAAAGGCTTGACGCGCGTGCCTTCGATTGCTTACCGGCTTGTGAAGCTTGAAGGATGACCGCGGTTCGCGGA  
TGGAACCTGATTGTGATTGCGCGCGCTCCGTCTATGGTAAACCGTTTTCGCGGAAACATTCGCGGATTCGCGCTGAAGCAGGCGAAGCGAGTTTCATTTCCAAAGCTACGAAATGAGC  
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AAGAGTGGAAAGTTTGAAGTGAACCTGCGACCTGCTCAAGCTTGACGAGCTTTGCTTTTGGCTAAGGAGAAAAAATCACTACCGGCTTGAATTTGTTGCTGCTGATCACTTCATCAT  
GCCAAGGCGAGGAGGACGAGTGGCGGAGTTGGGGAATATATCGCGCGTTTGAACAACTTGGCGGCGAGAGTGAATACCCCGCTGCTTGGTTGCCAGTTGAACAGGGGAAACACA

AAGCAGCAGACAAACGCCGGAACATGGCAGACATTCGGGCGAGGGGCGGATTGAGCAAGACGCAAAATCATCATATGCCGACCCGGAAGCTACTACGACGGAACGAGAATCCGA  
GCATTGCCGAGCTGATTATCGCCAAGAACCGGACGGCGAATGGGAACGGTGGTTTCGGCGTGGAAAGGGCAATTTATGAAGTTCGAGGAAGAGCCGTGATTTGGCATGGCAAGCCGCCAA  
ACATGATGAATATGACCCCTTACAGTGTC

**SEQ ID 6400**

MNRTEFEAVQSLASVGAENQLLGGILIEPTALARCAILTPEKPYQAHRIIFRALDMAAANEPIDITLNDKLEARGEAEENAGGLAYLIDLNQTPSAKNI SRYVGI VDRFVERGLLK  
ASAAIEKIAVSDGGTVAEKL SKADELAAVGDVAVKRETKTFGTTFVEDLIGGLDKRLDGVRFPLTGLMKLDGMTGGLPDGNLIVIAARPSMGRFVLAENLARFALKQKAVHFOSTYEMS  
AVELARRGMAAECNIPMQLKTGNLTQSDYANMPTIYVQAKENKFDVNCDDLNVDELCLAKEKLLTGLDLLVVDHLHIMPRAGRDEVAELGNTSRRLKNLAELNTPVVLVAQLNRGNT  
KQADKRFNMADIRGSGAIBQDANI IIMPHRESYDGNENPSIAELILAKNRDGEKTVVCGWKQPMKFEZEPDLAWQAPKHEIDYDPYSV

**SEQ ID 6401**

ATGCAATATCAACAGCCCCGAACCTTCAAATCAACATTCGGGGGGTGGGAACCAACAGCCCCGAAATGCAATATCAACAGCCCCGAACCTTCAAACCAACATTCGGGGAGTGGGGAATCA  
ACAGCCCCGAAATGCAATATCAACAGCCCCGAACCTTCAAATCAACATTCGGGGGAG

**SEQ ID 6402**

MQYQQPRTSKSTFGGAGTNSPEMQYQQPRTSKPTFGWGINSPENQYQQPRTSKSTFGE

**SEQ ID 6403**

TTGATGATGAAGCCGCTGAAAGTTTGAGAGCGGCGAGGCAATCGCGTATTACCGAAATTTGGCAAGCCCTTTGGCGGTGTAATTCGGGCAATATTATTTCGGCATTTCTTCTACT  
GGAACGATAAGACGCAGTATGAATCAGGCATTTACGGAACAGCGGAAGAAATGAAATGAAACCGGGCTGTCGCTTCAGGAACAAAGAACCGCACGGGCAAGCTGAGGGGAACCGCGCT  
ATTGATTGAGACTGAAAAACGAATTGAACACCGCATTTACTACAACTGAATTTAGACGCTTTTGTATGATTGATGTTGCAACATTCGGGGGGTGGGAACCAACAGCCCCGAAATGCAAT  
ATCAACAGCCCCGAACTTCAAATCAACATTCGGGGGGTGGGAACCAACAGCCCCGAAATGCAATATCAACAGCCCCGAACTTCAAACCAACATTCGGGGAGTGGGGAATCAACAGCCC  
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AAACCGCGAAACCGCAAGGCGGTTCAGCGCTGACCGCTTGTTCGCTGACCGGAAACGTCGGGGCGGAAACCGCGGAACCGACTTCGCGCAAGCGCGAAAGCGACAGTAAACCGG  
AACCGCGGCTTTTCGGGAAACCGAAATGCGAATGTTCCGCGCGCGCAAAACCCACGCGCTACCGCTTCAGGAATTCGCGGATTTGTACAACGAAGTTTGGGCGCGCGGTTCGCA  
CGCTCAAGTGCTGAACGACACGCGCAACCGCGGATTCGAACCCGCTGCTGCGAGATGCTGGGAACCGCGCGCGCAACCGCAAGGTGAGGTTTCGGGACAAGGAACCGGTTCGCGCTG  
GTTTCGCGGTTTCTTCGGAAGTGCGGATGAACCCGCTTTCGATGCGCGAAACCAACAGGGTTTCGCGTTCGCTTCGATTCGATTTTCAAGCGCGGCAATTCGCTCAAAATCCTTGAA  
TGGCATCCGCTTAAACGAACCGCGGCAAGGGGAAGGGCA

**SEQ ID 6404**

LMMKPSSESLRAAGRPJAYYPLAKPLGGVNAALFPHFPYWNDRQYVESGIYRTABEIEITGLSVQEQRTARAKLRERGVLIETEKRIEHRIYKINLDAFDLMLQHSGGGEPTAPKCN  
INSPLELQHSGGGEPTAPKCNINSPLELQHSGGGESTAPKCNINSPLELQHSGGSESTAVIRTEDELTEDLAVYTPPLPNAENGKGLNADAFVSADBTGREGTGEPTSPKESDSMG  
NGGLSGPKINANVPRRRKTHGVPLQBIADLYNEVLGRLPSVQVLNDRKRALANRWEZLGTAAAPNGKVRPGDKETGLAWFAGPFRKVMNPFWHGENQTGFVGFDMILKAGNPFVKILE  
WHPPKTNQAARGRA

**SEQ ID 6405**

ATGAGCCGGGAACAAAGAAATACGCGAGCCCGCTTCGCGGTGCGCGCTCATATGCAAGCGGAAGCGCGGGCAAGGCACGGGAAGCGTTCGACGCGCGGTTCGAAGAGTGAAGGGGTTC  
ATGATGAAGCCGTC

**SEQ ID 6406**

MSREQRIRGARLPVPAHMQABGAGKAREALDGRVEEVKGVDDDEAV

**SEQ ID 6407**

GTGACGAGCTTCGCGCAGGATAACCGACTTGAAGGCGAGGGCTTCGTGTTTGCCAAAGCCGAAATACAAGTTCGGTAACTGTAAAAATCCCGTTCGCCATTACTCAATCGCAAGTCAG  
GAATTGAACCA

**SEQ ID 6408**

VTQLAARITDLEGRGFVFAKPKYKVGNCNPNVAHYSIAKSGIEP

**SEQ ID 6409**

TTGTTGCAITTCGCTTGTGTTTTGATTCATAATCGCTTTCGCGGTTCCTGAAACGCTTCCTGCAATTCAGGGGGATTACCGCGCGGTTCGCGGTTCCTTTATCGCGCGCGCTG  
TCCGGCGGTTCAGCGCTTTCGGAATTCGCGTCAACCGGTTCACACACCGGGTTCCACACACCGCGCGAG

**SEQ ID 6410**

LPALRLFLIENRLSPLPELPCNSGGLPAPCGFFFI GRPSVRAVSRLSDLPSRYNRVSTQRPTE

**SEQ ID 6411**

ATGCCGTCGCACTTATCTTCATCTCGCCAAAGAGCTTATCCGAGCGGTTCATCCGCTTAAGCGCGAGTACGGCCAAAGGACAAGCGGAGAAATTCGCGGTATTATCCGGAACACTTC  
GTCAAAACCCGAAAGATCGGAGCCAAATACCGATGACGAATATTTAATCGGGCTGCTTTCCAAG

**SEQ ID 6412**

NPSDLSPILAKELIRSGSIRLSGTAKGAGELAVFIRTRQKPEESEPNTDDEYLIGLLSK

**SEQ ID 6413**

ATGAAGAGCAGGACAGAAACCGCTGTCGAAGAAAGACAGACCGCTGATTAAGAGCGGATGCTGAAGCCCGCCCAAGGCTGCGATGAGGTTTACAAATCGCGCGGTTTGAAG  
ACGGCTTTGAATTACTTTGAAAGCAGCCGAT

**SEQ ID 6414**

MKKQDRNLSKKDRRLIKKAMLAARAGCDEVYKIAPGLKDFELLGKQPD

**SEQ ID 6415**

TTGCTAGATTCCCGCTGCGCGGGAATGACGAATGGCGGTGTAAGAGTAACTCGAAATTCAAAAAGCCATACCGCCCGGACTTTTGCCCGATCGGTATGACTTTTGGATTCAAACCGCT  
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CGCATCTCGGCACTTCGTTCAATTTGATGATGTCGCGCGAATTCGGTTCGCGACAGCGCGCGGACTTCGCGGGTTTGAGCGCGTGGACCGCTTCTCAAAGCGGGAAACCATPACGCC  
GTGCGCAAAACGAGCCAAAGTCCCGCCATTCGCGCGCTTGGGAATATCGCGGTGCGCAAACTTCGGAATTCGCGCGCTTCGCGCGCTTGGCGCGCTGGTCTGAGATTTCGCGGATGGTACTT  
TCCGCGCGGACGCGCGGCTTTTGTCTGCGCTTAAATCAGGATGTTGTTGGCGCGGTATTCGCGCAACCGTTCGCGCTTCGCGCGGATGATGCTTGTGTTTTCGCGCTCTCTCGAGGAAG  
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**SEQ ID 6416**

LLDSRLRGNDENRCKNSKFKKAIPLGLLFDYDFWIQTALADVDIRAGMVAQVQDGLSGFLLEDVLPFHGLADTFLRRAGIAHFVQFDDVPAELGDRRADLSGFERVDGPFKGNHYA  
VGKPAQVAIARACVLGISACQTCIRAVARLVDFADGTFRADGGVFAVGPNQDVLGAVLAQRCAFOQGDALFLRLLEGINFSAHAAVLHHCLLADFFGNDVVGKLAALGAEVPEGG  
ILCDGIDFRFTCLNVAFAFRLYNQGLVDKLHQHLSGQLGFTTLRVPGCGGFGNGFGKPAVGDFVVGNDGNAV

## SEQ ID 6417

ATGGACGAACCAAGAGATTAGTGTGTTTTGAAAGAAAAATGAGCAGCGCGCTATCGCGAAAGAGGTGGCTGCTCGAAAGAGTTTATTAATAAAATCGGTAACGGCAGCGAAAA  
ACCCGCGTTATCAATTTGTTGATTCTTTAAGGAGTTTATACAGAAAGAAATCAAAACCAACCCAAA

## SEQ ID 6418

MDPRDLVLFLEKEMSSAAIAKEVGCSEKFEINKIGNGERKNPRVQIVDSLRLSYRENQNPQK

## SEQ ID 6419

TTGGCAAACTGGCAGAGTAAGTCAATCAACATCGCAGCGTTGGAATCGGTAGGAATAAAAGGCTACCAATATCGCGAACTTGCCAAAATTTAGATGTATCGGCTTTTGGCTTG  
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TGTTCCTGCTCCCTACCTCAAGAGAGCTGCTTCAAGGCGGGGCGGGCGGTATGAATCCCGACACACGGCTACCGCTGCGCTTGGCAATCAACGTTAAGGCGCAAGGCGATC  
AACCCCGACACGCTTCTGCTGACCCGTGACCGCGACAGCATGGAGGAAAAATCGCAGAGACGCGCAATCGCGTAGATACGGCGGAAACCGCCATACCGGACGGCAAAATATACG  
CCTTTGCCCAAGACGGCATGTCCGCGTCAATACCTGATACGGCAGCCCGCAACGCGTGTGATACGAGCCACACAGCGGCTTCTATCCCGACGAAACCGCCCTTTGGACAGCT  
GACCGTTATCGGACGGCTTTTGGTGGAGCGTGTGGAT

## SEQ ID 6420

LAKLAESVQSSTIAALESGRNKAATNIAKLILDVSAFWLETGEGSRTPALINPDLPEHVKDHRPMWSSNDPLFDDYVFPYLLKESCFKGGAGAYEIPDYNVRLFPFKSTLRRKGI  
NPDNVFCCTLTGDSMEKLAEDAAIAVDGTETAIRDKIYAFADGMPFVKYLIRQPGNSVLIRSHNSGFYDETAFLDSLTVIGRVFWNSVLD

## SEQ ID 6421

ATGCTGAACCGCTACGAGTGGCAGATTCTTCCTTTCCCTTTTGAAGAAGAGGACGGGAGCAAAATCTCCAATCTCAAACTTCAAAACTCTGTATTACGCAAGGCTACGCCCTTG  
CCATATCTAACCGCCCTGTTTGGCGAAAATATCGAACCTGGCAGCAGCGTCCGATGTCCTTCATTTACCGCACCTACAAAAATACGGCGCAGCCATTCGCTGCGGCCATAT  
CGAACCGGACAAATATGCGGACGAAGAGTTGTTGCTTCAACCGTGTCCGTAAGAGCAGGGCTGTACACCGCTTGGGCAATTACGCAATAAACCCATCAGGAAGCGCGTGGATACAG  
ACCCGCGAGGGCGAAGTCATAGGATTGCGCTGATGGGGAATATTTCGCCCATCGCTGCGCAGACGAGATTACAATTCAATCTTGAAAACTCAAAACAGCGCTTGAAGACAGCTTG  
TCAGCGTCCCGATTTCACAGCGCGCGACGCTTGAATAATGTTGGAGCAG

## SEQ ID 6422

MLNAYDVADFLLSPFEEDEQIENLKLKLYYAQYALAILNRPLFAENTIEHQHGFVVPVCIYRTYKKGSGFLPAAHIEPKYADEELVVLNRVRKEQGCYTAALNRKTHQEPWIO  
TRQGEVIGIALMGYFRHALPQTDYFNLEKLKTAVEDSFVSVPHPFGADDEKLEQ

## SEQ ID 6423

ATGCAGGTGCTGCTGGCGAAGACTTCAAAAGAGCGTTGAAAACCTACCCCAAGAGACCGCAGAAAAATTCGGAATTTATCGCACAGTCCAACAGAACGGCTTATCAGGGTTACCGG  
GCAGGAACAAATCCAGCGCAACGTTACCGGCAGACGATCTCAATGGCTGGAAAAAGTCCGATTTCGCCAACGGCACAACTTTGGCACTATCACATCGGCAATTCCTCAATACAGCGCG  
CAGGTATGGCGATTGACATCCGCTATATCTTCACTATACCTTTGCGCAGCGCTTATCAAAATCATCGGTTTTCAGACACACCCGCTTTTATCTGCCGATATTCCTCAAA

## SEQ ID 6424

MQVLLGEDFKRLKNYPKEDRRKIAEFIAHVQNGLSGLPGRNKSNDVPPADPQWLEKVRFAQRHNLWHYHIGIPKYNNGRYGDLTSAYILHYTLCDGFIKIIGFDRHPPFLLPDIKX

## SEQ ID 6425

ATGTTAGACAAATATCCCCCGCGAAATCGAATCAAAACATATCAAACTGGGAAAGCCAAAGGCTATTTCGCGCCGATATGGATTGACCAAAACGCTTTTCCATCCAATCGCGC  
CGCCCAACGTAACCGCGACCGCTGCACATGGGTGATGCTTCAACCAAAACCATCATGGACGGCTGACCCGCTACTACCGCATGAAAGGCTGCAACACCGCTGGATTCCCGGTACCGACCA  
CGCGGGCATCGCCACGCAATCGTGGTGCAGCGCTCAGCTTCCCGCGCAAAACGTTGCCGTCAGCACTTGGGCGCGAAAAATTTCTGGAAAAAGTGTGGAGTGGAAGAAGTTTCCGCG  
GGCAGATTACCCAGCAGATGCGCGCGCTGGGCTGCTCCGCCGACTGGACGCGAGTATTTCACGATGGACGGCTACCGCGGAAACCGTACCGCAAGTGTCTGCGCGCTGTATGAAC  
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## SEQ ID 6426

MLDKYSPABIESKHYNWESQGYFRPMDLTKPSFSIQLPPNVGTGLHMGHAFNQTINDGLTRYRMKGCNTAWIPGTHAGIATQIVVERQLAQNVSRLDGRKFLKRVWKEVSG  
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ELILPLTGRITPVIADIEYVEKDFGTGCVKITPAHDFNDYEVGRHDTRLINVFDLEAKVLANAEEVFNPKGEAQPGFSLPEKYAGLDRFAARKQMVADLQEQFLVEIKPHTLMTFKGDRTG  
SVIEPMLTSQNFVMSATPNGEPDNEFKGLSLADKAKKAVDSGAVRFIPENWNTYTNQWMMNIQDWCSRLQWNGHQIPAWYDEAGNVYVARNQAEAEKQAGKTGLTREDVDLDTWFS  
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SMGADALRFTMASYASLSGPF

## SEQ ID 6427

ATGGACAATCTGAATCCGAGGAAATTTCCGTGTTGCCGGAATCTGCCGCTGTATGCTCGGACCGGCAACAGCAGTGAACGGGCATCCGAGGTTGTTTTACTTTTGGCGAAG  
GAGAATCGGCGAGCGTTGCCGTGCCGTAATGCGGCAACCGCTACCGCCTTGACGGCAAGATGCGCATCATTAACGCG

## SEQ ID 6428

MDNLAPQEI SVLPENLPLYCSGPDNEQWNGHPRVFLPLGEGESGVACPYCGTRYRLDGKMPHHYTA

## SEQ ID 6429

TTGCTGCTTGGCGGAGGACGCGATTGATGCGCCCTGCTGCTGCTTTTACGCTTGGCCAAATCCAAACGCGCGCGCTACCGAAGAATCGTCCCTGAAGAAGCGCTGACCTG  
ACGACCGCGGACGACGCGCATAAAAATCACTTTGCCGAAGTCGAACTCCGCAACCGCCGACCGCTCCGAAAAACGATGTAACGACACACTTGCTTAGGTGGGGAATCGAAGA  
AGAGTTATCGGCAAAACAAACGTTGATGTCGAAACCGGATACGCTTCAACCCGATCGACTTGGATTTCGACAGCTTGGCAGCGCGCGCAAAACGCAATTTTGTCCGCGCACTTACGCG  
GATGAAGAAACCAAAACGCGCGGATGCCGAT

## SEQ ID 6430

LLLAGGGTALIALLLLLLRLAQSKRRRTESVPEEPDLDDAADDGIKITFAEVETPATPEPAKPNVDNLTALGGSESEELSAKQTFDVEITTPSNRIDLPDSLAAQNGILSGALTQ  
DEETQKRADAD

**SEQ ID 6432**

**SEQ ID 6433**

**SEQ ID 6434**

**SEQ ID 6435**

**SEQ ID 6436**

**SEQ ID 6437**

**SEQ ID 6438**

**SEQ ID 6439**

SEQ ID 6440

**SEQ ID 6441**

**SEQ ID 6442**

**SEQ ID 6443**

SEQ ID 6444

**SEQ ID 6445**

**SEQ ID 6446**

**SEQ ID 6447**

SEQ ID 6448

**SEQ ID 6449**

ATGATGAAAAATCAAAGCCCTGATGATTGCCGCCGCGATTGCTGGCAGCAGCCGATGTCACGCGCCGACCGCAAAGGCAAAAACCGCGCCCGCCAAAGCGGTCAAAGCTGCCGCCACGCGGC  
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ACATCATCAAAATGAACGAAGTGGCGGATGCCGCGACGCGGAGGAACGATATCCGCAATTTCCGTGGCGGCAATACATCTTTCCAAACAAAAGCCGGACAGGCAACCGTCAACCTGTTGCCGCA  
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**SEQ ID 6450**

MMKIKALMTAAALLAAADVHAAPQAKTAFAKAVKAAATAQKEAAPAQOQGTRFSDGLAVVAIDNEVTNRRLEAEVAEKATLPEDAQISEZLSRQVIMQVNVQSLIVQAGKRRNIQAS  
EAEIDAVVAQNPAIKNLSPTRRELADNTLAEKVRQAAVMQNSVSEAEIDAFLEAQKQGITLPEGAPLQRYAQHTLTKADSKNAAVGABSTIRKTYDQARNGTDFAGLARRYQDASA  
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**SEQ ID 6451**

ATGAGCTTCCATCCCGAAACCGCTTATAACGGCGCGGAGAAACAGAGCCGTACGGACCAAGCCCCGAAGAAATCAAAATACCGGCAAAGCCCGGAAACCGCGGATGACCG  
AAAAACAGGCAGAGGCCACATTAAAGCATTATCAGA

**SEQ ID 6452**

MSFHPETAYNGGGETEPYGPSPERIKYRQSPETAETRMTEKQABGHKSIIR

**SEQ ID 6453**

ATGCCCTTCGCGCGGCGGCTTATCTGATAAATGCTTTTAAATGTGGGCTTCTGCGCTGTTTTTCGGTCATCCGCCGAGTTTTCGGCGGTTTCCGGGCTTTCGCGGTAATTGATTTCCTGGGGGCTT  
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**SEQ ID 6454**

MPCAAALSDNAFNVAFCLEFGHPFCFGGFRALPVDFFGANSVRLCFSAAVISGFGMEAKSLPSGTSASPCTERQPASSSAFRCRSSQISALNSATCAG

**SEQ ID 6455**

TTGCTTTCGTCTTTCACACTTAAATCAATGACATTTTCGGTCTCCTGTTAAAGGTCGTTTCGTCTATCGGTCTCGCGCTGTTTATGCCCTTGC GCGCGCGCGGTATC

**SEQ ID 6456**

LLSSFTLKINDIFGLLLKVVSSIGLALFYALRGGVI

SEQ ID 6457

TTGATTTTAAAGTGTGAAGACGAAAGCAATTTTCAAACCATGCCCGCAGGCAGCCATCAGCCACCTGCATCCGCATCATCGATTGGGTACGCAGCTCGTCGAGTACCAAAACGAACAAA  
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SEQ ID 6458

LILSVKDESNFKPCPAGSHATCIRIIDLGTQLVEYQNBQRQHKILVQWEIDPEGDPEMLMPDGRPYLISRRYTASLHKSQLATDLKSWRGEDFTPEERDNFDLRLNLGKPCLLSIAHQ  
ESSDGKTTYANISAI SNKMSYTPKHPDNVAFDLSDPDNANYGLLNEKLRBQIAKSPEYAEAVNGROPPAPPQKQAQAEAGRPEHPQGNAAPAEDIEDDIPFN

**SEQ ID 6459**

TTGCAACTGCTTCGGACGGCAACAGAGAAAGGAAACAAAAAATGCGAAACATCGACCTGACCCAAATGGGACGGGAAAAACATTGGCGCCGCCCAATCCGGAACAGGGATACATCAACA  
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SEQ ID 6460

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SEQ ID 6461

ATGACCGCCCTCACACTCTACCGGTGCGCGGCAGAGCTACAGCGGGGGCTGGATTACTACTTTGACAGCGAAACGAGCGCGAAGACACGCTGGAAGCGGTTATCGGGCAGTTTCGAGGTC  
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AGACTACTTGGCGCGCAATATGACGGCGGGCGGCATTACCGAAATCAAAGCGGATGACGGCACATTTTAAAGGCTCGTTCGCGAAATCCGAAGCCGTCGTGATCTTAGACGAGCACAAATC  
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TTAGA

SEQ ID 6462

MTALTLYRCAADVQAGLDYDFDSETEREDTLEAVIGQPEVKAQSVIAYIKNQETETKMLEGHIROMTGKLLAAKARNQSLKDYLRARNQAAGITEIKADDGTFKAFPRKSEAVVILDEAQI  
PAEFMREAVKTEPDKTAIRKAIESGROVAGAKTEGKNLQIR

SEQ ID 6463

ATGAGCTATTTCGGAAGATGTA AAAAACGCATTAAGGGTAATAGATAACTTATGCAAAAGACGCTAA AAAGACGCTGAATCGTTAGAGGGTTTATATAGACGA AANTTAGGGATAAAAGCAGAG  
AAGCGGATACCTCTTTGGAATTCTTAAAGGATGTAATAAATTATGGTATTAGCGATT TAAAAAATGTAATTGAGGTGTTTGAAGATTGCGTT

SEQ ID 6464

MSYLEEDVQNALRVIDNLCKEALKEPESLEGYIDETRDKADEADTSLEFLKDVINYGISDLKNVIEVFEDCV

SEQ ID 6465

TTGATGAACACCGAAACCAGACTGCGGCTACGGCGCAACCGCTGCCGAACCGCGCGGCATTCTCTCCCGATATGTGGATCATAGGTCGCTGAATCAGACCATCGAGCAGGTTACGC  
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SEQ ID 6466

LNMFENQDCGYGATAAEFRGHSPFDMWIIIGRLNQITQEVQTQAYETTRFDLAAETLYSFVWNDYCDWYLELAKVLQQTGCASRQRATRTHTLLFVLEAALRLHPIIPFITEELMQTVAPMCD  
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KLOKALDKLNKLSKPGYTEKAPAHLEVKDKADLAELEDKMAKVOMOLAKLRD

SEQ ID 6467

GTGATTTTCCTTTTCGCTGGTTTGGCGTGCGCCCATTTTACGCCATCGGCAGGCTAAAGGATATTTTTCGGCGCAAAGCCGCAATCCGCTATAATCCCCACTTTTTCAGACGGCATACCATGACT  
GGCGTACCCCTTCC

SEQ ID 6468

LIFLCVVGVRPEYATGRIKDI EGAKPOSALIPTFOTAYHDCAYPS



**SEQ ID 6469**

TGGGCTCGTTTATTTTCACCTCAAACCCACTGTGCTGGCAATTGGGCTTCTGTTTCGGCAGCGCATTTGCGCCGCGGATACCGTTGCGCGGGAAGAGGCGGACGGGCGTGTGCGAGAAGCGGTTGCGAGGGCGGTTCGGAATCCGCACAAGCTTCCGATTTCAGCCCTCGGTTTCGACCTGCTGTTTTCAGTAACGAAAGCGGACGCCCGGAGAGAACCAGAGCCGCGGTCCAAGGCAGCGCGGAGCATCCGTCGCCGAAGACTATACGCGCATTTGCGGACAGGATGGAAGGACAGTTCGAAGGTTAAGGTGCGCGCGGAAGGAAGCGTTATCATCTGAACGGGACGGCGCAGTCTCTAATACCGATTGGGCGGATTACGACCACTGCGGCGACACCGGTTACCGTAGGCGACCGGTTTCGCCCTCCAACAGGACGGTAGCGTGATTTCGGGGCGAAACCCCTGACCTTACAATCTCGATCAGCAGACCGGGAAGCGCAGACGTCGCTGATCGCAACGAACAGGCGCGCGCTCGCAAGCGCTCAGCCGCAACCGCGAAATGTTGGGGCAGAGGGCGGTTACAACCTGACGGAAGAACCAATTCAACACTGTGCTCCGCGCGAGGCTGCGGCTGGTATGTCGAAGCGGCGCTCTGTCGGAAGCGGATCGGGGAAAGGCACTAGGCGCTTGCACCAACGCGCGCTTCTGTTGTCGGCGGATTTCCCTTTGCTCTATACGCCCTTGGGCGGACTTCGCCGTTCGACGGCAACCGCAAAAGCGGACTGCTGCTCCCGTCCGTTATGCGCGTTCGAGCGGGCTTCCCTTTCCGTCGCCCTATTTTCTCAACCTTTCGCCCTACTTCGATGCCACTTTTCGCCCCCGGCAATTATCGCGGAACCGGGCGGACGTTTGCAGGACAATTCGGTTACCTCGGTCCCGATTACAGCGGACAGACCGACCTGACCTGGTTGCCCGACGATAAGAAAAGCGGCAGGAACAACCGCTATCAGGCAAAATGCGAGCAACGGGACGACATTTCGACACGCTTCAGCGGGGTGTCGATTTCAACCAAGCTCCGACAGCGGCTACTACCGGACTTTTACGGCGGCGAAGAACTCGCCGCAACGCTCAACCTCAACCGCGCGCTATGGCTGGATTATGTCGGCGAGGGCGCGCGGAGGCAAGCTGAATGCCCGCTTTTCGGTTTCAGAAATACCAAGTCGCTGGCAACCAAGCGGACTACAAGACGACCTTACGCCATCATGCCCCGCTTTCTTCGCGGATTTCGCGATAAAAACGAGGCGAGGCGCAAACTCGCGGTGTCGCGCACAATTTACCCGCTTCAGCAGAGCGCGCGCAAGACGAGCAAGCTGCTGTGTTATCCCGGTTATCAATGGGATTTCGCAACAGCGCTGGGCTACGCTCGCCCAAACTCGGCTGCAAGCCACTTATTACAGCTCGACAGTTTCGGCGGCAAGGATCCCGCAGCGTCGGGCGGCTTTGCGCGTGTGTCAATATGACGCGGCGCAACACTTTCGAACCGCAATCGCGCTGTTTCGGGCGGAGTGCTGCAAACTATCGAGCCGCGCTGTCTCACTAATATTCCTGCCAAATCTCAAAAGCACTGCGCCAAATTCGATTCTGTCGGAAGCAGCTTCGGCTACGGGCGCACTTTTCGCGGAAACCTCTATTACGCGAACGACCGCATCAACGCGCGCAACAGGCTTTCCACGCGCGTGCAGAGCGGTATTTTGGAGCGCGCAGCGGGGAGGAGCGTTTCGCGCGCGGTATCGTGCAGAAATCTATTTCAGGATGATGCGGTGATGCTTGACGGCAGCGTCGCGCAAAATCCGCGCAGCGCTCCGACTGGGTGGCAATTCGCTTCGGGCGGATAGCGGGCGTTTTCACCTTCGACAGCAGCATCCACTACAACCAAGGCGACAAACCGCGCAACCTATACGCGCTCGGCGCAGGCTACCGCGCCCGCCCGCGAAAGTGTGAACGCCCGCTACAATACGGGCGCAACGAAAAAATCTACCTTCGAGCGCGGACGGCTCTATTTCAGCAGAACTGACCTCTGACCTTCGCCACAATTCGCCACAATCGCGCGCAACCTCTGCTGCCGCTGCTCCGCTACCAACTTCTGAAAGCGAAAAACCGATAGAAATGCTTCGGGTGCAGAATAACAAGACGCTGCGGCTGCTGGGCGCGGCGGTGTACGCGCAACCTGCTTACGCGGGAACCACTTACAACAAACGCGGTCTTTTTCCTCACTTCAGTTGAAGACCTCAGCAGCTTCGCGAGAAACCCCGCAGGCAGGATGGATGTGCGCGTTCCCGCTACAFTCCCGCCACTCTCTTTCCGCGGACGCAACAAACGGGCC

SEQ ID 6470

LARLFLSLKPLVLALGFCFGTHCAADTVAAEADGRVABGGAQGASEAQASDLTLGSTCLFPCSNESGSPERTEAAVQGSGEASVPEDYTRIVADRMEGQSKVKVRAEGSVI IERDGAVLNT  
DWAADYDQSGSDTVTVGDRPALQDQDGLIRGETLTYNLDQQTGEAHNVRMETEQCGRRLOSVSRTAEMLGEGRYKLTETQFNTCISAGDAHWYVKAASVEADRGKIGVAKHAAFPVGGVPLFY  
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FYGGEKILAGNVNLRNRVWLDYGGRAAGGSLNAGLSVQKYQTLANQSGYKDEPYAIMPRLSADWHKNAGRAQIGVSAQPTFRPSHDGRQDGSRLVYVPGIKNDPFSNSEGVSVPKLGILHATYS  
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DDAPVGLDSGKVNKR.SRSDVWFAASGIGGRTFLDSSHYNDKNRAEYHAGVDPAGPKVLNARYKYGRNEKILYLQADGSYFYDKLSQLDLSAQWPLTRNLASVVRYNYNGFEAKFKIE  
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**SEQ ID 6471**

TTGACGGCGCGTTCCTGCCCGGTGATTCCCTTCCGCCGCGCGTTTGGCGGCAAGCATCTGTTTTCGCGTCGGTTTTGTGTCTACTGTTTGCATTTTGTTTTCTCGATTTTTTGATGCCGTTCTCTCAATGCCCAATCATAAAGCTGTAATCTCTCAGAGGTGCGCGCAATTTAAAT

**SEQ ID 6472**

LTARSCRVDSFAARLAASICFAVG FVATVCILFSRFFDAVLSMPNHKAVSLTRSPNLN

**SEQ ID 6473**

ATGTGTCCTGGCGCAAAAGGTATCGGAAGACGAAGCCCTGACGTGCGGCATCATGATGCGGCTGTCCCTGCAGGATATGCGCTATGCTGCAATCAGGAATTAATCAACTTCGCGCAACATA  
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TGACAAATTTAAGCCCGAATCAGCGCCCACTGCTGCTGCGTCTGTCGTAATCTCTTCGCGCGGTACGAAGAAATTTCTGAAAGACGCGCTGCACGGCTGATAGCCGAAGTATCGGCATAC  
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CCCCGACGTAATGCGACGCTGCGCGCCGGCATGATAAAATGCTTTGTTGGGACAAGCGCGCGCTGTTGTCGGGCGGTAAAGACGATCGGAAGAGCTCATCCGGCATTTGGGACAACGGC  
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**SEQ ID 6474**

MLSGAKVSEDEALTCGIMRLSLQDMRYACNQELINFAEHIVKQVQRGLGYNCTDDPANGESVLFPACREASQAVAQWTKDFDNLSFNQRQLVLRPLSNLPAAYEEFLKDAPARLIAEVSAY  
 SLAVKVAKKAMAFLELDGGLISAVGKVVNGADSRAEARRLKMPYAEFTGRILLHAANLNYDVGIGQADKELSAMYGKPLNPNVRPRRISDVRPMMKMLVADKGKGLVRAVKDSDEVIRKHCNG  
 AGFSCFNWTETPKRTANLISLHREAAA

SEQ ID 6475

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CTACGCGCAATACATACGCGGCGCGGAATGCGCCATTGTGCAACAAACCGCTGCCGCTTCAAAGCGCCCTCGAAACGGCGCGGTGGAAAACACTAGCTCCGCGCATCAAGAATCCGAG  
CGGTACCGGATCGCGAAGCGCGCGGAAGCGGAAAAACAGGCGCG

**SEQ ID 6476**

MHTHRTCVYHDSGKFGSNTASGISGTAAGAAEQAFFSAAKTANRASAASANAPHPDPKPKNGRKPMTPQGHNNRKKAGGYAEYITGGELRLLLQQTACRFKAALETAANKHYVRAIKES  
 PVPDAEARRRKKQAA

SEQ ID 6477

ATGGTAGCGAATACCTAGACCCGAGCAATGCGCAGATATTTTATCGTAAAAAAGCGTACATTTTATAGAGCGGTACGCAACCCGCTCCGGATTTCGCCGCCGAATATCGTATCGAAGA  
AACGTTTTTGGTGGAAAAAGAAGAAGTCGAAGGATGGCTAGACCCGCAAAAAAGAAAAACGCCCGATGATG

**SEQ ID 6478**

MDSEYLDPOCCADILSVKKRTFLERYAPRDPFPARISVSKKRFWNKKEEVEGALDROKEKRPMM

SEQ ID 6479

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**SEQ ID 6480**

MPGGRIADPTAAKHKPKQLLRPKPCAIGQNLNLYNHPYADVAKLVDAFDLGSQAERCESSLSVTRTKIFTSFIMLYATWCKCGANHIIGRPSFWRSSHPTSSFFHQKRFDDTDIRAGKSGRG  
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## SEQ ID 6481

TTGGGTATGCTGCTGCTTTGATTAAAGGATTTTCTGCTGACTCAGGGTTTGAAGCTGCCGCTTGACAGAGTTCCGGCGCGTATCTGACGGCGCAGACGGTAAATGGATATGGGGATGCTT  
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CTTCCGGCGCGCAAAATTCCCATTCCTGTCACGGAGAGCGCGGCTGATTTGGCGCTGGTTTATGTTGAATTTGAATGCGCAGAGTGTGCGGATACCGCGCGCGAGCGGGAATGGGTGGC  
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## SEQ ID 6482

LGMPAALIKDFLLTQGLKPLDEVRAAYLTATQVMDMNASIDRSVLWCNDEGWLADYLPCCDVREDALKRLFNALDSVFSRSTGVRSAAYVYALMPSENAALRLVCLSQQEGLENINWQ  
DGNITDVSLSACRSAQSGWMNVASDVRRMLNLGELSGERNHASAAQISIPVCTESGGVLGVVHVEFBCACADTAAQAENVALALALEPLKQLLIGITAABGDENV

## SEQ ID 6483

TTGAGTGAAATAAACGAGCCAAAATGCCCTCAAGTCGGTTTACCGGTTAGAAATAGTGTATTATGTAACCCGAAATGCCCGGATACGTGTATGCAACGGCAACCGAAC

## SEQ ID 6484

LSENRKRIAPQVGLFVRIVFIVTRNARILLCNKPN

## SEQ ID 6485

GTGTTCTGCAAGCAGGGCGAGGCTTGTTCGGCGGCTCTGATGATGCGCGCTCCCATCTTCAAGCTCGGGAACTGTTTGGCAGGGATTCGATGCTGCGCTCCGCTCCGCGGAGGGTT  
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AGCCGAGGCGATAGCTGTACGAAGCCGCTTCTTCCGACTTGGCTGTGAGGTAGCAGAATGCGGTGACGCTGTGCTGCTGCTGCGACAGGCAGGAGAGGGATTCGTCCCGGTTTGGCG  
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## SEQ ID 6486

VFCQSQVLFGGTVVCAVPPFKVGEFAQGFVDCASVGERFDGFAVLVVEGFGVQDFRHFDFPAAQAVGKVAENVFAVAGGDKLYEAFDFDLAVEVAECQORVLVVGQAGEGFAVLG  
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## SEQ ID 6487

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## SEQ ID 6488

MMSEILLDHVASCRLLPTWGVFTMHGFEEANGQEHVALTVGNCSDGNFVLTRIHSECLTGDAFLSRKCDGQLEAAMRAVQAEGRIIVYLRQEGRGIGLINKIRAYHLQEQMDTVEAN  
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## SEQ ID 6489

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## SEQ ID 6490

LKLLIALSSYGNLPPERRRRMPVPCNFALFRHQPQLVCFGLEITLVFQIPDVQGNAPDHVNFPIFQGLDFFGVVGQDFRADAQIFVDRLRQTEIAGIDGQPECQIGFNGIHTLFLQMI  
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## SEQ ID 6491

TTGATATTATGATTTTCTCTATCATCTGCTCCCTATTTACAATGTGGAATAACCTTCGCTGCTGCGTGGATTCCGTGCTTCCGAAAAATTTTCCGATTATGAAATGATTTTGGTCCATG  
ACGGTTCCCGCGAGCGCTGCGGGAAGATTTCGACGAATATGACGCAATATCCGCATATAAGGGTAATCCCATGCGTAACGCGG

## SEQ ID 6492

LIFMIPSIIPIYVNEKYLRCCVSVLAENFADYEMILLVDGSPDGGCKIDCEYAGKYPHIRIVPCVTP

## SEQ ID 6493

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## SEQ ID 6494

LIYPIILRRYANDYPIMRIFACIFVANLPAAVRRTVIDQNHFIIGKIPKGHIHAAKVFFHTVNRDDRENHXYQYVVLRLVCLKPALAMRLHPHPAT

## SEQ ID 6495

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## SEQ ID 6496

LDSKILFFDASAMVGKTEHSAPFDNDKGLDQFSDRLKSLGYQNLHICMEATGSYYEEVADYPAQYYSVYVNNPLKISKYAESRFKRTKTDQDAXLLAQYCRSAKESLVRQKPTDQY  
RLSRMTAAYAQIKSECAAMKRNHHAADDEAAKAYAQIIKAMNEQLEVLKEIKETEPNCKEKGVRLETIPAGRMATAVLPFHLTSSKFETSNKPAAPAGLSPQKESGTSVRGKGL  
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## SEQ ID 6497

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**SEQ ID 6499**

**SEQ ID 6500**

**SEQ ID 6501**

**SEQ ID 6502**

**SEQ ID 6503**

SEQ ID 6504

**SEQ ID 6505**

**SEQ ID 6506**

SEQ ID 6507

SEQ ID 6508

**SEQ ID 6509**

SEQ ID 6510

SEQ ID 6511

**SEQ ID 6512**

SEQ ID 6513

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**SEQ ID 6514**

MTNEACRFILAAATRGSDGIALFPHYQLLRCTPPPCVPCPAIRHNPQTTPRCGFOTAPLPAQVALFIGNIKKEQMKGSFVQTLAAGSDSGGAGIQADLKTQMRGVFGTCVITAV  
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**SEQ ID 6515**

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**SEQ ID 6516**

HKQKTVQCTILGFAAASMAHQAAGAAANSCTIRKTDKYLVLAKQEQENNYTLNGSTEVKPLNLSLIIAANGGTNNITIKGLADGPADAPPTIDNNSIERNINKNYTYAWQNSGAVMLV  
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**SEQ ID 6517**

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**SEQ ID 6518**

MKIHTCKLKKEVQKEPLRSFVPEVTARSAADILGIHPDAAALFYRKIRTVNHRLLAALDEVFERPAGPGGSCFGRRRGRRRGRGAAGKAVVFGIPKRNGRAYTVAADNAEPETLPFAVKK  
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**SEQ ID 6519**

ATGAACGCTTTATTTCTCGCGGTCTTTTATCCGCAACACCGCGCGGCTTCTCCGATTGTCGGTACATGGCATTGCATCGGCACTGATGAAACATTCACAGTGATACAAAAGTCAAAAT  
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AAGCCAAATCAAGTACGCTGAAGTTTACGACAGCAGCAGCGCGGAAACGCTGGCGTGGTTAGAAAGTCGAGGATGACGAGCTTTCGAAAGCATGATGATACCGGATTTGGTCCGCGAG  
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**SEQ ID 6520**

MKRFLPVLISATTFAPASPIVGTWHICIGTDENHSITKVYKLDGSGFRDAILKIDDDGNI LAYRVVAGKWRPANNALTSQIKYGEVSRQHSPEFLANLEKSEARLLESMMYTLGLVAQ  
MDPKGKDDVYQLDKSGKLVSSEDGTSREACTKVE

**SEQ ID 6521**

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CAAGGCAAAACGACGGGAGGGAATATCTGAACTGGTCAAAACAGGGCAATCAAGAGCAATAAAGCATCAATAAAGCATCATACAAATTAATGTCCTCGCTACGCAACAGGCA  
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TATTA

**SEQ ID 6522**

MSNGARWTVTNDMLKELDLSEDAQVEFSDNNKPVKVSVKLGDDGVPMYGDIVKGESDKLITRKSGBTHII EYMDDAKAKTTGREYKLVENKGNQEDNKASNKASYKLNVRCTEQG  
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**SEQ ID 6523**

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ACTTCCCGAGCCTGATGGGCGGTTCGGCTTTCCGCGCGGCGTGGACGTTTGGACGCGCGGAGGCTGAACATCTACGCGAAGCTGATGTACAAACGCGAGTTTATCGGCACGATCCGCCA  
CAGGTTCAACGCTCTCGCTGGAGGAATTAACACCGGGCGGCTGGTTGGAATACGCTTGGCGTGGTGGCGCGCAATGCCGAAACGGACGCGAGCTTTATTT

**SEQ ID 6524**

LVANARYKSGYLTNYAGKRVESEARLNAVMSAEAGRRMEKQDGGKNSVAAGSAVLLVYARLRLSAVKRAVCRDQLPQPDGAVRLSGGRGRFRRQASHLRQADVQTRVYRHDPF  
QVQRLCRGGIQTFRGLVIGIRLGRGAPQCRKRTAALF

**SEQ ID 6525**

ATGCTATATGCTTTCCGCGAAGCGGTAGGCGGATGAAAAACAGACGCGCGCAAAACCTATCGGTGGCAGCGGAGGTGCAATTTGCTTACTGTTTACGCGCGGCTACGGCTTTTC  
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AACGACGCGAGCTTTATTTTGGAGGCGAAAGTCTTCGATGACACAGATGCCAGAAATGGCAGGTCAATATGGCGGTGGCAGTATGTC



## SEQ ID 6526

MPICPPKPVGGWKNKTAATYRNQPEVQLSYWFTGYPPLSNGLSABTUNFRSLMGRFGFRAGVDGLDGGRLNLYGKLMYKREFITGIRHRFNGSAVEEFKHRGGWLEYGLGVVRNAG  
NGRQLYPAQRSSMHTMRQNMVNHGVRSMF

## SEQ ID 6527

TTGCCGCTTCCAATGGTCTAGATTCCCGCTGCAACGGGAATGACGATTTGGAAATACCAGAAACCAAAACAACTGAAACCGAACAGCGCGGATTCGCCCTACCGCGGAATGACCGGG  
GGCGGATGCCGTC

## SEQ ID 6528

LPLSNGLSRLHGNDDLEITRNPKTTETBQAGFPLRGNDGGADAV

## SEQ ID 6529

GTGGGCTTCAGCCACCGCTTCAGACGGCATCCGCCCGCCGCTCATCCCGGTAGCGGGAATCCGGCTGTTCGGTTTCAGTTGTTTGGGTTTCGGGTAATTTCCAAATCGTCATTCC  
CGTGCAGCGCGGAATCTAGACCATTTGAAAGCGCAATATTCAAAGGTTAGCTGAAGCTTTAGAGATTCTAGATTCCCGTTTTACGGGAATGACGAAAGGTTGCGGAATCCAAACCAT  
GAGCAACGCAATATCAAGATTATCTGAAAGTTTGAAGTTT

## SEQ ID 6530

VGFSPPLQTAAPSPFPRSGNPAFCSVSVFGRVLSKSSFFCRRESRPLESGNIQRLAEALILDSRFHGNDRLRKPLSNSNIQRLSESLF

## SEQ ID 6531

ATGGGTGCCCGGTGATGAATGGTGGATTGTACCGCAACCGCGCGGAANTGCCGTCTGAAGGCAGATTTTGGCTTCAGACGGCATTCGCCCTTCAAGACTGACCGGGG

## SEQ ID 6532

MGRVRMKHIVPQPAEMPSEGRFCVQTALRPFKTRRG

## SEQ ID 6533

GTGAGGCATGTACGAAAGTGGAGTGAAGCAACTGTATTTTCCACCCCGTGGGCAAAATACCAAACTCAAACTAAGCCGTCCGGAATACCGTTTTCGGCGGTATCGTTTGGCGCAAA  
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CAGGCATGCAATGTACGGAACCGGTTGCCCTGGTGCTTGGCGCGCT

## SEQ ID 6534

VRHVRKSEKQLYFPERRAKIPKLSSRPNTVFGGIVCGKIITHPGIRYRRQFAHTCENGLRL/LVWRINKNQDKAAGRQYQYEWYGTGSPGAWAP

## SEQ ID 6535

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CAAGACTTTGATTATTATTTGAACAAACGGTATGTTCTTTCAGCGGCTTGAATCCCGCAAGTTGACCGTTTGAAGAACGAGTTTGCCTATTATGCGCGTCCGTTCCGCGCGCATCA  
ACGTCGCGCGCATACCGACGACAACATCGATTATCTGTGTGAAGCATCGTGAAGATA

## SEQ ID 6536

LRLFPARVKQRKIGPELSSVPIKEQAMFFKHLEAAPADPILGLGEAFKAETREPKVNLIGVYDKASGATPIVKAVKEAKRLLESSETTKNYLTIDGVADYNBTQILLFGKDHETIASR  
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QGFNGLEEDAYGLRFLKHNTELLIASSYSKNFGMYNERVGAFTLVAEDEETAARHSQIKTIIRTLVSNPASHGANTIALVLKNDLKAQWIAELDEMRGRIKAMRQKPFVELLKARGST  
QDFDPIIBQNGMFSFSLTPEQVDRLEKNEFATYAVRSGRINVAIGTDDNIDVLCESIVKY

## SEQ ID 6537

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CCTTTCAGCGCAAAAGTCTTGCAGCTTACGAATCCCGCAAGTTCAGCGCGCGCGCGCAAAATGCAGGAGCTGACCGAAACCTTCCAAATCGACGGTACGCCACGGTTATCGTCCG  
CGCAAAATATAAGTCGAATTTGCCGATCGGAGTCCGATGTAACCATCGACCTTTTGGCGGCAAAAGTACGTAAGAACAAAAGCGCGGAC

## SEQ ID 6538

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## SEQ ID 6539

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## SEQ ID 6540

VKILLIGNQVGSVAQNLAATNNDVTVIDIDEKALQETGSRLDVQTVFNGASPTFLERAGAEDALLALSRSDETNIIVACKVAADLPNIPGRIARVRSEYLEYLSPKLENNENGSL  
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VASWTKGVILLANGKILLTRDRAADAKRLVMDLKGKELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDFTRQMLKQTGLLGMIGKSERGAATCEADNKAIVYLMVGGAAAYLVAK  
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[illegible]

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[illegible]

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## SEQ ID 6554

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LAQKSVIISDNARFRMGALRGTAERLGHKVLPPAPYSPEFNPTEKVMANKRYLRTVLSYARFDDALLSYDFN

## SEQ ID 6555

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## SEQ ID 6556

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## SEQ ID 6557

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## SEQ ID 6558

MENPYESVKMRHYIKLRFGRGFARLQRLTGSRNKYKQSG

## SEQ ID 6559

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## SEQ ID 6560

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## SEQ ID 6561

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TT

## SEQ ID 6562

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## SEQ ID 6563

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## SEQ ID 6564

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## SEQ ID 6565

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## SEQ ID 6566

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## SEQ ID 6567

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## SEQ ID 6568

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## SEQ ID 6569

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## SEQ ID 6570

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## SEQ ID 6571

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## SEQ ID 6572

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## SEQ ID 6573

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## SEQ ID 6574

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## SEQ ID 6575

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CAGGGATGACGAGCGTTCATAGACCAATCACTTTCACGATACATGAAATTCATGACGAAAGTAAACCGGAAAGGGATTGGTATCAGATACGGAATTCGTGTCCGGTATAGCGAGCTG  
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## SEQ ID 6576

VKAFEDKALAVSADMALADGAAATAVGCPPLRIGGEQNKTPNPKGAERTENQEPQFYFPHVSDGKGRFIEIPLRRGRDDGAFIDQITFTIHENSMKVTGKGLVSDTEFVVRYSEL  
LEEILPGITKLPFGKFFYQSCYQCPDNVEYGVHYGGQCEHMLVELNGTGMALPQWENRLYEFLSKCVRPKITRIDVAHDFPNGEYTPDQANLHDHNGHYDVHMRPKSECRGTA  
WRNEDSGRTFTYIGKRNKSFTRVYEKGRQLGDVDSFWVRFGSDIEIPLDVLVSSYLGGAYPEICKIEFTAKRMEVKVKNVNLIPDVKLFHARNQVGMVNPFLRDIWDSDSRIVDELV  
KGVGYPKGLQPEQYDCKNQTPQFYIHEBQKAINALNIETLFDLLIERECAPPDREW

## SEQ ID 6577

ATGTTTGAACCAAGCCAGTAACCCATATACCGCCACTTTGTTGGGCGCAAAAAATTCAAAGGCGAAATCGACGGTAACAAAATCGATTATGACCGCTCTTGGTAGCCAGCCCCATGC  
CGTCAACCGCAATGCCGTGGGCTTACCTCGGAAGCATGAAGTTTGGTGACAGCCATAATTTTGAATAATGAAAAACCTTAAATTCCTCTGCGGTGATCTAACCGTTGCCATGGA  
ATCAACAGGAAAAGCCTTAGTGAGAAATTTGTTGATTTCGAAGTAAAGGCGCAGCACCTAAAGCC

## SEQ ID 6578

MFETSQVFTYATLIGAKRPFKEIDGNKIDSVLVAAPMPNNGNAVGTSESMPGDSHNFELKLNLFCAVDLTVAMESTGKGLVQKLLDPQVKAAPKA

## SEQ ID 6579

ATGAGCAGATACCAACAGAAATTTATCTGACAGGAATGGAAAAATCAGAAATTCATCTATCCGATTCTGTTGGCGATATTGGATTACCTCGAATCAATACAGCCGGTAAATATGACA  
GCTATGAAGACGCTTTAGCTCGGCATGGAAGAGATAGCGGGGAATTTGTAATTTTCGGATTCTACGAAAAAGAAGAT

## SEQ ID 6580

MSRYQKFTVQLENEHFIYDPSFGDIGFTSNISAGKYDSYEDAFSSALREIGGEFVIFGPFYKED

## SEQ ID 6581

ATGAAATTTATTACACCTGCCGTAATAACGGCCAAAATCGGCTGTTGTAACAGCCGCCCGCTGCGCTTGGCGGCACAGGCAAAACCGAGCTGCCCCGAAACGGCAAAAAACGCTTTGG  
AAGCCGCAAAAGCGGAGGTATGGAAGCCGGTTGGATTGTAGTGGCGCTTTTCGCCCGCTTTTGTATTTTCATCGTTAAGAGGGTGTATGAAG

## SEQ ID 6582

MKFINTCRKYGAKLAVVTAAPLALAAQANAALPETAKNALBAKADGNEAGWIVGVFAALFVFSIVKRVMK

## SEQ ID 6583

ATGCCCGCTTACTTCATACCCCTCTTAACGATGGAATAACAAAAAGCGCGGCAAAACGCCACTACATCCAAACCGGCTTCCATACCGTCCGCTTTTGGCGCTTCCAAAGCGTTTGTG  
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GAAATTTTAAAAAATGTGTTTCGGGCTTTGTGAAGTTTGTAGAGACCGCTCCCGGCGCTCTTAAACTTAATCTCTTTTTCGTAGAATCCGAAAAATACAAATTCGCCGCTATCTC  
TTCCAATGCCGAGCTAAAAGCGCTCTCATAGCTGTATATTTACCGC

## SEQ ID 6584

MPPYFITLTMENKSAAKTPTTIQPASIPSAFAASKAPFAVSGNAAFACAASGAAVTTASFAPIYLRQVLNFMIFSTFKLKKCVGLCEGFRDLPLGLNLIFPVESENYKFPAYL  
PQCRKASVFLAVITG

## SEQ ID 6585

CAGGATAGCGATTCTGAGCACTGCATCCAAACCCCCCCCCGAAACACTCCCAAAACAGCCCGCGCGCCCGGGCGCTTGGCGTTTCCCTGCAAAATCTGCGATACAATGCAGTCTGAA  
CATTTATCCGAATCCAAACCGGATGATACCGCACAAAAACAA

## SEQ ID 6586

QDSDS\*QLHPTPPPEQLPKQRRAPRAFAVSLQNLRYNAV\*TFIRIPNPDQAQEQ

## SEQ ID 6587

GTGCTTCTCAAGACATTTATTTCCGACTTGGCAGTACATGCCGCTTACTTCATCACCTCTTAACGATGGAATAACAAAAAGCGCGGCAAAACGCCACTACAATCCAACCGGCTTCC  
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GGCAGGTGTTAATAAATTCATGATATTTTCCTTTACGAAATTTTAAAAAATGTGTTTTCGGGCTTTG

## SEQ ID 6588

VLLKTFISDLAVHAALLHPLNDGKYKRGNAHNPFGHTVRFVCFQSVFCRFQRCVCLCRQSRGGCYNQFCVPTAGVKNKFDIFLYEIKKMLRAL

## SEQ ID 6589

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GATACGCGCGTAACGCCCACTGCCGGAAGGATAGCGGTTTTCACGCGCCGACAGGTGCAACCCGATTTACGACGCTTCGACGATCCGAGCGCATACCGCTTACCTGCTCGAA  
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TCCGCGCGCGCGGGTGCAGGCAAAATCCCGCTCAAAACCATCTACCGCGCGACCTTACCCAAAGCGCGGACTCGTGGCGCTCGATTTCACCGCAACGCCCTTTTTCACCCACATGGT  
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CTTTACTCGACGCGCTGACTATCCCGGGGATACGGCATCGTCCGCCCCAAATCCCGGAATGGCTT

## SEQ ID 6590

MDTAQKQRWATLSYDGRFYQWQKQAGGVPTVQALETALARIAGESVATTVAGRTDTGVHATAQVVFHPTAAVRPAQAMIRGVNAHLPEGIAVLHARQVAPGFHARPDASGRHYRYLLE  
SAPVRSPLLNKRWGTHLELDIGPMRRRAALLVGEQDFSSPRAAGCAQSPVKTYIRADLTQSGAGLVRLDLHGNALFHHMVRNINALGVYVSGSRLSVEGPAALIQRERSLKAPPTFMPDG  
LYLTGVDPGAYGIVRPQIPEHL

## SEQ ID 6591

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CTTGGCGAAATGCTGCTGCGCTGCGCGGATGTCGCGGAGCTGTCGCGCGGCTGCTGCGCTGCTGCAATGGCGCGACGCGCGGGAATCGGAAAGCGGGGAGCTCTGCATC  
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## SEQ ID 6592

MNMLGALAKVGLFHVSRVLFVVRDVIARAFAAGMATDAFVFAKLEPNLLRRVFAEGAFAQFVPIIAEYKTRSKATEAFIRHVAGMLSPVLIVVTALGILAAFPWVIYVSAPGFTKDA  
DKPQLSISLLRITFPYILLISLSFVGSILNSYHKFIPAPFTPLINISIFVAFVFPYDFPVTALANAVFVGGIILQGLFQPLWAKLGLFLKPLKFNKDAANVRVMKQHPAILGVSV  
AQISLVINTIFAPYLSQSVSWMYADRMELPGVLGAALGTILLPTLSKHSANQDTEGFSALLDWGLRLCHLLTLPAAAGLAVLSFPLVATLFMYREPTLPDAQMTQHALIAYSFGLIG  
LIMIKVLASGFYARQNIKTPVKIAIPTLICTQLMNLAFTGPLKHAGLSLAIGLACINAGLFFLLRKHGIYRPRGWAAFLAKMILLALAVSCGGLWAAQALCFPEWAHAGGNRKAGQIC  
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## SEQ ID 6593

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## SEQ ID 6594

MLNPSKRLVELVRLDEGGFVPSGDPVQATEALRRVDGSTEEKIIRRAEMIDRDLRLDRLERVRAGSFWLVVVAAMFTAGFSGYLLMDNQNLNFTLVLAGVLMNTLHLAVWLATLP  
LRVKVGRFFSSPATWFRGKGPVNAVRLRYADQWRQPSVRWKIGATAHSLNWLCTLLGLMSVLLLLLVRYQTFNWNSTLLSNAASVRAVEMLAWLPSKLGFPVPDARAVIEGRINGNIADA  
RAMSGLLVGSIVCYGLPRLLAWVCKLILKTSENGLDLEKTYQAVIRWQNKITDADTRRETVSAVSPKIVINDAPKWMLETEMQDQGWPEGRLAQEWLDKGVANRBOVALETEL  
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## SEQ ID 6595

TTGATGGTTCGGATCGCTGTAAGAGGTATTCGAAAGGCGTTAATATACAGCGGAACCTTAGCAACGCCATCATGCTGTTTCAGGCGGCAATTTTCTTATAAAACCTTTCAGCAAC  
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## SEQ ID 6596

LMVRNPSERCIRKALISGTLANAIMLFAAFPLIKTFQOYLAKLQTKLLITADLPSKIRSNF

## SEQ ID 6597

ATGCCGATATCTTTTTCGAAACCGCTTTTTCGCGCTTATATCGGGCGGCAATCGCCCGCTCCGACCGGCGGACGGGCTCCGCGATCAACATGCCGTC

## SEQ ID 6598

NPISFFGRFFRAYIRARIARVETGRTGCRITWAV

## SEQ ID 6599

ATGCCATACTCTGCGACTTAAGAAACAAAGCTTTAAACCATAGCGGATTAACAAAAATCAGGACAAGCGCGGACCGCAGGCGATGCAATGGTACGAAACCGGTTTCGCGCGGCTCC  
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TCAAGAAACAGCGTTTACCTGCGGATTCGCTTAAAAAACAAACAGCAGCC

## SEQ ID 6600

MAYSADLRNKAHLNLSGLTKIRTRRRTAGSTNGTEPVRPALHHLRESFPLGRGGATFYRLLIRYITDNAKTPAKPQQLTCTQETRTGCFALKKQAA

## SEQ ID 6601

ATGAAAAATCCCTGATTGCCCTGACTTTGGCAGCCCTTCTGTTGCGCAATGGCGGATGTCACCCCTGACGCGGCCATCAAGCGCGGCTACAAACTTACCCTTCTGTAGAATACATACAG  
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TGCTTCCGTGCGCGCACTAACACCGGCTGGGGCAACAAACATCTTCTGCTGCGTTGAAGGGCGGCTTCGGTACCATCCGCGCGGCTAGCCTGAACAGCCCCCTGAAAAACACCGCGGCC  
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TTTCTTACGCCCGCGCTTCAAAGGCACTGTGTAGTGTGCAAAACACGCAACTACTTATGACCAAGTGGTGTGGTGGCGGAATACGACTTCTCCAAACGCACTTCTGCCTTGGTTTCTGC  
CGGCTGGTGTGCAAGAAGGCAAGCGCAGACAAAATCGTATCGACTGCCAGCGCGTGTCTTCCGCCCAAAATTC

**SEQ ID 6602**

MKSLIAL/LAALFVAAMADVLYGAIKAGVQTYRSEHTDGKSVKVTGSEIADFGSKIGFKQEDLGNGLKAVWQLBQASVAGTNTGNGKQSFVGLKGGFGTIRAGSLMSPLKNTGA  
NVNAWESGKFTGNVLEISGMAQRHRYLSVRYDSPEFAGPSGSVQYAPKINDSGNSESYHVLGNQNSGFFAQYAGLFQRYGEGTKKIEYDGYTISPLFVEKLQVHRLVGGYDNNALYV  
SVAAQQQDAKLYGAMSGNSHNSQTEVAATAAYRFGNVTFRVSYAHGFKGTVDSANHNDYTDQVVGGAIEYDFSKRTSALVSAGWLQEGKADKIVSTASAVVLRHKF

**SEQ ID 6603**

ATGATTTTGACACCGCGCGACACGCCCTTTTCTCCGCAACGGCAATGCCGACACGATTGCCGCCAAATTTCTGCAACACCCCGCACCCGCATACCGCGCGAGATGCTTCCCGACAGCA  
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GCTCGCGGTACGCAATCGGGGTTGGCAGCGCGAGTCTCCATTTCGCGAGCTGCGCGCGGTAGCGGAACACCGCCCGGTGTCTTACCACTTGGGTGATACCGCGCAATCGCTTTGCT  
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CTGCTCAAAACAGTTTGCCTCAACCGCTGCTCTGCTCAATGCCGCAACGACCCCTTCTCGCGCGCGGAGCCCTGCCCGTGCAGACGAAGCGTCCGAAGCGCTTACCTGTTCACCACTG  
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**SEQ ID 6604**

MILFPPDTPFFLRNGNADTIAAKFLQHPAPAYRREMLPDSTGKTKTAYDFSAGGISPDAPLVVLFHGLEGSSRSYAVELMLAVRNRGWHGAVVHFRSCGGVANTAPVFYHLGDTARIAFA  
LDLTARYREIYAVGVSGLGNAPAKYLGEGKKALPHASAAVSAPVDAEAGSRFDSGTRILLYTRYFLRPLI PKARSLQGPQTAFAPAGCKTLGEFDRPTAPLHGFAADRHDYRQTSCKP  
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**SEQ ID 6605**

ATGAGCGAACAACCAATCCGCAACCGAGCGCAGTTGGACGAAAACCAATCATGCCCTTGGCGCGCAAAACTGAACAACATCCGCCCAACAGCGCAACGCTTATCCCAACGATTTC  
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CAAGCGCAGCTTCCGCCACCATTCAGAGCTTACCGGTCAATCCAGCTTTATCTGAACAACAAAGCGGTGAGCGCAAGAGTTTGGAGCACTTCAACCATCGGACTTGGGCGACATCGTC  
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**SEQ ID 6606**

MSEQNHQPTSPQLDENQIIALRREKLNINRQORNAYPNDFKRSFAADLQAQYGEIGKEELDFQAVPVKIAGRMMLKRMKGASFATIQDVITGQIQLYLNKGVSEVLDDFNHNDLGDIV  
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LKRLVVGGLERVFIEINRSPRNEGMSVRHNPETMIEFYRAFSDYERMOMQAEIIRNASRTVNGTANTITNGKEVDLESPPERLITILEAIKKYNPHYDEQLNDAEWLKEIKVKGESLFP  
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**SEQ ID 6607**

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**SEQ ID 6608**

LRMLVFAHRVFRKNKSGAVCFRRPDRTKFAFILRDVGVFPQERAMPSENADGIIQLKMPKVR

**SEQ ID 6609**

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GATAGCTTCCCGCGCTCGTGTGTAATAATATCGTGTGCTCCGCTCAAAACAGAGAGCGCAAGCTCTTCTTCAANTTTCTTAATGGCAATAGACAAAGTGGGCTGGCTGACAAACAA  
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**SEQ ID 6610**

VVDKTYPVKLRHLRRLRRRLRTDKITAIROYDPPAWRRTPKRNNAEQHMLVIGRGRQRHADQCTAGHMDCIDRAALQCIQGLYALFRPQFTA\*EYLIPIHTVAFRQQNLLITQ  
HPGRNGIQLK\*MPFRDNEHKKRFVIQPGNNARLLKRFNGDNRVNPAPERLQSHRVLVFOHQRHFRCTAQDNDQFRQVWRNRKNQPEFERTLQLVLFFIQCMPDLRLFLQYLTRLCN  
DTYFRLGRNNIVAAPVKQRDGLFFQFLNGNRQSLADKTRPRPAEMTFLGCDVDPQFG\*GH

**SEQ ID 6611**

ATGTCCGAACACATATTCGACTTGGAAAAAGCAAGATCAACGCAATGGGACCGGGATTTATGATGGCTTCGCGCGCTGTGCGCGGTTTCGACCTGATGCTCGACGCGCGCGCGCGC  
TTTACCGCTGGCAGCTCGCGCTCATCATCTGACCAACCTCTTCAATAACCGCTTTTTCGCTTCGCGCGCATTACACTCTGGACACGGGCAAGAGTCTGATGGAAGTTATGCGGA  
GAAAGCTGCGTTTATTTGTGGGTTTTTTGATTGTTGTATCGCTCCGCCAGATTAACGGGGCGGGTCCGCAATGTAACCGCGCGCATGCTCAAAATGGCGATTCCCTCGCTGATG  
TTTGATGCGCGCAGGTTGCCGCTTGTATGATGCTGCTGCTGATTTTGTGTAGCGGAGCTTACCGCGCTTGGATCGTGTTCGCAAAATCATCATTTGTTACTTTGAGCATGCGCA  
CGCTTCCCGCGCGCGCATGCTATGTGCGCGGTATGACAGTGCAGCCGATTTTATCGAGCGGACACCGTGGACGCTTGGCGGTTTGGGCTTCTGATGCGCTGATGGCTGGATGCC  
CGCGCGATCGAAATTTCCGCGCATCAATCTTTGTGGTAAACGAAAAACACCGCATCACTCTTCTGAATACCGCGCGGATTTTCGATTTCACGCTCGGTTATATCGCAGTGGCGTT  
TTGCTTTGGTTTCTTCTGCAATGCGCAACCGCGGAGCAGTGCAGATGGCGGGCGCAAAATATATCGGGCAATGATTAATATGATGCGGTAACCACTCGCG  
GCTGGTCTCGCTCGCTGGTGGGTTTTATCGCGTTTGCCTGATGTACGCGGACGAGATTTACCTTGTGGAGCGTTATGCGCGTCCGATTCGCGCAACCGCTGCGCTGCGCGCGGAGGA  
TAAACCGCGCAACCGCGAGTTGTTTGCCTGGAATATTTGGGTGGCGGGCAGCGGTTTGGCGGTGATTTCTGGTTTACGCGCGCAATGGCGGAACGCTCAAAATTTGCGATGATGGCGC



TTTGTGTCGCCCTGTGTTCGCTGGCTCACTACCGCTCGTCAAAGGGGACAAACGCCACAGGCTTACCGCGGTATGAAGCCCTTGCCATTGTGCGGCTGTCTACCTGGCCGGGT  
TRGCCGTTTGTTCCTCGTTGAACCTTACCGGACTTTTGGCA

## SEQ ID 6612

MSEQHSITWKSINALPGIMMASAAGVGSLLIASTQAGALYVQLALIIILTNLFKYPFRPSAHYTLDTGKSLIEGYAEKSCVYLWVFLILCIASAFINAGAVAIVTAIVKMAIPSLM  
FDAGTVAALIMASCLIIIVSGRYRALDRVSKIIIVTLSTATLAAAGIAMSRGMQMPDFIEPTWTLAGLGLFIALNGWMPAPIEISAINSLWVTEKQRIINPSEYRDGIFDFNVGYIASAV  
LALVFLALGAFVQYNGEAVMGAGKYIQLINMYAVTIGGWSRPLVAFIAPACMYGTTITVVDGYARAAEPVRLIAGRDKTGNALFPAWNIWVAGSLAVIWFWDGAMARELLKFAMIAA  
FVSAFVPAWNLVRLVKGDKRRRLTAGNALAIVGLLYLAGFAVLFLNLTLGLLA

## SEQ ID 6613

ATGTTGTTCCGACATAAAGTCTTCCTATTTTAACTGTGTTTCAACACACAGAGCCGATATTCGGACACAGCCCTATCTATTGTCTCAATTTGGCGGGATTGACCCCAACAAACCA  
ANTCTTACCGTCTTCAAAAACAGGATACCGCCCGG

## SEQ ID 6614

MLFGHKVFRIFNCVSTHRAAYSDTALSIAPIWAGLTPNPKSYRLQKQDAR

## SEQ ID 6615

TACCTTTTTCGTTCGCGCAAGTAATGTTCAACTCAAGCACATCCATACCTCTGCTTTCTTGGGAAATACGGATATTGTCTAATGAAACATTCACATATTGGACAGGACTTCCATC  
AACTCTTTACGTAAAGTCGGCAGGTAATCCGAGTCTGACCTTCTTGGGCGCGCTCTTGGGCAATGATGATTGAAGCGGTGCGGGCAACGGTTCGGCTTTCTGCTTTCTACCGAATA  
AAAGTTCGATCAATGACAT

## SEQ ID 6616

YLFPRQSNVQLKHIHTILLFLGNTDIV\*\*NIHIFGQDFHQLFT\*SRQVIRSLTFLGALLGNDLKAIVAGNGCRFLSTE\*KPDQ\*H

## SEQ ID 6617

TTGGCGCGCAACTTCTGTGCTTGGTGGCAAGATTTTATTGAGGATGTCGGTCATGTCGTGTTCCGTATTTGTCCGGGAAAGGGGAATATTAGCATCAAAACCGT

## SEQ ID 6618

LGGNFLCLGGKDFIEDVGHVFRICPGKGGILASNR

## SEQ ID 6619

TTGTCCGTACTGACCGACGAACCCCTATTTCCAAGGTTGCGCCGAATACCTCAACAGCGCGCGAAGCCGTATTGCTGCGCGGTGCGCAAAGACTTCATCATCGACGAATACCGGTT  
ATCAGGCGCGCGCATGGGGGGCGGATGCCGCTCTGCTGATGCGCGCGCACTGGAACAGGGACAAATGGAACGCTTTGAGGCGCTGGCGCACGAATGGGCATGACCGTCTGCTCGAGCT  
GCACGACGAACCGCAATTTGGAAATGCGCAACCTGACCAAGCCGTTGTGGGCGGTAAACACCGCAACCTGCGGACTTTTGAAGTCTCCCTCGAACCAACCTGTGCTGCTGCGCGCG  
CTGGAGGCAAAACCGTCTGTACCGAAAGCGGCATTACAGGCAAGCGGATGTGAATTTATCGGGCGCGCGGCTGCATACCTTCTGATCGCGGAACGTTTATGCGTGGCGACGATA  
TTGGGCGGAAGTGGGCAAACTCTTC

## SEQ ID 6620

LSVLTFDEPYFGSFEYLKQAREAVLLFVLKDFIIDYQVYQARAWGADAVLLIAALEQGQLERFEALAHELGTMVLLLEHDETELEKCRNLTPPLWGVNRRNLRTFEVSLDQTLISLLPA  
LEGKTVVTESGITGKADVEFMARGVHTFLIGETPMRADDIGAEGKLF

## SEQ ID 6621

TCTCCGAACAGACGTTTGAAGAAGCTTTTTTCTCAGCTTCCAAGAAACGCAATTTACGGTTCTCGCCCAAGACGGGCAATAACGCTCTATATGCTCGGAAGCCGTTACGCTGTCC  
TGATGATGACCGGTTCTCCGAATGGATGCTGCAAGACGTTTGGGATTCGGGAATCACACCCAGCAAGGAATACGAGAAATATCGCAAAATATCTGTACAGACAGCATTTCCGCTT  
TGCCACACGTTTGGGGAATAACGCGTAATTAACAGATGTTCTTAACCGAAACCGCTTGTCTCCGCTTACGGGATTTGCTTTGCAAAATATCCCAAAATCTGTGCGGATTCAGCACACT  
GGAAACCTCAGGATTGGTCTGTTACATGCTTCATCAGCAAAATACAACGCCATCAATGACACCTGCTCAATACAGCAGGAGAGTGCAGAAATATATCTCAAAGCCCATTTTCTTGGCG  
GACAGCTCTGCTACACTTTTCTACGCGCTCGCGTGTCAAAGCGCTTTTATCCGAGTCTGGGAAGCGCGCAAAATAAACAGGTTTTCACAAATTTTATCTTTAATCAAAGCGCTGGTTGA  
CGCTCGCCTCACCTCGAATGACATTTGATCAGTCTATAACGACACGCGCTCGCAACCCATAATGAGGTCGAGGTTGCGCAAAACCCATCAAAATCAATTACCGCAGTTTATATCGCG  
TAATGCCAAACCTGTGCAATACTGCACTGCTAGTCTGTTTACCGACACCGCCCTTGCCTGAAGTTACTACAATAATTTTGGCCAC

## SEQ ID 6622

SSEQTFEAPFLSFQETHFTVLAQKTGNVILICLSRYAVLMDRFSIGICLQDVLGFGNHTQQRNTQNIANILYRQHFACHTFGRITRN\*QNFNRTALLRLTGFALQNSQNPVGVTHF  
GNLRIGRYNGFISKIQRHQCTLLNTSRVANNILKAHFLAGQLLHFFYALACQSVFIPSLGSRQNKQVFTPIFQSLVERRLTINDIDQVINDTTLATHNEVEVAQTHIKINRYSPISA  
\*CQTCNCTGSRFTDIALA\*SYNNPCH

## SEQ ID 6623

ATGCTCTCTTTTGAAGTAATACGGAATATAGTCAGGTTTGAGCATGAAGTCTAATAGTGTGTGTTGGCAGGTATTGGATTACGTTACAATACCGCTTTCATCAAAATTTCCCTAC  
CGGCGGTATCTCTTTTGAAGACGGTAGGATTTGGGTTGTTTGGGGTCAATCCGCCCAATTTGGAGCAATAGA

## SEQ ID 6624

MPSFSGNTENIVRFEHEVLIVCVGRYLDYVTIRAFIRISLPGGILFLKTVGPGFVNGQSRPNWSNR

## SEQ ID 6625

CTCTGAGCCAATTGCATGATAACCAATCGGTTATCTGCAACAATATCTGTACCGGCTGCTGTGTCAGATGGTCCGGCAATCTGTTCAAATACCGTAATCCCGCGACAGAAAC  
AACTCCGCTGCATGGAGTGGATAAATATGCGGCGAGAAGTATCACCTTTGGCGCGCGCAAGCAACCGCTCTCATCGGCGCATAAATATGCATATGGCATCTGCAATCAATTCGCGCC  
CCTGGCTGACCGCCCCGTAACAATCAAAATCGCATCTTCGGCATAAACTGCTGACCGGTACGACAGGGGATGTAATCAATCTGTTTCTCTGCTTCTGACCAATCTCCGCTTTCTG  
CACCTCAACCTGACCCAGTCTTTTAACTTTTCCGAATGAGACAGACAAACAGCAATGATCTTCAATAGCCACAGCAGCCCAACGTTTCAATAGAGTCTCAGACCCAAATTTGCATA  
CCATGCTCTGAAAACAAACAAATGCAAGATCCAAAGACTCGGGATAATCAAAATCTTGAACATCCAGAACAAATGGAACACACAGACTTTGAAACTCTTGGCCCAATTTGA  
CCAGCACATCTTCCAAATCAAAACAGTCTGATGATGCAAGATATAGACAATACGTCATCTTGTGCACTTTATATCGAAGGCAITTCATTTATATAAACATCATAGAAATTTTATGA  
TGTAAGTTTACCGCGCAA

## SEQ ID 6626

L\*ANCYDQSVILQYVLYRLLVQWVRIQILFKITVNPDRNQRLHGVDKYAGRSITFGAGQSTPSHRRINMHIAICNQFRPLADRPNNQIAIFGINLLTGTDRGCNQYCFPCFLITLRF  
HLNLTQFPNIFRMQTKQQMILHSHSPTPIRMLQTNLHMP\*\*QRNQCSKIQRLGIILKFNQKNWNTRLLKLLAQDQHIQIQV\*\*CMQRYRYVHLRLTYEGIHYNHHRIP\*\*  
CKPTAQ

## SEQ ID 6627

TTGCAGCAGGCTGGCGATTGATANTATGGTTATGTTTTCAGACGGCATTTTCAGATTTCGCTCCATGCGGCTGGAAGCGCGAAACCTGATTGGAGGATCTGTTATGAATACCGTATCGA  
ATTACCTGTCCGATTCGCGAAGCCATGAAGCGCAAGGCTTGGACGCACTGTCATCCCTCCGCGGACCCCACTTCCGAATACCTGCGCCGAGCATTTGGCAGGCGCGCGCGGAAT  
GTCAGGCTTACCGGCTCGGTCGGCACATTCGTCTTACCGCGATGAAGCGGCGTATGGGTGGACAGCGCTATTGGGAACAAGCGCGCAACAGCTTTTCGGCAGCGGCATTTGAGCTG  
CAAAAAGCGGGCAAGTGGCGCGTACAACGAATGGCTCGCGCAACCTGCGCGCAACAGCTGCGGTCGGCATCCCTTCGGATATGGTGTGCTCACCGGCAACGCACTTTGGCGCAAT  
CGCTCGCGCCAAAACATCCGATCCAAACCCGACGACCTGCTTGACCAAGTGTGGACAAGCGGTCGCGCTATCCGCGCGAAACCGGTTCATCCAGCAACGCGCTACGCTCTCGA  
AACCGCGCGGAGAACTCGCGCGGTGCGCGCAGTTATGGCGAAAAGCGCGGATTACCACTTGGTTTCTGCTGACGACATCGCTTGGCTGACCAACCTCGCGCGCAGCGAGTG  
CCTTCAACCTGTTTTCGTGCTCTCCGCTGATCGGCAAGACAGTGGCGCTGTTTACCGCAACATGCGGCTGAAGCGCGAAGCGCGCGCGCTACAACCGCAGGTATCACGG

TCGAGCCTTACGCCCAAGTTGCCGACAACATCGCGCAAAATCGGCGCGCGCTGCTCATCGAGCCGAACAAAACCGCGTCAGTAGCTCTGTCGCCCTGCCGAAGCGCGCGCTGATTGA  
AGGCATCAACCCGTCACCTTCTTCAAATCCGTCAAATCCGAAGCCGACATCGCCCGCATCCGCGAAGCGATGGAACAAGACGCGCGCGCGTTGTGCGGCTTCTTCGCGAGTTTGAAGAC  
ATCATCGGCAAAAGCGCGCAGCTGACCGAAATGACAGTGGATACGATGCTTTACGGCACCGCAGCGCGCGCCCGGGTTTGTGTCCTTGAATTTGCAACCAATGCAAGGCTTCAACGCCA  
ACGGTGCCCTCGCGCATTACAGCGCAACACCCGAAAGCCACAGCAACATCAGCGGCAACGGTCTGCTGCTCATCGACTCCGCGCGCAATACAAGGCGGCAAGCCGACATCACCCCGGT  
CGTCCCCGTCGGCACGCCACAGCAGAACAAAAACGGCAACAACGCTGCTTCTCAAAGCCCATATCGCGCTTCCGAAGCCGTGTTCCCCGAAACATCCCCTCGCGCTGATTGACGCG  
ATTTCGCCGAACCCCTGTGGCAGGCGCAATGCTACCTACGGACACGGCACCGGCCCGCGCGTAAGCTATTTCTCAAACGTCCACGAAGGCCCGCAGCGCATCGCCTTCGCGCCGCCGCCA  
CGCCCGAAACCGCCATGAAAAAAGGCATGGTTACCTCCATCGAACCCGGCTCTACCGTCCGGGAAATGGGGCATCCGCATTTGAAACCTCGCGCCAAACCAAGCGTTCGCCGACCGCA  
GGAAACCGGATTCGGCAGCTTCTCTGCTTTGAAACCTGACCTCTCGCCCATCGGATACAGCGCTGATGAGCACGCGCTGATGAGCAGCGCGGAAATCGACTGGGATCAACCGCTACAC  
CGGGAAGTCTCGCGCGCGCTCTGCGCGCTTGACCGAAGGCGCGGCAAAAGCGTGGCTGATCAAACGCAACCGCAACCGCTGGCGGCT

**SEQ ID 6628**

LQQAGDLITLWLCFS DGI SDPRCRLKPPN LIGGSVMNTVSNYLSALREAMKAQGLDALVIPSPADPHLSYLPPEHWQARRELSGPTGSVGTFVVTAD EAGVWVDSRYWBDQAARQLSGSGSIEL  
QKSSQVPPYNEWMLAANLPENAAVGI PSIMVSLTGKRTLQAGSLAANKIRI QHPDDLDDQVWTSRPAIPASTVFIHCHAYVSTAEAKELARVRAVMAEKGADYHLVSSLDDIAWLTNLRGSDV  
PFNFVVFVSLIIGKDSAVLFTTEQCRLNARAAAAAQTAGITVEPYAQVADKLAQIGGALLIENPKTAVSTVLRLPESARLIEGINPSTFFKSVKSEAD IARI REAMEQDGAALCGFFAEFED  
IIGKGSILTEIDVDITMLYRHRSARPGVFVLSFDITLAGFNANGALPHYSATPESHSTISGNGLLIDSGAQYKGGTDTITRVVFGVTPAEQKRDNTVLKHAHLAAEAVFPENIPSPILIDA  
ICRKLWQAQCDGHTGAGHGVSYFLNVHEGQRIAPAPATPETAMKKGWMTSIEPLGLYRPGKWGIRIENLAANQA VADPQETEPGFSFLCFETLALCPIDITRLMDTALMTGEDIMWNRXH  
AEVRRRLLEPLTEGGAOKAWLIKRTLEPLAR

**SEQ ID 6629**

ATGACGACCCGACCCACCGCCAGACAGATTTTGCA CGAAGTATTTCGGCTATCCCGAATTTGCGGCGAGCGAGGAGTGTATCAATACCTTTGCGAGCGCGCGCAGTTTGACGCTGCTGA  
TGGCGACGGGCGGGGCAAGCTCTTTGTGTTACAGATTTCGGCGCTGATGCGCGAAGGCGTGCGGTTTGTGATATCGCGCTGATTGCGCTGATGAACGACCAAGTGCCGACGCTGCATGT  
GGCCGGGATTTGAAGCGCGCGCAGTCAACAGCGGCACATCGGCAGTGAAGCGCGCGAGATTGCGCGACAAGCTTGCACAGGCCGCTGTAAGCTGCTTTATGTGCGCGCGGGAACGCTTGST  
ACCGACCGCTTTTACGTTTTCGACCAACAACCCGTGACGCTGTTTCGCCATTGACGAAGCGCACTGCGCTACAGCGGTGGGGACACGATTTCCGCCGCCGAATATCAACAGCTCGGTATG  
TTGCCGGAACGATATCCGAATATCCCGGATCGGCTCGGCTAGGACCGCCAGCGCGCGGCGCGCATCAAGCAATATTCGTCACTTTGAGCAGCGCTCGGAATTTGCTTCCAGCTT  
TGACCGCGCAAGTAATTTATATCAGTTATTGACGAGTATTGACCAAAAACAGCGCAAAAACAAATTTGCTGGATTTTCATCGCGCAAGAAATGACGGGGCAAAAGCGGATTTGTGATTGCGCTACCGCGAAA  
AAGGTTGAAGATTCGCGCGCAGTTTTCGTGAAAAACGGATTAAACGCGATTTCGTATCATGCCGGTTTGAGCATGGACGTGCGCGAGGAAAAACCAACCGCGCTTTACGATGAAGACAATA  
TTATCTGTGTTGGCGACCGTGGCGTTTCGGCATGGGCATAGACAAAACCGACGTGCGCTTTTTCGCCCATCTCGATATGCCCCAGAGTGTGCAACATTTCTATCAGGAATCAGGGCGCGCGG  
CCGGGACGGGCTGCTTCCGTGAGTTGGCTGTGTTACGGCTTGAACGATTGGGTGTTGTCTGCGCGAACGGAATTGCGGAAGGCAACGCGACAGAGTGCAAAAGCAAAATCGCAATGCAAAAA  
CTCGATGCCATGCTTTCCGTCTGCGAAACCGCGCGCTGCGCGCGGCTATGCTGCTCAAAACATTTGCGGGAAGCATCGAAACCTTGGGGACATTTGTGACAACCTGCTGCATCCGCCGCTAC  
GGTTTGACGGCACGGTGTGTTGTGCAAAAATTACTCAGCTCGGCTGTACCGCGCGCGGACAACGCTTTGCCGCCGTTGCACATCACCACCTTTGCGCGCGCAAGCGAGCATTTGGATACGGG  
CAACCGGCACAGGCAACTGTCCACATTCGCGATTCCGCTCGGCTGCGGATTTGTCGCAAAAAGTATGGCGGACGCGCTATCCGCGAGTGCATCTGCTTCCGCTACCTCAACGCTCAACATTTGCCGATG  
CAGCATTTCCAACTGACCGAAGCGCGCCAAAAAAGTCTCAAAGGGTGAACCGCAAGTATGCTGCGCGCGCTCAAGCGCGACAGCCGCCACCGGCACCTCTCAAAGACAACCTGCTGCGGTA  
CCGAACCGGAAGAAGCGCTTGTGGCAGGCATTGCGCGTTTGGCGCATGAACAGCGCTGAAGCCGAAGGCATCCCCGCCTATATGATTTTTCGGCGACAAAACCTTGCAGCACTTTGTGAAAA  
AATGCCGCAAAACCTCAACGGGCTGCACGACATCTACGGCTTTGGGCGAAGCGAAAAACCGAACGTTTCGACACGGCATACTCAAAGCTGCGCAAAACGCTGCCGACTTTAGCCACGATGCC  
GTATCCGCTCCGCAAAACCGAAGCGGAACAACACTGCGTCAAAAACCTCGAAGCCTGGCGGTATGAACAGGCAAGGGCGGAAAAACTGCGCCCTGCATACCGCTCTCTTCGACGAAAGCGCTTG  
CCGATATGCTTGCGCCACGCGCGGAACCGGAAACCGACCTCGCAAGCCGTACACGGCTTGGGACGCTACGCGCGCCCAATACGGACGGGACATCTCTGCGCGTCTGCCCTCCGTTTTCAGA  
CGGCATCGATGAAAACCGCCAAACACAAACGCTGCTGATGCGCGCCCTGAFTCAATGGTGCACGAAACCGCAAAACAGAACAGTCCGAACCCCTACCGCATTTCTCAGCAAGCGCGCGCTG  
CGCGCATTTGCCGCGCAACAGCGCGGAAGGTTTGGCGGAGCTTGCCGCCGTATACGGCGTAGGCGAAGAAAAAGCCGCAAGCTTACGGTGGCGCGGTGTTGGCGGTGTTGGAACGGGATGCGG  
TC

**SEQ ID 6630**

MTHRPTRARQILHEVFGYPEFRGRQEDVINFLAGGGSLVFLMPTGGGKSLCYQIPALMREGVAVVVSPLIALMNDQVASLHVAGITEAAVNSGTSADEARETADKLQAGRIKLLVYAPERLVTDRFLRFLDQQLVSLFAIDBAHCVSRRGHDFRPEYQQLGMALBRYENIPTRIALPATAADATRIDKHLYLHDLADASEPVSFDRTHIYIYQVLEKNKKQQLLDIRKMETQSGSIVYCLSRKVEDAAQVLETRGLNGLAIPIYHAGLSMDVRENQRPTHEDNIIIVATVAFMGMDKDPDVRFAVHMLMPTQSVHEIFYQESGRAGDGLPAVSLYGLNDVLLWRRIEAGMSDEVOKEITQXLDAMLSCVETAAACRRVLLLLKHPEASEPCGHCNCLNHPVRFDTGLVQKLLSCVYRAGRFAAGYITNLLRGKSDDWIRGNRHBQLSTFGIAGELSDKEWRSVIRQCTISLGYLTVNLIARYQALQUTEAAKVLKIGETEVMILRPLRKDKPATRFLKDNWNLTEREERLLWQALRVWRMKQAEAGIIPATYIFGDKTLRLDLVEKMPQNLGLNGLHDYIYGLGEAKTERPFGHGIKLVQCNAAADPSHDAVIRPQTERBQQLRQLLEAWRYEQARAENCLHTVLSDESLRADMLAATPETSTDLEAVHGLGSVRAAKYGRDILAVCRPFSGDIGETAHKHRCRLMRALIQWCNETAKHEQSEBPYRILSKAALRLAAKOEGLAEALVYGVGEKAARVYGAVALVAVLERDAV

**SEQ ID 6631**

TTTCATTATAATTTTAAACATGATAGCCAATACCATATTATCTATCAGATATTGCAAAAAATACGCCACTGCTTTTCGGCAGATGGCGTTATATGACTAAAAATTACTCAGCAGCGGTTT  
GTCAACCAATTCAA

**SEQ ID 6632**

FN\*YFKHDSOYHI IYQILOK\*RELLFGRWRYMTKITOOPVCOPIO

**SEQ ID 6633**

ATGATACAGCAGCGCAACCATGCGGCTGTGGTTCGATCCCTTCGGAACCCFCGCCGCTTGGAAATTCTCGTAGCAACCGACTCATGTCGCGCCAAACCTGGGTAAACGCAACCCCATCCCG  
ACCACGAAGCGCGGTGCGCGGCACTCTGGCGCGGTACATGGAATGCGCGTTTACGCGGAATCGACATCGAAGCGGCCACCCACACCGTAAACGCGGACACAGATTACACCTTCGCGCAA  
CGGTGAGTTACCGTTTGGGCAACACCCGGCCACACAGACCGCCACACCGACTACTTCTCGAAATTCAGACGCGCATACACGTTTCTCGCGGCAACCCCTTTTTTCGCGCGGTGCGGA  
CGCGTGTTTACCGGCACGGTCGAACAGCTTTACGACAACCTTCAACGGTTTCAACCAATTACCCGAAGGCAACCTGTCTTCTTCGCGCACAGTAATACACCGCGGCAACCTGCGTTTTCGCG  
CCCATATCGCGCCGACAGTCGCGCACTTCAGACGCATTTGAAGCGCGGCAACACGCGCAACCTGCGCGTTTTCGCGTTCGCGCACAGGACGCGCGCTGCAACCCGTTCTTACGACAGAAAT  
CCCGCGCTCGCCGCAACGTGCGGAAGCCCTGGTTCGCGCAAAACGCTGAACAGCGGTTTGGAAATTTTCGCGCGCTTCGCGCACTGAAAAACGCTACCGC

**SEQ ID 6634**

MIQHGNHVAVCVPSEPSVPLEFLVRNRLMAQTVWVTHPHPDHEGGAAALWRGYMESPVYGESDIEAATHVTTAGTRFTFGNGVTVWATPGHTDRHTSYLLETSDGLHVFCDTLFSAAGC  
RVFTGTVEOLYONFORPNOLPESTLFYPAHEYTAANLRFAAHI EPNADIOTAKAAEHTPTLPVLAHERRVNPFRTET PAVROARAALVGKTLNSGLEVF AALRELKNAYR

SEQ ID 6635

GTGTGGGATTTACTCTTTGCCCTACACTGTGAATATTCCTTGAAAATGCCGTGTGTTAAATTTGTTTTTTATTTTCAGACGGCAITTTTATGT

## SEQ ID 6636

VNDLLFAYTVNILENACVKICFLPSDGILC

SEQ ID 6637

CTCAGCAGCCGGT<sup>1</sup>TTGTCAACCAATTCAACAGTGCCAGAGGTGCATTTATCACTTTTACGGAATCCGTA<sup>2</sup>TTTCAACACTCGAACAATAACCACCGT<sup>3</sup>TACGAGCAGTAAACGAGGACCCAAA  
TGC<sup>4</sup>CAAAACAGTTT<sup>5</sup>TACTACAACAATCA<sup>6</sup>CGGTTCGGAGTACGGTCAAA<sup>7</sup>TGCCAAACGGCGGCTTGC<sup>8</sup>CAATGACGGCTTTT<sup>9</sup>TACCAATGTAAT<sup>10</sup>CAACGGCTCT<sup>11</sup>TACTACACGGCGCAATTCTCT<sup>12</sup>

TGGCCTTAGGCAGAGTTGTTTACAAATAGTTTCGTGAGTCAATAATGAATTCGCCATATTACGACGATTCGACGACGATGCTGCTGGTACGGTTAATTTGCGATTGCCATTACGATGAG  
CAT

## SEQ ID 6638

LSSRFVNFQNCQRCIIITFTESVPHSNITFTVSSKTRTQIAKQFYINITVASTVKQTAACQ\*RLFTQCNRQLYTTAQFLGLRQSCYNFVSQ\*\*IRHITQHCSTNTAGTV\*FAIATITHT  
H

## SEQ ID 6639

TTGGACTGGCGGGCAACAAACCGCTTGGGGCGCGGAGCTGGCGGATTTGAAACCGCTTTACAAAGACTTTATGTATTGGGAACCGGCTGTCACATGTATAAGGCAAGTCCCGTCTGTC  
CGACGGGATATGTACGGGTGGGAATACCGCGCGCTGTGCGGCGAAGACACGACCGGTATGCCCTTTTGGGGCGACGGCTACGACGTGTACCGTCAGTTGAGATGCGCGGACAGATACC  
CGAAAAACAGAGAAAGGCATTCAAAAAAGCCGCAAAAGCAAAATACCGGTATGTTGCGGACGGGAATACGGCATATCCAAACAGAAATTGAGCGATGTTTGGGATGATTTTGAAGAC  
CGGATGGAAGTGAAGCGTTTCCCTGCTGCTCTGCTGTTTCTGACCAAGTGGCATAAAAATCTATATGAATATCTGGAGGAATATCCGTTTATACCCGATTTGTGCTGGAAGAACGAG  
GTGACACCGTGTGCTGATTTACGAATACGCGCATACCGACCTTCTGTGATATGACCGGCTGGAATCCCTTATTTGAACGAAGGCTTGGACACCGCTGAACTGAAAGGCGAAATCAA  
GGAAACTGCAAGGTCTGTACCGCGGGAAGGCGCGGCTGTGATTTTGAAGTGGGCAAAAGCGTTCCAAAGTGGGGGTTTGGAAACCTGACCGGCTCAACGTTCATGGGCAATGGCC  
GATTTGATATGCAAAACCTGTGCGGAACGTATCCCAAGCTCAAAACCATACGGCTGTGGGGCAAAACCGGCAATATCGCAATTTTCCGCGATATCGGATTTGAGGATTTGGAAGTGT  
TCACTGCCGTAGATTTGTTGGTTCGGCGCGGACGACATCCCTCATCCGACCGGCTGCCGAAGTGCACAGGCTGTGGATGAGCAGCGCTGCCGAGAGGCGCGGAGGCAAGTGAAGAA  
ACTTTAAGAAACGGAAGAGAGCGGCTGGAACCGTGGATAGAAAGCCGAAACCGGAATGGTGGCGCAAAATTTGCAACACCGCTTCCGCGATTTGGGACGCGCGGAGCATATC  
CCGAAAGCCATGCCAAAAAGCGCGGAGCTGTACCGGAAACCGGCTGCCGCGGTGTCAAACGCTCTGGCAATCCGCTGAAACATAGGGGAGGGGCTGGCAGAGGCGGTCAAGCGCT  
ATACCGGAGGTTTCAACAAATGGACAAAAACCTTTATCGACACGGTAGAGCGGGAAGATATGCCGAGCGGTTGGAACAGATATTGGACCTGATACCGGATGGGTCTGTGCGGACAA  
GGAAACTGTTTGAATAATTTGATAAAAAACGGAATTTT

## SEQ ID 6640

LDWRGNKPLGAELADLKPLKYDFMYWERGLHMYKASAVVPTGYVVGNTAPLCEGDTQRYASFWGDDYDVYRQLRWQRQIPEKQKAPKKAASKNTVMFAGREYGISKQNLSDVDDDFED  
AMELKAPCLSSFLTKWHLNLYELEYFPITRLCLNHGQTVLDFSNTRITDLSVDMTGVSLSYLNELGLSLNLKGBLEKNCVCTAGKAGLILEVGKSVPKVRGLENLFAVNVGIA  
DFDMQNLSETPYKLTITRLWGPKNIANP/SAVSGFEDLEVFTAVDLFGFGADDI/PHPRDL/PKHLRLMNSLPEREAAKAVKLYKKRKEDGLDPWIEKARKPEHLQNLNPNFRDWDGAET  
PKSHAKAELRYKTRAGVVKLLGNPPENIGELAEAVKAYTGGFNKDKKPH/IDTVEREDJAELEFILDOLI/PDGSADKEKLEI/FPDKNRNF

## SEQ ID 6641

AGGCTTTTCCAGCCTACAGGTGGCCATGCTTCCAACTTAGAACCCAGTGTCAAACTTTAGATGCCAATACTTCTTAATCTCATTTCAAAGATTACGTCCTCAAAATTCGGCGTTTGAAG  
AGCTCGGTTTCAGTGGCTTGAATCAAAATGCCAATATAATAATATCTCAGCTTTCAACAATTAGCTGAACGTACTGTCAATTCAGATCATCCCGGATGCAAGAACAGGCTCGA  
TAGGAGGTGATTTTCTTCAACTCTCTCACAGGATACCTGCAAAATCAGCAAAATAGACATCTGTATCAATCAAAATACGTGCCGCACTCGGTACAGCTTCTCTCAGGATCAATAGAAC  
GTGCGTTTCGATATCCAAACCAACTTATCAAGATCCGTCCGCTGCTCTACAGTGCAGGTTCAACCTCAAAGCTAACACGGCTGATGGCGAAAGCTCGCATCAACTGGATTCACCA  
ATCTGACGGTCTCATCACGAATACCTGACGACCTGAAACAGATTGATAACACGACCTTGTCTACTTTAATTTCCATTTCAATTTGACCGTTATCAGCCAAATGACAAATGACATGAC  
CAGGATTCAGAAATTTCTACATCATGCGGCACTCAATATCACCGGAGATACGACACCTGAACCTGATTTCTTCAACACAAGTGAACCTGGCTACGACCATGGAGTTTAAACACAATATACC  
TTTAATATTACGCAAAATGTCAACACATCTTCTGAACACCAACCAAGTAGAATATCTGTCGCAATACACCGCAATAGCTACTTTCAGTAGGAGCAAAACCATTCATGGATGACAGTAAG  
ATACGGCGCAAGCATTACCTAAGGTATGACCGAAACCACTTCAATGGCTGCATAGATACTTTTGACAGAGTTGCAGAAAAAGTATTATCATCAATTTGACGAGGTTTCAAAATTCGG  
TTGTGCTATTCTGCAT

## SEQ ID 6642

RLFOAYRWPCFQRLTQCQTFRCQYFLNLIQRPTSQIRRFKLGFSALNQIANIINILSFQITIS\*TYCQFI IHRMOKNRVDR\*FPFNLLHRSTLQISKNRHLINQNTCTAYSFRLINRT  
VGFDIQNLIKIRPLLYTCTFPNLKANPADGRKARTQLDCTNLVFLITNYLIT\*NRLLITPTLLYFNHFNLTIVISQMTNDMTRI QNFIYIMRQIATITGRYDT\*\*FLQHKLNLTATMEFKHNT  
FNIQQNWNINPLATNNSRLFVQYTGNSYFSRSKTIHG\*Q\*DTAQSI\*GMEFTTFKWLHRYFCTSCRKSIYINLITRQKFGCAILH

## SEQ ID 6643

TTGGCGCAAGCAGACACCGATCCGTTTGGCGCAATGCACAAAAACCAATGCCGCTTGAAACGCCAAACAGGCTTCAGACGGCATCGGTAGCGGATGAAACAGCAAAATCCGCATATC  
GTCAATTCCTCGCAAAACAGCTCTTTCACAGCCCTCCGCTCCCGCCATCTTACCTCGAAATCCCGCTATTCGCGCAAGTGGGAATCTAGGAATGAAAGCAGCAGGAATTTATCGGAA  
TAACCGAAACCGGAGCTGGATCCCGCTCCGCGGAATGACCGGAAAGTGGGCTGTGGCGGAGTTGGTGGA

## SEQ ID 6644

LPQADTPFCGKCTKNPMPSETPNRLQASVADENSKAYRHSCENSSQPSGRNLYEIPSPFRKWESRNEKQDEFGHNRNRTDWI/PACAGTRKSLHAGLVE

## SEQ ID 6645

TTTAGATAGAACTCTACCAACAGCTGTTCATTAATATCACCGGTCAATTCAGAGCGATCCGGCATGTTTTTGAACACACCTCAAGTTTATCTGCATCTACAGAAACCAACCCGCGCAAG  
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TTACACCTATGACCTTATGAGAAACAAAGTGTCTTGTCTGAGTCCGGATGAGAACCCCAATACGATTAACAGACATTTATCCAAACAGAGATTCCAGCACTGCAACAGCAACTGCCAGT  
AGAACCTTTACGGCGATCAGCTTCTGCGAAATAACGACGGAAGTACGCTTCAATACGCCATAAATACGGCGGATTTTTTGTGTTTTTACGCAACTGCAAAACATAGTCTGACAAACGCGGT  
TTTTTTGACCAATGCTGACCGGAGCGGAATCAATTTTACATTTAGAAATCCAAAGACGGCGGCACTTCAAAACAAATCCGTACCTTCGCGAGCTGCCAACTTACATTTAGGCGCAA  
TATAACGTGCCAT

## SEQ ID 6646

FRVELYHQLFINITGQFRAIRHVFEHTLKFCIYRNPTQADLSCQTCPLNTYLPFGFFTN\*DNITSFHLERRNIDNLSIYNLSLHNRKLSCFSSGRTEHTPTINDIIQTRFQQLQQLAS  
RTFTALSFCEITTELFF\*YAINADFLFFTLQITIV\*QTRFPCTHLT/SGSINFTFRIQRAARTLQKQIRTFATCQLTFRANITCH

## SEQ ID 6647

TTGGAAACGGCTTCAGACGTTCATTCACATCATCTTTCGGAACCAACACGACCGTCTCCCGCTCGGCGACGACAGTTTTCAGCGGCTGTCCGTACACCGTTTCAGCGTAATG  
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ACAGCGCGCAACCGCTTCGCGATGCTCAAAACGCGGCTGTGCGGCTTTTCATCAACACGCGCTGCTTCTTCAAATCCGATGCGATCTCGCCATACGCGCGGTGTAAT  
CGCGCTTTTCGCGCAACACGAGCATCGGGAACATCTATCTTGTCCAAATGCGCGCATCCGCGCTTTCCGCGCGTCCAAAGCTTCTGTGAAGCT

## SEQ ID 6648

LEFASDVICTSLRKKTHHVLPLRQHQFFHGVSVHRFQRNAQTAFPPKYRPGTETRGVVFVVRHPRPNAQRVHIRPKRFLFVVQHLRRIQNVIVKAVFGEHIAQVHVHGHAAAFNAV  
FPQTGFPQRGTAPEAGEKQFPVRLQARFPVQHQKDLFRQQSEVRPOHIGTRFQRHGRGLAVLHHAAPARQFLPETALARGCGSRQKIRTVIFVFFKYRQRIALRQAAADVRIRTGKQD  
MPGRVADECCALVGMFGKMAVNLPAFVLRHVKPPSTKSRHSAANASAWLKNGACAAPSTITSLLPFKCRCRYSPITRSGVIASLPWTSSGTSTLSNKRASALSASKASCA

SEQ ID 6649

AATACGACGTTTTTTAGGCGGACGGCAACCGTTATGAGGCAACGGGGTAACGTGAGTAATGCTGGTAATCTTGAAACCAAGAGCATTCAAAGCACGTACAGAGGATTCGGACCTGGACCT  
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CGCCAGAGGTAGCCCAAGACAACGCAATTCCTTGACGGTCAGTGATTGTAATGATGGTATGTTGAAAGATGCATGAACGTGCACAATACCTCACTCAGGTTTTACGTACTTTTTTACG  
TACACGTGAAGCTGTGTTTGGCTTTAGCCAT

SEQ ID 6650

NTFFRRRTATVMRQGNVSNAGNLETKSIQSTYRGFATWTFWTFNL\*IFNAILGNFTSCFCCNLCCKNCTFTRFTKTSAAAGSPRQRIALTVDNDGIVERCMNVHNTLTHGFTYFTT  
YT\*SCVCFSH

SEQ ID 6651

ATGTCCGTGCGCCGTTCCCGTCCGTCAATCCCGCACAGGCGGAATCCGGATTGTCCGACAGGAACTTATATTTCTGTCATCCCAATCCCGCCACAGCCCACTTTCCGGCTCAT  
CCCGCGCAGCGCGGAATCCAGTCCGTTCGGTTTCCGTTATTTCCGATAAATCTCTGCTCTTTCAATCTTAGATTCACACTTTCCGCGGAA

SEQ ID 6652

MSVRRSRPSFPHRRSEGFVRTETFISSFHQSRRPQPTTPRHSRAGGNPVRSVLSIDKFLLLFIPRPLSRE

SEQ ID 6653

GTGGCGGGATTGGTGAATGACGAAATATAAGTTTCCGTGCGGACAAATCCGGATTCCCGCTGTGCGGGAATGACGAGCGGGAACGGCGCACGGACATTCGCGGAATTTTTATGTCT  
CCATTCCTCATACTCTTTTATGCGCTATTCAGAAATAGGTTGTGCGAGCTGTTTACTTTTCAGACGACCTGAAATCAACGGTTGTAATCAATCTGTTTTTCAAAACCGCTGCA  
ACCGCAAATCTGCTCAACCTGCCCTCCCGCTGGGGGAGGGCGGGGAGGCGGCAATCTCCAAGTTGCGGCAACCTTTCCCAACAACCTTAACCGCCCAATACAGCCTTGCCTGCT  
GTGCGCTCTCTCAGCCCTCTCCACGGGGAGAGGAGCAGGGAGGCTGTGGGGT

SEQ ID 6654

VGGIGMNTKYKFCQGIIRIPACAGMTDGNAGTAFIYVSLILFLMRYSKKIGCAGCFYFSDDLKSTVVPNICFSNRLQPPNLLQPAFSPVGEGRGGILQVAATFPNNLTAPIQALRL  
VALSPALSHGERGRCGCG

SEQ ID 6655

AAATTTATTTCTTACCAGCAATCGCTTTACGCGGACCTTTGCGAGTACGCGCATTTGTACAGTGCCTTGACCGCGCATGGTAAGCCGCGACGATGACGGAAGCCAC

SEQ ID 6656

KFISYQQLYADLCEYAHLYECVDRGMVSRDDGSH

SEQ ID 6657

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GCGCAAGGGCGGTTTCTGGCAAAACTGACGGGAGGGCGGTGTGCGACACTGCAATCCCGGACCGTGCCTGCCGGAAGCGTGTGCGGATGATGTTGTGGTGGAACTCGGACCTGTG  
GCGCGCGAACAATCTCTCCCGTGTGCAACAATGGGCGCGCGCTGAAGACGGAGCGGCTGCTGTTTTTACCTGCTTCCGCGCGGATACCTTGGCGGAAGTGAATCCCGCTGTGAAG  
AAAACGGCATTTGAAGCGCGAGCGTGTGTTCCGATATGACGACTTGGCGGATGCTGCGCGAAACGGCTTTTACGATCCAGTACCGATACGCGGAAGCTGTGTTGGACTACAA  
AAAGCGGAAACGTTTTGGCGGATATGACACGCTGGCGGTTTGGCGCGGCTGGCGTGGGACGACGAAACCGCGCGCTTCTGCTGCCGGGCGATATTTGAACGGGAAGCGGTTT  
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SEQ ID 6658

VPRLCRGFMFQDKCWQVHRHLAEHTDQRLFLVFNAPGHILLAGADADISRLSLAKRYPLAVFEYDSRADFLAAAAARKGGFQKILTRGVVQHCQSFVPLPEACADMLNSNLGLL  
AAEQILPVLHNWARALKTDGLLFFTCFGRDTLAELKSLKENGIESRSVMPDMHDLGDLAENGFDYDPTDTAKLVLDYKRAETFWADMDTLGVWRAVANDDENAARSCAGAIPEREGGL  
GITLBTVYGHAVKILVLPQGENVVRFPFKR

SEQ ID 6659

GTGCGGACAAATCCGATTTCCCGCTGTGCGGGAATGACGAGCGGGAACGGCGCACGGACATTCGCGGAATTTTTATGCTCTCATCTCTACTACTTTTTTAAATGCGCTATTCAGAA  
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GGAGGGCGCGGGAGCGGCGCATTTCCAAAGTTGCGCAACCTTTCCCAACAACCTTAACCGCCCAATACAGCCTTGGCGCTGTGTGCTCTCTCCAGCCCTCTCCACGGGAGAGAG  
ACGGGGAGGCTGTGGGGTTAAGGGTTTTG

SEQ ID 6660

VRTNPDRLCNDGRERRTDIIRNFCLHSHTLFNLQENRLCRLFLFRPEINGCKSNLFFKPPATAKSAATCFLPRGGGPGRRHSPSCNLSQQLNRNPTSLAACPLSSPLPRGR  
TGRLLGLRLV

SEQ ID 6661

TTTCTTCCAGCAATCGCTTTACGCGGACCTTTGCGAGTACGCGCATTTGTACGAGTGCCTTGACCGCGGATGGTAAGCCGCGAGATGACGGAAGCCACGATAGCAGCCATGTCCATC  
AATCGTTTGATACATAGTACTTCAAGACGCAATCACTTCTACTTCTACTTGGCACTTGATCAGCAAGCATCTAATTTAGTCTCGTCCAAATCTTTTGCTTTAGTATCAGGCG  
CAATATTGCGAGCTCACAATCAATTTAGCACGAGTAGCACAATACCGTAATAGCTGAAAGCAATATACGATGTGTGCTTATAGGATATTTACCCTCGAATACGAGCCAT

SEQ ID 6662

FLTSNRFTTFASTRICTSALTAAM\*AAATMTATLAAHVHQSFDTHTSYPTQITFTYFILGNLITQSI\*LSLVQIPCFISIRRNICSLTNQFSTSTNTVNSLKTNYDVCVIRDIYPCMTSH

SEQ ID 6663

GTGCGGAACTTGCCAAATCGGTATTCAGCCGCGCGAGATGCCGTCTGAAACCGCGGACGAAACCGTGGCATAATACGCAACGCTGATAGTGGCGCGCTTCCGATGCGCGCCCAACAG  
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CGATTTGCCCGGACAGCGGGAGCGCGCTTCCGCAACCTTCGATATTGAGGCGAGTGGCGGCGCATTTCCGCTCAATTCGATACGTCGGCGGACATTTCTGGCTGGTCACTCGCGGA  
TTGGTCCGCTGTATCTGGCGGCGCGCATCCCGCAAAAGTCCGTCTGCTTGCCTGACGGCGAGTTTCGACCGGCTGACGCTGCCGAAGACTATCCCGAAGGGCTTGGCGCGCTGCA  
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CGGATTACACCGCTGGGTATGGCGAGTATCTGATCGGCATTTGAAAGGAAGCAGGCTGGTTGTGATGGAAGGCGGACACGCGCGCTTTTGAAGCATGCGGAAGCGTTTGGCGCGC  
TGTCCGCGACTTTGTGAAGGGGTTTGACA

SEQ ID 6664

VRKLAKSVLQPAQMPSETPDEPHWNTQRLIVGASAMRRQQRKFMPPDAKVKYLHGWGANRHFDDLMPLPATWPFVSAVDLPGHGDAFPAQPFPIEAAADGIAAQIDTSADILGWSLGG  
LVALYLAARHPDKVRSCLTASPARLTAEDYPEGLAAPALGKMGAFRTDYAKHIKQFLQLQLLHTPDAAEIIGRILFDLARCGTFQALQJALDAERADARHLIDKIDVPLLVPVGGKD  
AITPLRMGSYLHRLGSRLLVMEKAHAHAPFLSHAEAPALCRDPVEGGLT

SEQ ID 6665

TCTGTCTGAAAACGATTCGAGCCCTAGTTAAATCATAGGTGTGAGCTCTACTGTGACCTTATCTCCCGGAGAAATACGAATGTAATGCATCCGCTCTCCAGAAATATGACCCAAAT  
ACAATATGTCATCTCAAGTTTACTTTAAATGTTGCGTTAGGTAAAGTTTCAAGAAATTTACCTTGCATTGGATAGTATCTTCTTCGCCAT





GCGAGGAGGAAACGGTAGATTGGAGCATCTACCTCTCGGAAGAAAATATCCAAAATATGCAGATACCTGTTTCCCTCGGAATCTGTAGGTTCTGACGCGCTTCCGAAGCGAAATACGA  
CCTTCCGGAATGTATCTCGAAATCGGCGACCGCGATGCCGCTGCCGAGACAGTCGAGAAATGCTGGAAGAAGCGGAGCGGACGTACTCAAACGTGCCCAAGCATTTGCCGCGAGGAATTG  
GGTATT

## SEQ ID 6684

VYEPETFPNPVPEVIDTPEPESVAQTAKNPETVDTPYNNLFSNNHIGTEETASAKPAAPSGLAGFLKASSPETILEKTVAEVQTPERLEHFLKVYETGAETAPEPTDFNAAADDL  
SALLQPAEAPAVEENAEITLETPTDNTSEADALPDFLKDSEETVDWSIYLSSENI PNWADTCFPPSVSGDAPSEAKYDLAEMYLEIGDRDAAAEVQKLEAEAGDVLKRAQALAEQL  
GI

## SEQ ID 6685

ATGTATGCAGGGCAACGCTTCAATACTTACAGCCATTGAGCGGTTTGATTCTGGCGGGCGGAGGTTTGATGCTGATGCTGCTGAAAACCATAGGACACGGGGACGGCTACCGTATCTTCA  
GCGTATCGGTTTACGGCATCAGCCTTCTCTGCTCTATTGAGTTCTCGCTGTACACCGGAATTGACAGCCGAAAACCTGAAAAGCATTTTGAAGAAAACCGACCTGCATGATTTATGT  
GCTGATTGCCGGAAGCTACACACCGTTTGCCTGCTGTTTCTGAGAAACGGGCGGGCTGGACGGTATTCTCAGTCTGCTGGCTGCTGGCGGCTGCAGGAATCGCACAAGAACTCACCATC  
GGACGGAAGAAACGAAACGCTGCTGCTGCTATTCGATTTATATCGTAATGGGCTGGATGGTCTTGGCGGTAATGAAATCCCTGACAGCCTCACTCCCGCCGGCAGGACTGGCTTGGCTGG  
CGGACGGCGGTATGCTGTACAGCGTCGGCATTTACTGGTTTGTAAACGATGAAAAATCCGACACGGGACGGAATCTGGCATCTGTTCTGATTTGGGCGGCGACCATTAACCAATTTGTCAG  
CGGTACGGTTATGTAATC

## SEQ ID 6686

MYAGERFNTYSHLSGLILAAAGLMLMLLKTIGHGCGYRIFSVSVYGISLILLYLSSSLYHGIAGKLSILKKTDMCHYVLIAGSYTTPALVSLRNGPGWTVFSLWSLLAAAGIAQELTI  
GRKSEKRLLSIAIYIVMGWMLAVMKSILATSLPPAGLAWLAAGGMLYSVGIIYWFVDEKIRHGHGIWHFLVGLGGSITQFVSVYGYVI

## SEQ ID 6687

TTGCTAGGGTTCCGCTGTATATAACGCTTTTCGGATACACCTTTTCAGACGGCATCCGAACCATCAAGGAACACTCATGAAAATTACCCCGCTCAAAGCCCTGACCGACAACTACATCTGG  
ATGATACAGCAGCGCAACCATGCGCTGCGCTGCATCTTCCGAAACCTCGCCGCTCTGGGAATTCCTGTCAGCAACCGACTCATGCTCGCCCAACCTGGGTAAAGCAACCCCATCCCG  
ACCGAAGCGGTCGCGCGGCACTCTGCGCGGCTACATGGAATCGCCGTTTACGCGGAATCCGACATCGAAGCCGCCACCCACACCGTAACCGCGGCGACACGATTCACTTCCGCA  
CGGTGAGTTTACCGTTTGGGCAACCCCGGCCACACAGACCGCCACACAGCTACCTTCTCGAAATTCAGACGGCATACAGTTTCTGCGGGCGACACCTTTTTCGCGCGGCTGCGGA  
CGCGTGTACCGGCGACGTCGACAGCTTTACGACAACCTTCAACGGTTTCAACCAATTAACCGAAGGCAACCTGTTCTATCCGCGCACAGGAATACACCGCGCGCAACCTGCGTTTCCGCG  
CCCATATCGAGCCGCGACACGCGCATTCAGACGGCATTTGAAGGCGCGGGAACACACCGCCACCTTCCCGTTTACCTCGCGCACGAACGCCGCGTCAACCCGTTCTTACGAGCAGAAAT  
CCCCCGCTCCGCAACGTCGCGAAGCCCTGGTCCGCAAAACGCTGACAGCGGTTTGGAAATTAATCGCCCGCTCGCGCACTGAAAAACGCTACCGCTGACCTGCCCTCCGAAAAATG  
CGTC

## SEQ ID 6688

LLGFRCLITFPFYGTQTASEPSRNTHEHYPRQSPDRQLHLDFTARQPCRLRRSPRTLARIIGIPRTOPHTARPNLGNAPPSEPRRCGGTLARLHGTARLRRIRHRSRHPHRNRHTIHLRQ  
RSGYRLGNTRPHRPPHQLPSRNFRRHTRFLRRHPFFRLRLTRVYRHGRATLRQLTPVQPIRRHFLVSGTRIHRQPAFRFPYRAGQRRHSDGIEGGTHAHPARYPRARTPRQPVLTDRN  
PRFPPTCRSEFRQNAEQRFSGSIRRPARTKRLFLTCPKNAV

## SEQ ID 6689

TTGTGCAGGCTGTTTTTGTCTTTTCAGACGACCTGCATCAACGGTTGTAAATCCAATCTGTTTTTCAAACCGCTGCAACCGCAAAACCTGCCGCAATCCGCCCTCCCGCTGGGGAGG  
GCCGGGAGAGGGCATTTCTCCAAGTTGCGGCAACCTTTCCCAACACTCAACCGC

## SEQ ID 6690

LCRLFFAFQITCINGCKSNLFFKPPATAKPAAIRPLPRGGRGEGILQVAATFPNNSTA

## SEQ ID 6691

TTGACTTTAAACCCGAAAAACCTTTTCTCTCTCACCGCCGCTTCGGCACACACTCCCTTCAGACGGCATCCGCCGACGAGTGGTCAAGCCGAAAAACTGCAGCCTCCGCCAACCGCA  
GCTACAAAGTCCCGAATTACAGCAAAACCGCAACGCTCTGTGTTACGGCGGAGGTTTACGGGGCGAAAACTTCCGGCGGAGACCGCTACGATATGAACGCCCTTACCGCCGCCACAA  
AACCTGCCATCTCCAGGCAATGTCGCGTAACCAACACCAAAACGGCAAAAGCGTCATCTCGCGCTCAACGACCGCGGCCCTTCCACGGCAACCGCATCATGACGATATCCAAGCC  
GCCGCGCAAAATTTGGGCTTTGTGACGCAAGGACGGCACAGCTCAAAATCGAACAATCGTCCCGGCCAATCCGACCGGTTGCCGAAAAACAAAGACATCTTTATCGACTTGAATCTTT  
TCGCTACGGGAACAGCAAGCAAGCCTATCTGAACCAAGCCGCCAAATTTGCGCGCTTCGTCATCAAGCCGGAACCTCTCGGTTGAAAAACGCCGTTACGAATACGTTGTCAAATTTGG  
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## SEQ ID 6692

LTLTRKTLFLTAAPGTHSLQASADAVVKPEKLHASANRSYKVAEFTQTGNASWYGRFRHGRKTSGGDRYDMNFTAHHKTLPIPSHVRVINTKNGKSVIVRVNDRGPPHGNRIIDVSKA  
AAQLKGFVSQGTAVHKIEQIVPGQAPVAENKIDIFIDLSPFGTEHEAQAYLNQAQNFPAASSSPNLSEKRRYEVVVKMGPPASQERAAEAQAQARGHVRVAVLTSQ

## SEQ ID 6693

CATTTCATCTTACCACCAACATCTCGATAGCAGCTCTCGCACTTTGTTGTAATTTAATACCTTCAAAGCAACTGCTTTAGAAATTTACACAGAAGCAATACTTTAATATTAGAGACT  
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TTTTAGGGAGGCGTGTGCAAGGCGATTGACACCTCGAAACCCACCTTATGAAACCCACAGACCGGCTCTTTGACCTTTATGACCACGACACCGCGTTTGGCAAGACCACTACC  
AATACCGCGTCAACACGACGACGATGCGTAGCACCAACAGCAGGTGTAATTTGATTTCAAAAACT

## SEQ ID 6694

HFNLATNILDSSSTFGNFNTLQSNCLRNFTRSNNFNIRDCRNQTCLL\*D\*NINLINSN\*PQPT\*TKLCIS\*YC\*RFKTSFRESLQGHLLTLETHLMKPTRPALLTFMTTTRFAKTTT  
NTASNTTSMRSTNSRLNCIQKH

## SEQ ID 6695

AGACTCCACTTTCAACAAGTAGCTGATTTTATTAATCATACCACGGTTTTCAGAGGTATCTAAAACCTCTACCGTATGCTCGCGACGACGCAAACTAAACCGCGTGACATGACAGATGA  
GATTCATTTGATACCAATCAGGCTTTTAAACAAFTGTAACCTAATCTTTTTTGTTCAGCCAT

## SEQ ID 6696

RLHFQVADFINHFTVFRGI\*NLRYMLATTQT\*TACTCTMRFNCTNQAPNQCNPLPLFSH

## SEQ ID 6697

TTGTGCAAAATTCGGGAGCCCTCTCCCCACGGGGAGGGGCGAGGTTGGGCGAGATTGGCGGTTGACGGCGGTTTGAAGAACAGATTGGATTACAAACCGTTGATTTCAGGTCGCTGA  
AAAGCAAAAGCAGCCTGCACAAACCTGAT

## SEQ ID 6698

LSKFGEPSPPRGQVAAADLAVAGGLKNRLDLQPLISGRLSKKQPAQPD

## SEQ ID 6699

ATGAACATCAACACCTTCTCTTACCGCGCGCGCAACCGCACTGTTGGCGATTTCGCCCCCGCACTCGCCCAACGACGAGCGGACGCGGATGACGACCAAGGACGCGCGCACCAAC  
ACGGCAAAACAGCAAAATCATCAGCGCGGCCAAGCCGAAAAAGCGGCTTGGGCGGCTGCGCGGCAAAATCACCGACATCGATCTCGAACACGACGACGGCGCTCGCAGCTATGATGT  
CGAAATCGTCAAAACGAGCAGGAATACAAAGTGTGTGATGCCGTACGGCGCGGTGATTTCCTCCCGCGGACGAC

## SEQ ID 6700

MNIKHLILLTAATALLGISAPALAHHDGHGDDDDHGHAAHQHGKQDKILSRAQAEKAANARVGGKITDIDLEHDDGRPHYDVEIVKNGQYKVVVDARTGRVSSRRDD

## SEQ ID 6701

GCCATGGTTAACTCCCAAAATGCTTCCACTGTCAAGCCACGTTTGGCTGCGATATCAGCAGGAGTATGCAACTTAGACAAACCATCTAATGTTCAGCTACGATATTATATGGGTTAGTAGATCCGTCACCTTTGGCGGAAATATTATGAATGCCATAGCATCAAAAACCAAAACGATAGTCCACCGGCTTTTACGCCACTACCTCTTTAGCAGGCTGCATAAATACCTTTAGTAGCACCATGTGCGACCAATAACCTCATGATGGATCGTACCAATTTTAAATGGTACCTTAATCATAGAGCGCTGCTGCTTATCCATCGCTTTTGGACTGCAACAGGACCTCTTTTGGACTTACCTTTACCCATACCAATACGACCATCTCCATCACCACACAGTGTAGCGCAGAGAAAGCCATAATGCGACCACCTTTAACTACTTTGGTTACACGGTTAACTGCGACCATCTTTCAATCAGACCGTCACCGGCTCTTCAATTTCAATGTTTGGCAT

## SEQ ID 6702

AMVNSQNVFHCQATFGCDISRSMLQRTT\*CTTYDIIWVSRSVHPGNNIMNAHSIKNQTHRSSTGYATTLLFSLHKYFSSIMSTNNLMDRTIF\*WYLAHRASCLIHRLDNCNRRFF\*LTFTHWITLISITNNS\*RRSHNATTFNYFGYTVNCDHLFNQTVTAFFNFMFCH

## SEQ ID 6703

TTGCCGCGGCTTCCACCAATCCCTTCAATATTACOGATCCCGCATTTGCCGCGGATTCCTGCAAAATCCATCAATTCGCCGAATCAOGCTTATTOCCAAAAACCTTGATCGCGGGG

## SEQ ID 6704

LPPASTNPFNITDPAIAADS VKS INSAESRLFPKNLDAAG

## SEQ ID 6705

GAAGCTTAAACCTTTTTCAGCAGCAGCTTACGCAAGGCTTACACGACCGTGATATTGGAACCTGAACGATCAAAAGCAACCTTTTCTACACCTGCTGCTTTAGCCTTCTCAGCAATACTTTTACCACTATTCAGCTGCTTCAACATGCTTCCAGATTTTACAGTACCGCGACCTCAGCTTCCATGTAGAGGCTTGAGCCAATATCTTATCACCCTCAGCACAATTAATTAATGATGATGCTTCCGAACACACATAATCTTACCATTTTCAAGTCCGCAATACGAGCAGGGTTTTCGCTGCAGCAGGAGTCCGGTTGATGTTATCCAT

## SEQ ID 6706

EA\*TIPTSSPSQSLETTVILET\*TIKSNLFYTCCFSLLSNTFTNYCSCFNIAIRFQYTAHLSFQCRGLSQYFITFTSNYLSINMIASEPT\*SYHQVWNTSTGFACTPESGCMFIH

## SEQ ID 6707

TTGATGCGCGGGCTGAAGCCGCGCTTCAACCTCTCTATGCAACCCCTTTCGAGCCGACACTACGCAACATCTTGAGAACCCTCTCTGTAAGATACCCGAACCGTCCCGATACCCGTAATCTTAAACCCGCCATTCGCCGCGAGCGGGAATCCAGTCCGTTCCGTTTTCAGTCATTTCCAAAAATTCGCTAGCGTTAAGTTTCTAGATCCCACTTTCCGGAAGATGACGCGTGCAGGTTTCGTCGCGAGGATTCGTCAITCCACACAGACAGGAATCCGGAATTTGTCGCGCGGAACTTATGCGCGCTCAITCCCGCACAGCGGGAATCAGGTCGTGCGCATAGGAATTTATCCGATAAAGCGTTGCCCAACCTGCGTCTTAGATTTCCACTTTCTGCGGAATGACGATTCAGGTATTCCTAATAGCAACCGGCCACAACCCACTACGCCCATCTTACGCATCTGCCATACAGCCCTGTTCCGAGCGCGGATAAGTGCAGTGCCTCGCGCGGGCATCA

## SEQ ID 6708

LMRRABARPATLSMHLASPTLRNLI RTHPVKNRTTFPIHRNPKTRHSRAGNPVRSVSVISKNCRSVKFLDSHFRNDADVQSVRTDSSPHRQSGFVRAETYPSPFHRREPRSVGIGTYRIKRLPQPCVLDSHFRGNDSDGIPNSNPPQPTYAHPHLPSVPERADKVRERRAS

## SEQ ID 6709

TTGCACCCGACACTTCAGGATTCGGCACATGATCAGCAGACTGACCGGCAAACTGGTTGAAAAAAACCTCCGCAAAATCGTCATCGATGTCAACGGTGTCCGTTATGAAGCCGACGTATCGATGCAGACTTCTACAACCTGCCGCCGTGGGTGAAAGCGTACAACCTGTTTACCCAGCTTATCATTCGGGAAGACGCACATCTTTTATTTGGTTTGGCACTGCGGAAGAACCGAAGACCTTCGCGCAACTGATTAAGGTTCGGCGGCATCGCGCGGAAACGGCTTTGGGCAATTTGTTCGGCGATGACGGCAGACGAGCTTGGCGCGGGCGGTTCAGAGAAGAGATGTCAAACGGCTCTCCCTCCGCTCCGGAATTCGCAAAAAACCGCGCAAGCTATGCTTGGAACTGCGCGGCAAGCTGCTCGCGCATACGGTAACGGACGGGCTGTTTTCGCGCTCACCCGCGCGGACGAAACCGAAGACATCGTCAGCAGCTGCTTGCCTGGGTACAAACGAAACCGAGGCAAAAGCGCGGTCAAAGCGGTTCCGAAGGGACGGACGTGGGCGAAGCGGTGCGCTTGCCTTGAAACCTGCTGAAA

## SEQ ID 6710

LHPTLQDSAMHISRLTGKLVKNPPQIVIDVNGVYADVSMQTYNLPVVGESVQLFTQLIREDHLLFGFATAEERKTPRQLIKVGIGAKTALGILSAMTADELARAVAEEDVKRLSAPGLGKTAERINVLRLGKLVAFVTGGLFAASPAADETEDIVSTLLALGYNREKAAAVKGVKPGTDVGEVRLALKMLLK

## SEQ ID 6711

TTTTTCTTGGCTTCTTTCATTACCACTACTTCGCTACATAGCGAACCTTTTACCTTTATAAGGCTCAGGAGCAGCGAACCGCAATCTCAGAAGCACTTGACCAACAACCTTGTTATTCGAGCCAGTTAAACCAATCTCTGTTTGGCTAGGAGTTTGAACGGAGACACCTTCAGGCAITTCATATACGATCGGATGAGAAAAACCCAAAGACAGATTCAAGATTTTACCTTTGCTGTGAGCAGATAACCCACGCCCATCAATTTGTAATTTCTTCTCAAAACCTTCTGAAACACCTTTAAACCATATTGCTGACTAATGCGCGAGCAGTACCAGACATTGCATTTGCTTGTTTACTGCTATTATTCGCAACAAAGTCAATTTGCCATCATTAATTCATGGCTACATCAGAATGCAAGGAAAAAGACAATTCACCGTCTTACCTTAAATACCAATGCCTCTGTTCCAAATTTTACTTCTACACAGCGGAAACCTGCTACTGGGTTTTTTGCGACACGTGACAT

## SEQ ID 6712

PFLGPFPHYHYFATYANTPTFIRLSTERTNLSNLTNNLFIAS\*NNILCLARSLNGDTFRHFYIDRMRTQRQIQDFTLCLSTITHAQL\*FLLETF\*WTFPHIAD\*CASSTRBCICLFTAIIIRKSSQPAIKFNGYIIRMQRRQFTVLINQCLCKSFYFTSGNRHVVPCDT\*H

## SEQ ID 6713

GTGACGGCGGATCTGGCTTACGCCTACGAGCACATCACCGCGATTATCCCGAAGCAACCGGTGCAAAAAAGGCACAACAATAAGCAGGTAAAGCGATTATTTCAAAAACATCCGCACCGCTCCGCTCCACCCCGACTGCTCCCTCGGCTACGATTTCCGCGGCTGGCGCGCTTTTCCGCCCCCGCGCTTGCAGCGGCTCCCAACATCCCTTCAATATTACCGATCCCGCATTTGCCGCGGATTCGTAATCCNTCAATTCGCGGAATCAGGCTATTTCCCAAAAACT

## SEQ ID 6714

VQADLAYAYEHTRDYPEATGAKGTTISTVSDYFKNIRTSVHPRLALGYDFGWRVFSAPAVAAGLHQSLQYYSRHRRRFRQIHQPRITPIPKP

## SEQ ID 6715

ATGTTCCGATTATAGTCTGAGTTATGCGCTCTGAAAAATGCCGTTTGGCCGACTTTCGCGCTTAAAAATGCCGCTCTGAAGTTTACAGCGCATCGGAATCGCGGAATCAGAAAAATGCCGCTGAAGGTTTACAGCGCATCGGAATCGCGGAATCAGAAAAATGCCGCTGATAGGCTTTATAGGCTTTTACAGCGGCTTTTCCGTAATAATGGCGTTATTTGCTCTCTTTTACAGCGGCTTTG

## SEQ ID 6716

MFLGYCQLCLRLKMPFARSCALMPSGSDGIGIGESEKMPSESDGIGIGESEVAHAQ

## SEQ ID 6717

ATGCCGTCGGAAGCGCGCGCGCTTTGCCCTGACGAAACCTTGGCTTTCCGCCCCGCGCTGCTTCCGACGGCTTTTCCGTAATAATGGCGTTATTTGCTCTCTTTTACAGCGGCTTTGTTGATGCCGTC

## SEQ ID 6718

MPSEGGAAAFATKPCVSAPRCLPDGFSRKMALLSFLSDGIVPDAV

## SEQ ID 6719

GGCTACAATGCATAAACAACCTACCAACCAACCTTGAGAACGCTGCTTTACGATCAGTCATTACACCTTTAGAAGTACTAACCAGTACGAAATCCCAAGCAATTCATAACCTTGAATCTCATAGACGCTTTATAAATACGCAAAACCGGGCGAGATACGCTTGATTGTTCAATTACAGGACGACCTGCATAGTATTTTAATTGAATTTCCAATATAGACTTACGTCAGATGAACTG

CGAAGTCTCTCAATATATCTCTCTCTTTCFAATACCTTTGCAATAGCACCTTTAATTTTGAAGAAGGCATTGCAACTGCTGCTTTATTAGCACGTTGCGATTGGGGATACGAGTCAACAT  
ATCGGAAATAGGATCATGCATCTACTCAT

**SEQ ID 6720**

GYNA\*QLPTNLRCTCFIISHYTFRSTNDSNQALHNTWNLRFRFINTQTGARVYTLDLFNYRTTCIVF\*INQVRLYVR\*NCEVLNLSPPFYQLCNSTL\*F\*RRHCNCCFISTLRADTSQH  
 IGRNRMETH

**SEQ ID 6721**

CCAGCTGGCTTTAAACAACACCGGGAATTTTCGCCACGCATGGCGATTTCACGGATTTTAATACGACCCAAACCAAATTTACGGAAAGTACCACGAGGGGCGACCTGTCAAAGCACAAACGAAGA  
CGTTGACGCACAGGTGCCGATTACGAGGAATGGATTGAAACCTCAAACGAGCCTCAAACGCTCTTCTCAGTTGCATTGCAATCATTTGATTACCGCTTTAATGCGCGCGCTTTAGCGG  
CATATTTTTTAGCCAAAGCTTGACGTTTCAGATCACGATTAAATAAGTGCCTTTCTTAGCCAT

**SEQ ID 6722**

PAGFNNTRNFATHGDFTFDNFTQTKFTSTTRATCQSTTTTLTHRCRITRNLKPKQTSKTLFLSCIRIIDYRNCRAF SRIFFSQSLTFQITINKCFLSH

**SEQ ID 6723**

TCCTTTGAAACGGAAATTTAAACAATGACAATAAAGCTTTCGCTTCCTCATCGGTTTTTGTCTGTAGTAGTAATAGTAATATTCAAACCACGCAAAAGCATCAAAATTTATCGTATTCAAAATTC  
GGGAAAAATAATTTCCTCAGACACCCCATATTGTAATTGCCACAGACCATCAAATGATTACCCGTCACACCACGGAAATGTCAGTACCGGAGGTAAATCCAATAGTAATCAAACGATCCAAGA  
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CTCTAAATTGCGAAACAGCATGTTCCATAACTTTTTGTGACGAACACGCCCTACCCACACCCATATTCAAGGTGATTTTTCAAATACGCGGAGTCCATTACTGATTGTAAACAAATTGT  
TTAAACCAATTGAGGAACAACGTCTCTTTATAAAACACCTCTCAACCGGACCAT

**SEQ ID 6724**

SFRKFKQ\*Q\*SFRFLIGFCCSSNSNIQTQSQINFIVFNFRNNLLTNTHIVLATTIK\*PTAHTTEVTYAR\*CNSNQTIQEPKHLITQCYFATNRIVITDFKTCDRFTGNSNNRSLTGS  
L\*IGNSMFHNFVVSNSLTHTHIQGDFFNTRDFHY\*PVTKLFPQFNRNCLKPIKLSQPSH

**SEQ ID 6725**

[illegible]

**SEQ ID 6726**

LICIRSTKNFSSLLFSSLLFSSLLFSSAARAAGEHGRGPYVQADLAYAYEHITRDYDPAAGANKGKISTVSDYFRNIRTHSIHPRVSVGYDFGGWRIAADYARYRKWHNNKYSVNIKELE  
RKNKNTFGGNQLNIKYKTEHQENGTFHAVSSLSGLSTVYDFRVNDKFKPYIGVRVGYGHRVHGIDSTKTKNTLTAYHSAGTKPTYDDIDSGKNQKNTYRQRSSRRLGFGMAGVGIDV  
APGLTL DAGYRYHYWGRLENTFRFKTHEASLGVRVRF

**SEQ ID 6727**

ATGTTGAACAAAATATTTTCTCGTTCGAGTCCCGAATCGACCCCTACCCCGAAGCCGCCGCCGAAAAACGCCGAAAAAGGCTTGTGCGGFTTGTCTGGAGCAGTATGGACGGGGTGCGGA  
AATGGATAGCCGCCCTAGCTGCGCTGACCGCGGCAATCGGCATTTATGGAAGCCCTGATTTTTCAATTTATGGGCAAAATCGTAGAGTGGCTCGGCAATACGCCGCCGCCGAACCTGTTTGC  
CGAAAAAGGTTGGGAACCTGGCGGCAATGGCGCGATGATGTTGTTTTCTCGTCTGTGGGCGTTTGC CGCGTCCAAAGCTGCGCTGCAAAACCTTCAGGGCGTGTCCCTATGCGCCCTGGG  
TGGAACTTCCACCGCTGATCGTGAACAGACGACCTCGGTTTTCTTACGAGCAAAATTTGCGGCCGCTGCGCTGATCGGCAAGATCATGCAGACCGCGCTGCGTTTGGCGACGCGGATGACGG  
TTCCGATATGAGTGGCTTATGTGTGCGGTGATTTTCACTCTTGGGCGGTGATTTCTCGCCCTCGCTGCACTGCTGCTGCGTGGTGGTCCCTTATTCGCGTGGAATACCGGTTTCGCTTCGGTAAT  
GCGCCTGCTGATTTCCAGATTTGGGGCAAACCGCGCACGGCAGGCGAATGCCCGCTCGCTGATGACCGGCCGCAATTACCGATGCTCATTTCCAAATATGCACATCGCTCAAACTCTTTTTCAC  
GGCGCGCGCGAAGCGGTCTATGCCAAAGCAGTGCATGGAAGAATTTATGTTTACGGTGC CGGCCCAAATACGCGCTGGCGACTCTGCTGCATTCGTGCAACTTCACTGCTCAACACTTCGCTGA  
CCCTCTCCACCGCGCACTGGGCATCTGCGTTTGGCAACAGGACAGGTGCGCGTGGGTGCGGTGCGCACCGCCACCGGATGCGGTTCGCGGCCAACGGGCTGTGCGCAATACATTTATGTG  
GGAATCCGCGCGCGCTTTGGAAGAATCCGCGCATCTGCAACAGCGGCATGGCGACCTGTGCCAAACCGCACACCATCTCTGCAAGCCCCAAGCCCTGCGCTGAAAGCTGCGCGCGGCGCAAT  
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ACAAGATACCTCGCTGCTGACCGTTTCCGTGCGCGACAACATTTATTACGGCGCGCCGACGCGACCGGATGCCGAAATGGTTTCCGCGCCGGAACGCGCGAAGCCGCGCTTCATCCCC  
GACCTTTCCGATGCAAAAGGGCGAGCGCTACGACGCGCAGTTCGCGCAACCGCGCGTGAACTCTCGCGCGGACAACGCCACGCGCATCGCCATCGCCCGCGTGATGCTCAAAGACGCAC  
CCATCTGCGCTGTGACGAAGCCACAGCGCGCTCGATTTCCGAAGTTGAAGCGCGCATCCGAAGAAGCTTCGACAAATFGATGGAAGGCAAAACCGCTCATCGCCATCGCCACCGGCTCTC  
CACCATTTGCCGATGGACAGCTTCGTGCTCTCGACAAAGCGCGCATCATCGAAGAAGGCACACAGCCGAACTCTCGAAAAACCGCGGCTTTACGCCAACTCTGGGCGCACAGAGC  
GCGGCTTCTCTACGGAACAGCTGCTGCTCCGACGACGAC

**SEQ ID 6728**

MLNKIPSWFESRIDPYEAAKPTPEKGLCRVWSSMDGVKRWIAALALTAGIGIMEALIFQFMGKIVELGKYAPAEFLAEKGWELAAAMAAMVFSVVWAFAPASNVELQTLQGVFFMRIR  
WNFHRLMLNQLSGLFYQDEFAGRVSAAVMQATALALDAVMTADMVVYVSVYFITSGVILASLSDMLLLFFIGWIIGFASVMRELLIPLRGQTAARQANARSLMTRITDAYSNIAIVKLFPH  
GARREAVYAKQSMEEPMVTVRAQMRRLATLHSCNPIVNTSLTSTAALGIWLVHNGQVGVGAVATATAMALRANGLSQYIMWESARLPENTGIVNDGMATLSKPHITLIDKQPALPLNVPGA  
IKFHEHVDFCYEAGKPLLLNGFLNLKPKGEKVLIGRSAGAKSTVNLILLRFPYEQSGTVSIDGQDISGVQTESLRAQIGLVQDPTSLHRSVRDNIYIGRPDATTDAEMVSAERAEAAAGTIP  
DLSDAKGRSEVQDADHVGERGVKLSGGQRQRIATARVLMKADPILLLDEATSALDSEVEAAIQESLDRKMBEGKVTIAIAHRLSTIAAMDRLVVLDKGRIIEGTHAELEKRGLYAKIMAHQS  
DGLFSEHVEYDH

**SEQ ID 6729**

TGCTCCAATGATAGAGCCATTGATTGGAAGAAACGAACGCGCTTAACTTTCGCTTCATTTTCAATCAGCTTAATACCAACACGGTCCGCTTTATAGTTTCCGGATTACAGGATTGCGATA  
TTAGAAATATCCAAAGGCATTTCCTTTAGTAATAATACCGCCCTTAATGCCACGCATTGGATTAGGTTTTTATGGGGTTTTTACAACATTAACGCCCTCAACACAACTTTTACCAACCAACA  
CTCGAACTACTTGACCTGCTTACCTTTATCTTACCAGCAATTACTACAACCCCTATCGCCTTTAATGATTTTATTCAT

SEQ ID 6730

CSNDRAI\*FEETNAPNPAFIFNQLNTNTVRFISFRIQDCDIRNIQRHFFSNNTALNATHWIRFLMAFYNNALNNNFTTCHSNYLTLTFFILTSNYYNPITAFNDFIH

**SEQ ID 6731**

GTGCTGTTTCCAACCCCTGCGCCTGTACCGTCAGGCTTTTATTATGGACCTTCCAGTTCGTTTTTACTGAACACCCCTTCCGATTCCAAACGACAA

**SEQ ID 6732**

VLFPRLRLYROAFIMDLPSFLNTPSDSKRO

## SEQ ID 6733

TTGATGGCGTTTACACATTAAAGCCCTCAACAACACTTTACACCCCAACTCGAACTACTTGACCTGCTTACCTTTATCTTACCAGCAATTACTACAACCTATCGCCTTTAATG  
ATTTTATTCATCGCTGCTATTCCTTATAATACCTCAGGTGCCAATGAACGATTTCATATAATCGCTCAGTACGCAATTCACGGGTACCGGACCAAGATACGAGTACCCAAAGGTCAAG  
TTTATTTATTCAGCAACACGGCGGCGATTGTTATCGAATTTAATTAACGCACCATCAGGACGACACCCCTTAGCAGTACGAACAACTACCGCATTTATATCATCGCCTTTTGTGACACGG  
CCACGGGAACCGCATCTTTAACTGCCACTTTAATAATATCGCCACAGAAAGCG

## SEQ ID 6734

LMFYNINALNNFNTQHSNYL/LLTFFILTSNYNPIAFNDFIHERAIPYNTSGANETIFINRSVRNSRVTPKIRVPKSSLLFSNTAALLSNLINAPSGRRTPLAVRTTTLTYTSPFLTR  
PRGTASLTATLIISPTEA

## SEQ ID 6735

TTGTTTTGCGGGATATGATTTTTTTTGTAAAGATGATTTATTTTTTAAATTCGGTGGCGGATCGGATATGGCGGATTAAACAAAATCAGGACAAGGGCGGAAGCCGACAGACG  
TACAAATAGTACGGAACCGATTCACTTGGTGCTTCAGCACCTTAGAGAATCGTCTCTT

## SEQ ID 6736

LPGRDHFFVKECIYFLKFRGDRWRINKNDKAAKPQTVQIVNRNFTWCFSTLENESL

## SEQ ID 6737

ATGCCGTCGGAACACCCCTTTTCAGACGGCATTTCCACACCCCAACCCAAAGAAACCATGAACGACACCGCCCAATTAACCGCGGCTACGGCGCGGCTACATGTCGCCACGCCCGGACG  
GCACAACTTACGAAGCCAGCACCCCGCAAAAAACGGTGGATTTCGCCCTGCGGCGACCGGCTCGGCATCAGCCCGCTCAACGCCGAACAGTGTGATTGAAGATTTTTTACCGCGCCAAAG  
CCTGCTCTACCGCCAAAGACCGCTGGAAACCAAACTCATCGCCGCCAACGTTACCAACTCTCTCATGTAACCGCGCGGCTCCGAGTCCGAGCGTGGCGCTGCTACAGCGCGCCCTGCTT  
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CGCCCGCACCGCGGACATTTCCGCGGCACTGACTCGGAAAAACACACCAACCCACGCGCGGCTTTATGATTTGAACGGCGAAACCCAACTCATGACTCCCGGGTTTGAAGAATTT  
GGTTTACACCACTTCAAGCGCGGATTGCGGCACTATTTCCCGGATTTCCGCCACCTTGTGCGGCAATGCGGCTTCCCAACTGCACCCACCGCGCGGAACCGCGCTGCGCTTCAAGG  
CCGCTGCGGAAACCGCGGCGAGCAAGCCCGAAGCCCTGCGCTTTTTCAGGGCATCACCGACGAACCTGCTCGGG

## SEQ ID 6738

MPSEHPFSDIGISTPNPKETMNDTAQITAGYGRYIVRTPDGTYEASTRKKRVDFACGDRVRI SPVNAEQVVI EDPFLPRQSLLYRQDANKTKLIAANVTQLLIVTAAVSPSVRLLRALL  
AAEAAGIRAVTVLNKADLPETALHLEKLFYETLGYPIVETRVLENADSLRPVLQHSNILLQSGMGKSTLANALLGSGTARTGDISAALDSGRHTTHARLYDLNGETQLIDSPGLQEF  
GLHHLQADLPHPYFDFRHLVGQCRPHNCTHRAEPGCAFAAAETGAASPERLAF/LQGITDELIG

## SEQ ID 6739

TAATACTTCAGGTGCCAATGAACGATTTTCATAAATCGCTCAGTACGCAATTCACGGGTACCGGACCAAGATACGAGTACCCAAAGGTTCAAGTTTATTATTCAGCAACACGGCGGCA  
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CCACTTTAATATATGCCCAACAGAACGCTAGCAGCGCTTAGATCCGCCAATACCTTGATACACATTACCGGACGCGCACCAGAGTTATCAGCCACATCTAAGATGCTCGCATTTGAAT  
CAT

## SEQ ID 6740

\*YPRCQ\*NDPHKLSLSTQFTGYRTKDTSTQRFKFI IQHGGIVIEFN\*RTIRTTHTLSSTNNYRIITYIAFFDTATRNRI FNCHFNNIANRSVATLRSQYLDTHYATRTVISHI\* DGLHLN  
H

## SEQ ID 6741

GTGTCATATTCCCGATACACCGTAATCTGAAACCCGTCATTCGCGCGAGACAGAAATCCGATTGTGTCGCGCGGAACTTATGCGCGCCATTCGCGGAAGCGGGAATCCGGAAC  
GTTCCGTTTCGGTTATTTCGATAAATCTGCTGCTTTTCATCTAGATTCCCACTTTTCGCGGAA

## SEQ ID 6742

VSSFPIHRNPETRRHSRADRNPDLSARKIMRRHSREGGNPDRSVSVLSKFLLLFI PRFPLSRE

## SEQ ID 6743

TTGCCGACCGGGCGGAAAAATGCGGCTGGAAGCCGATTCCGGGTTTCAGACGGCATCCGTTTTCGAAAAATGCTACAATCCGCTTTTACCGGAACACCGGAACTATGAAGAAAAACA  
CCCCGAATCGTTTGAAGAGGCTTGTGCGGCTTGAATCGCTGACGCGATCCATGACGGGCGAAATGCCCTTGAAGACGCGCTTGCGCCCTATCAGGAAGGCAACGAGCTGGTCAGGTA  
CTGCCAAACCAAGCTGCCCAAGTGAACAGAAATACAGGTTTGGATGCGGACGGGACGAAGAGTTGAACCTTGAATCCGACGAA

## SEQ ID 6744

LPTGAEMPEAGPGFQTSVLQKYNPLFTGTPETMKNTPKSFEEALSRLSLTQSMQEMPLEDALAAYQEGNELVRYCQTKLAQVEQKLQVLADGTEKLNLESDE

## SEQ ID 6745

AATAGAACGTGCTTCTTCAACCACTCACTGACAACCCAAAGATTAGTTTTTACAAATGGAGGGGATTCGATATAACAAACCATCACCAATTCATATTGATTATTTTCATCATGGGCA  
TGGATTTTAGTAGATAATCGAATAATCTTACCATACAGCGAATGTTTACTTTACGCTCAACCAATAGTGTACGGTTTATCCATTTTGTGCTGTACTACTTTGCTTGCAGAAAGTACGAA  
CATTTTATGTTTCGCTCAT

## SEQ ID 6746

NRTCFNLQITDNPFRSF\*QWTFRYNNHTNSLIIIFIMGMDPSR\*SNLFTIQRMFYFLNQYCYGFIHFVAYYFALQSTNIPSPAH

## SEQ ID 6747

ATGCCGTCGGAAGGGTTTTCAGACGGCATTTTTCGCTATTTACCGTAATCTGAAATCCGCTCATTCGCCGAGGAGGAATCTAGATGAGAAATCCATCTGTCAGAAATACCGGAATC  
GTCAGGAATACCGGCTGTCATATTCCCGATACACCGTAATCTGAAACCCGTCATTCGCCGAGGAGGAGGAAATCCGGAATTTGTGCGCGCGGAACTTATGCGCGGCTATTCGCCGAAGGC  
GGGAATCCGACCGTTCGGTTTCGGTTATTTCCGATAAATTCCTGCTCTTTTCATCTCTAGATTCCACTTTCCGCGGAATGACGAAGGAGTGGGAATCCGTTTGTAGTTCCGCGCAT  
TTCCGACAAATGCTTTGGCATTTGATATTTCTATTTTAAATCCACTA

## SEQ ID 6748

MPSEGPSDIGIFALFTVILKSRHSHAGRNLDENPSCQKYPNRQYEPCHSRVTVILKVPVPAQTIRICPRGNLCAAI PAKAGIRTVRFLFPINSCCFPLDHSFRGNDEGVGIRFLSSGH  
FRQIALALDLSFNL

## SEQ ID 6749

TTGAATCCGACGAATGATTGAAAGCGTGGCAACAGAGGGCGAGGCGACAGAGCTGCTGCTGGAACGCTTTTTCGCGTCTGGAACGAAATCCGCAACCGCTGCAAGAGCGATGC  
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CGTCTATTCTTTGGTTCACGACGATATGCCGCGATGGAACAACGACGCTGCGGCGCGGCAACCGACCTGCCACATCAAAATATGGCGAAGCCACCGCCCTTCTGACCGCGGACGCTTTA  
CAACCCAAAGCCTTCGACGTGTTGAGCGCTCCGACAGAACTGCCCCGCGCACGCCAGTTGGCAATTTGTCGGTGTGGCAAAAGCGGCGGCGGATGCGCGGCGGACAGGCAA  
TCGATTTGGCAAAATGTCGGCAACAAATGGTTCAAGCGGATTGGAACGGATGCACAGCTGAAAAACGGGGCGGCTGATCCGTGCGGCGGCTTTATTTGGGGGCGACGCGCTGTCGCGATCT  
GTCCGACGCGGAATTTGCGGTATTTGAGCGCTTACGCGGCAAACTGGGTTTGGCGTTTCAAGTCATCGACGATGTTTGGATTGTGAAGCGGACGCGGCACTTTGGGCAAGACGCGGCGC  
AAAGATGCCGACACGCAAGCGGCTTATGTGAAACTGATGGGCTTGAAGCGGCGGCTCATACGACACAACTGGTTGCCGAAGCAGTGGCGCTGCTGCAACCTTTCGCGGACAAAG  
CCCTGCGGCTGCGGCGATTGGCAGAAATTCAGTCCGACGCAATAT

**SEQ ID 6751**

SEQ ID 6752

SEQ ID 6753

SEQ ID 6754

SEQ ID 6755

SEQ ID 6756

SEQ ID 6757

**SEQ ID 6758**

SEQ ID 6759

SEQ ID 6760

SEQ ID 6761

TTGTGTGCTTGTTTATTCCCTGTTGCGCGTGTGCCAAAAATACCGCCGACGAAACACGGGAAGGCCGAAATGAGGTACAGGCAGACGCGTGGCGTAAAACTCCCAACCTGATTGTGT  
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TGGTCGTGAGGAAGGGGGCGTTGGCAAGATGAGTGCCAAAGACCAAAAGGATGTACATGGATGCGGTTCATGATGGGCTTTCGTGTTTGGGCATTGTGCGCGCGCATGCGGTCTGAACGCA  
TGC GGAA CGGCATATCTTAACAAAAACGGCAGCCTC



**SEQ ID 6762**

LFACLFVPIVARVPKIPPHETREGENEVQADDGGVKLPTLIIVYRSRTGFEDVGKRGGRQRETCRLDQVWSEMFALERGHAEQSGRZEGGVGKDECDQDQDVHGCCHDGLSVWALSAMPSELE  
CGTAYLNKNGSL

**SEQ ID 6763**

GTGTGGCTGCAGCATTACGTTCTACCTGCCCTTTCTTTGTTTACTCTCATGTTTCAGGTTTGGAAGATTTAATTAATGTGCCCTTCGGTATAAAACCCAACTTTTCAGACCCAATACACCATATGTGGTG  
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AGGACGGCGGAATCTCTTCAATATTTACATGAATAGGTACACCCATCAAGACTTGCAGTCACTGTTCCAAACTTCGATATCTCTCACTTTTTCACCGATAAACACACCCGGAGCAGCGGGAG  
TGAAATGGTAATGCGTCGACGATTTTGACGGGCGCTCAATAAATTAATCTACGACCAACCCAGCAATTTGGCCAAATTTTTCGACCAATAATTTGCGAACATCGATATCTCGCTTCAAACAGTAGAAA  
AGTCGGTACTTTTAGCAAAACCAATTTTGAAGCCAGCTCTTTAGTTACCGCCAGCGGAAAGCCTGTAGGGTTAATCTTTTGTCCCAAT

**SEQ ID 6764**

VGCSITSTCLSLPTLMFRGFRFNIAFRINPNFQTYTTCGVRFAGCIYIYC\*SMQWHAFTTIPFATGNIRTIQT\*SHNLNAPSTKTHCILHCSFHSHTETLNAPFQLGDTVSNNLSIQL  
RTANLFNIYMNRYTHQDLQVTFQNFDDILFTFDNHTFTSGVGNACRFCAFNMYSTNRISIQFLQIIANDILLQNSRKVGTFKPP\*SPVFSYQAKACRVNLLSH

**SEQ ID 6765**

GTGTCAAGAGCTGCCGTTTTTGTTAAGATATGCCGTTCCGCAATCGAGTTCAGACGGCATCGCCGCCGACAAATGCCAAACAGAAAGCCCATCATGACCGCATCCATGTACATCCCTTTTGG  
TCTTGGCACTCATCTTTGCCAAGCCCCCTTCTCTCAGACAGAGCTGTCGGCGTGGCCGCGCTCAAGCGCAAAATTTCCGGACACCACTGATCGAGCTGGCGCGAGGTTTCGGCGCTGAC  
CGCCTCTCTGCCATACATCTCGAAATCCCGTCCGGAGCGGTACACAATCAGGGTTGGAGATTTTACGCCACCGTCGTCTGCCTGTACCTCATTTTGCCTTCCCGTGTTCCTCGCGCGG  
TATTTTGGCACACGCGCAACAGGGAA

**SEQ ID 6766**

VSAAVFFVKICRSAMQFRHRRRQC PNRPKPIHTASMYILVLALIPANAPFLTTRLFVGAALKRKHFGHHLIELAAGFALTASLAYILESAGAVHNGHEFYATVCLYLIFAFPCFVR  
YFHTENRE

SEQ ID 6767

GTATCCCACTGTACACATTGATATGACAAGTTTGTGTTTTCGATGCGGTACCGCGACCTTTGGGGCGAGCTTGA AAACGTTTCAAGCTTGGACCTTTGTCAACAAAGATAGTTACCACTTTTCA  
AGTTTCATCAATGTCGCCACCGTTATATGCTCAGCATTAGCAATAGCTGACTCCAATAC TTTTTTGATCAGCTCGGCACCTTTTTTAGGCGTGAAAGCCAAAATATTCAAAGCTTGGGCAA  
CGTCTTTACCAAGAAATCAAATCAGTACCAAAACGAGCCTTTTGAGCAGAGATACGGGCATTTTATGTTGTGCAATTACTCTCAT

**SEQ ID 6768**

VTHCHIDMTSLFFDAVPATFGASLKTFAQWTFVNKDSYHPQFINVRTVIMLSISNS\*LOYFFDQLGTFFFRAESONIOSLGNVFTTNOISYOTPSLLSRDTGIFMLCIYSH

SEQ ID 6769

ATGCCGCAAGCCTCTGCTCTCCAATTTCCCTCCGCGGAAGCCCTGCCCTTCGGACTTCCCTTCACGGCTGCCGGAACCTGATTATGCTGATGAAAAGCGTATGCGTTTATTGTTGAAGAAG  
GATTTCCTTTAAGCGAAAAAGACGGCGGTTACTGGACAGCCGTCAAATCGACCACGCCGTTTTCGCCAATATGGCGTTTGGCGAACTCGGGCTGATTGTCAGCGATATGGATTTCGACGCT  
GATTACCATCGAATGTATCGATGAAATTCGCGCAGGTGTGGGTTCGAAAGGCAAGTAGCGGAAATTACCGAGCGCGCCATCGCGGAGAGTTGGATTTCGACAGCTCTTTAGCGACGCC  
GTTCGGTCTGTTGGCGGGATTGGACGAACAGATTTTGGCGGACATTTATGAAAACGTTTGAAGCTCTCGCCCGTCCGGAATTTTCTGTGGACGAATGCAAAAGGCACAATGTGAAATTC  
TTCGTGCTTCGCGCGGCTTCACGTTTTCACCGAAAGGCTGCAACACCGCTCTCGCTTCGAATACCAACACGCCAATATTTTGGAAATTGAAAACGGCAGTTGACCGGCCGCTCTGAAAGG  
CAGAATCATGACGCGCGAGGCAAGGCGGATTATTCGCGTCAATACCGACGCCGCTCGGATTCGACACCGCATCAGGTTGTGGCGATGGCGACCGGTCGCAAGCATATTCGATATCTCAA  
GAAGCGGGCATAGGCGTGGCTTACCGCGCAACCGAAAGCGCGGGCGCCGCGGATGCTTATCACTTCGCGCGGTTTGGAGCGTGTACGCGCGCTGTTCGGA

SEQ ID 6770

MPQALVLPFPSEALPSDFPSRLPEPDYADEKRMRFIVEEGFSLSEKDAALLDSRQIDHVLVPMAPGELGLIVSDMSTLTITIECIDETIAGVGLKGVAEITERAMRGELDFGQSLRSR  
VALLAGLDEQILADIYENVKLSPGAFFLDECKRHNVKFLVSGGPTFFTERLQRLGFEYQHANIIEIENGRLTGRILKGRIIDAQAKADLLREYRSRLGLQPHQVLAMGCDGANDIPILK  
EAGIGVAYRAKPKARAAADACTNFGGLERVRGLFG

SEQ ID 6771

GGTATTTCGATAGGCCAACCGAATCGTCGCCGCTTTCTCTTTGAACGAATCGATTTCGATCCGTCGGGCTCTCTACGAAGGCTATCACGTTGTGCGCGTGTTCATCAGCGCGGCTTCGCGGACGAGCTTTCGCGCCCTGCCGCTTCACGCGCTCGCAGGCTTCGTAGGCATCGTCCACTTCAACCGCGATGTGTCCGTAGGCGCTCGCCCAAGTCGTATCGTTTCGTATCCCAAGTTGTGCGTCAGTTCCTCAAAACCGTCTGTGCGGTTTCGTGCCGCTAACCGACGAAGGCAAGGGTAAATCTGCCCTTCGGGATAGTCTTTTCGGCGGAGCAGTTTCAT

## SEQ ID 6772

GIRIGNRIVAAFLNELDFASVGVFYEGYHCAVTHQAGFADDVSALPLHAFAGFVGIVHFNRDVSVGVAQVVSFRIPVVROFONRAVGFAVTDGKGSAPGTVFSADDPH

## SEQ ID 6773

ATGGAATAATATATTGCTGTTCTGGTGGGTACAGTCAATCGGTTTCTTTGGGGCTACCTGCTGATTATATCGCGCTTTTGGGTATACGGCGCTGTTTTTATACGCTGTATCTTGGTGGCGCGCAGATTACCAAGCTGGCGCGGGATTCAAAATCCGATTATCGCGCGCTTGTTTGGCCAAAGGTGATAAAGACGATAAGTCTTTATCGCAGTTTCAGGCGTTGGCGGTGCTATATCCGCGCAATCGTACGGGCAACGTGCGCGGTGTGGCGACCGCATTAACGCAAGCGGGCGGGTGCATTTTTCGATGTGGCTTCTGCGCGTTTGGGGATGTCACGATTTTGGCGAAGCACTGCTGGCGCAGAAATACCGCGCTGACGCCACGGCAAAATACATCGCGGGCGGGCTTTTATATTACGACCGGTGACTCCGAAATACGGCAGGGCGCGCGCGCTTTCCTGTCGGGCTTTTCTCCA TCGCGCTGATTGTTCGCTTGGGCTTTATCGGCAATCGCATACGGCAAACTCCATCGCTTCTGCGCTTACCAATTGCATTTATGATTGCTTCTTTGGCAGCTGGCATTTGTGTTTGGCGGCTTTCGCGGATGGTGTGATGTGGCGGCGTGAACCGTATTGCGCAATATTTGCGCGGCTTTATGCGGTGCTTTATGTTGATTTGTCGCGCTCGTATTCTGTTGAAATTTTCGCACATATTGTGCGGATGTTCAACCAATCTTTACCGCGCGCTTCAATCCGAGGCGGCTTTTGGCGGTGCTGCGGATATCGGTATCGGTGAAGCGATACGTTTCGGCTGGCGCGCGGTCTGT TTTCCAAGCAAGCAGGTATGGGTGACTCCGACGCCACCGCACTCGGATGTGAAGCATCTCTGTCAGCAAGGTATGACGGCATTTGTGCGTGTATTTATCGATACGATTTTGGTATG TACGGCTACGGCATTGATTAATCTGCTGACCGATGCCAACCTTTTCGGCGAACAGGGCGCGCGGTTACTCAATTTGCTTTTACAAGGCAITTCGGGCTCTCGGTGCGCAATGCTTGGC ATGTGCTGACCTTCTTCGCTTTACGACCAATCTCGGCTGTTATTATTCGGCGAGTCCAACCATCCGTTTCTTTTCAGGGGAAGCACTTGGGCATCTATCGCGCATTTGTTCTGCTTG CATTATGATGACTACCTGTAGTGCAGAAAAAGCGGGACAGGATTTATCCATATCAGATGAATTCACAGGATTCACAGATTCACAGAACAA

SEQ ID 6774

MENILSLVGVGNRFLWGYLLIYALLGIGLFFTLTYLGAPQITKLGAGKFSVPGGLFAGKDKRDKSLSQFQALAVASIAQIGTNVAGVATAITAGGPGCAIPFHWLSAVLGHMSTIFARALLA  
 QKYRVVSHGKYIGGPAYITHGLTPKIGRGAARPLSGPFSIALIYALGFIGNATQANSIASAVTIAFDVPSLAVGVIVFAVLAGHWVITGGVNRILANLARFPVPPMAVVYILCAVVILFEPSD  
 HIVPMFNHPTAAPNPEAVLGAAGIGMREAIRFGVARGLFSNEAGMGSTPHAHATAADVKHPVQCGMTAFVGVFIDTILVCTATALIILITDANLSGEQGAAVTQPAFNKAPPGFGSQLLA  
 MCLTFPAFTTIGWYTFGESNIRFLFRGRHLGIYRALVLLAIVLTGLGKVDLVVSLDMFNGFMVPIPLNIALFLLRKEIRATYDDYLMKKKAGODLSVOYEPHEPHDEQ

SEQ ID 6775

TTGGAGGACAGGGGCTTCGGCGATACGCGGGCTCAAAAAATGCGGATTATATAAGTTGAAACGGCAAGAAATGTTACGGGGGGCTGCCTGCAATCGGAAACGACTTCAAACGCAAAACGGCAGTATGTCTGGACAACACGGGAAAAATCGCGCACTATTGCCAGCCTGATGAAATTTCTGTATTAAGGGGAATTATC

SEQ ID 6776

LEDEGLRHNGGSKNADYIVKROMLRACLOSENDFKRRKROYVSDITGKCATTASLAKIRYEGHI

**SEQ ID 6777**

TTTCCTTTTAGCCTTTTATCGGCCAGGTGGCTTTAAAGGTACGGGCTCAATGAGAAATCGCCTAAATTTATGACCAACCAATATTGTGCGCTGATAAACACAGGCACATGGGTGCGACCGTTG  
TGCACGGCAATGGTCAGACCGATAAAATCAGGCAGAAATGGTAGAACGACGAGACCAGGTTTTTAATCGGGCGTTTGTGCTGTGCTTGGCGGAACAGCATCTACTTTTTTCAGCAAAATGCAGGT  
CTACATATGGGCCCTTTTTCAATGAACGAGCCAT

**SEQ ID 6778**

FLFSLFIGQVAFKGTGQ\*EFA\*FMTNHIVADKHRHMGATVVHNGNGQTDKIRQNGRTTRPGFNRAFVVACANSIYFFQQNQVYTWAFQ\*TS

**SEQ ID 6779**

ATGAAAAATCGGTATCCCAACGCGAGTCATTATATCCGGCGAAACCCGCGTCGCTGCAACGCCGCCACCGTTGCGCTGCTGGGCAAACTAGGCTTTGAAACCGTGTGCGAAAGCGGTGCAAGTGTGCGCGCAAGTTTGGACGATGCCGCTTACCAAAACGAGCGCGCAACCGTTGCGCGCAAAAGCGCGGGTTTGGCGCGTGCCTTTTAATTTATTAAGGTCAACGCGCGCTCCGAAGGCGAGCTGCCCTGCTGCTCAAGAAGGTCAAAACCGTATCGAGCTTCTCTGTCGCGCGCAACAGGAGCTTTGTCGAGGCTCTTGCGCGCGCAAGAAAGTCAACGCGCTGGCGCATGGATGTTTCCCGCATTTCCCGCGCTCAGGCGTTTGGACGCTTTGTCTTCAATGCGAAACATCAGCGGCTACGCGCGCTGATTAAGCGCGCAACGCTCTGCGCGCTTCTTCAACCGGTCAAACTCATCTGCGCGCGCAAAAGTGGCGCGCTGCGCAGGTTTGTGTGATTTGGCGCGGTGTGGCGGGTTTGGCGGCAATCGGTACGCGCAATTCGCTCGCGCGCATGTTGCGCGCTTCGATACCCGCTTTGGAAGTGGCGGAACAATAATCGAATCGATGGCGCGTAAGTTCCTGAAACTCGACTTCTCGCAAGAAATCGGGCGGACGCGGAGACGCGTACGCGCAAGTGATGAGCGACGAATTTATGCGCGCGGAAATGAAGCTCTTTTGGCGCAACGCGGAAAGATGGACATCATCATCACACCCCGGCCATTTCGCGCAAAACCCGCTCCCAAGCTGATTACCAAGAAATGTTGGGAAGAAATGGAATTCGGAATCCGTCATCGTGAATTTGGCGCGAGCGGGCGCAACTGCGAACTGCACTACCGACCGGCGAAATTTGTGCTGAACCTCGGCAACCGGCTGAAATCATCTGCGCTACACCGCATGGCAAAACCCGCTTGGCCGAGCATCTTCCAGCTTTTTCGACCAACATTTGGTGAAGCTGACCAAGCTGTTAAGCCCGCAAGCAAGACGCGGAAATCAGCTGCGACTTCGAAGACGTTGATTTATCGCAATATGACCGTTTACCGCGGACGGCGAAATCACTTCCCGGCTTCGCGCGATTCAGGTTTCCGCGCGCGCGCAGCAAAACGCGCTGAAAAAGCGCGCTGCGCGCAAGCCCGAGCCGAAACCTGTTTCCCTCTGTGAAAAAAACTCGCGCGCCCGCGCATTCGCGCGGATTTGTGTGTTGCGGTCGCGCGGTGCGACCCGCGAGCATCTTTGAACCATCTTATCGTCTTCGCTCTCGGCTCGGCTCATCGGCTACCATGTCGTTTGAACCTGACCATCGCTGCGACCAACCGCTGATGTCGTAACCAACCGCATCTCCGCGCATCATCGTCTGCGCGCTGTCGCAATCGGTCAAGGCAACGCGCTCGTTTCTGCTGCTGTCGTTGTTGCTGCACTCTGTATGTCGCGGATCAATATCTTCGCGCGCTTTCGCTGACACCGGCTATGCTGAAATATGTTTAAGAAAGGG

SEQ ID 6780

MKIGIPRESLSGETRVACTPATVALLGKLGFEITVVESGAGLAASLDDAAAYQTAGATVADKAAVWACPLTIYKVNAFSEGEPLLLKEGQITVSFLWPNQNEALVEALRAKKVNALAMDVPRI  
 SRAQALDALSSMANISGYRAVTEAANAPGRFFTGQITAAKGVPVPAQVLVIGAGVAGLAAIGTANSLGAVVRAFDRLRLVBAEQIESMGKKFLKLDLQESGGSGDGYAKVMSDEFIAAEML  
 PAEQAKEVDIIITTAIPGPKAPKLIKTEMVESMSSGSVITVDLAAATGNCBELTRPGLELVTNGVKKIIGYTDMANLAGOSSQLYATMLVNLTKLSPNKGTEITLDFEDVYIRNMIVTRD  
 GEITFPPIQVSARQPQTSKEAAPAKPEKPVPLWKKLAPAAIAAVLVLWVRVAPAAFLNHFIVFVLACVIGYHVWNVNSESLETPMLSVTNAISGITVVGALLQIGQNGFVSLLS  
 VFAVLJAGINIPGQVATRMMLPAKKE

**SEQ ID 6781**

ACCTTTATTTGAGTAAACGGCGACGAACAATCATATATCCGTGCGTTTGTATTACGAGTGCAGTACGCTTTAGCAGGAGTACCCCATGGACTAACCGGTTTCGGGGCTTCGCCGGTACGG  
CCTTCACCAACCACCATCGCGGTGATCGACGGGATTCATGACAACACCGCGTACGGTCGGACGAATACCGGCCAACGGTTAGCACCGGCTTTACCGATTTTTTTCAGCGTTTGCTCTTGCT  
TACCGACTTCACCGATGGTCGACGGCAATCTACGTTGATTTTACGAACCTTCGCCAGAGCGCAGACGGACTTGTAGCGGTATGCACTTCTTTAGCCAAACAATACCGCAGAAGCACCGGCAGA  
ACGTGCGATTGTGACCACTTTACCGGGTTTCATTTTCGATACAGTGGATAGTCGTACCAACCGGGAATGTTCGCCGATCGGCAGGGGTGTGCCCTACTTTGTATGGCAGCTTCAGCACCGGAAACC  
AATACGACACCGCGCTTGAATACCCGAGGAGCGGATGATACCAACGCGTCGCCGCTTCGATACGACCAACAGTGCAGATGAAGGCAGTACGGTTAGGATCGTATTGCCATACGCTCTACTTTTAG  
CAGAAATGGCGCTCTTTGTACGTTTAAAGTCTCAACACGTCGTAATGGTTTATGACCGCCGCTCTTTGTACGGGTGGATATGACCATTAATGTTCAGCCGGCAGTATGAAATTTTCTT  
TTCAAGCAAGGGTGCATAAAGTGCACTTTGTGCAAACTTGTGTTACACCGCGAACCATTCGCCGACGGCCTTCAGAGGTGCGGCTTCATTTTAAGCATTTGCCAT

**SEQ ID 6782**

TTFTVATNMNHHIRAFVITSVAFAFSRSTPFTNRFAGFAGTAFTTTMVRVIDGHDNTAYGRINTAFTVSTGTFDFFQALLFVTDFTDGRTAIYVDFDNFARQDTLSVCTFFSQQYRRSTGR  
TCDLSTPTGFHFDTVDSTRMGNVADRQGVAYFDGSPSTGNGYDTGLNWTARSDDVFTLAVCIAQQCDGSGTVRIVPDTLYFSRNAVFTFKVYNTVMVFMATAAFVTGGDMTIIIVTAGSRIFL  
FKQGCIRCTCFVOTFCYHANHAATAACRGRLHFNDCH

SEQ ID 6783

[illegible]

SEQ ID 6784

MWSDDLNLMPALPEVALLSLVLVLLPADLWASDDKCRWTHYGALATVAVTAAVQLAVWBGQSTSSFGMYIADGMSRLAKMVLVYALFVFLVYAKPYNVQVGIKGEFVTLSLFALLGMSV  
MVSAGHFLTAAYIGLELLSLALYALIALRRDSGFAAEALKYFVLGALASGLLLYGISHWYATGSGLEFAGVLASSFNEEANEWLLKLGLVFIIVAVAFKLAGVPPHMMMPDVYHGAPTSVT  
ALVGTAPKIAAVVFAFRILVTGLGTVHHDMSLMPALLAAASLLVGNLAAITMCTNIKRLAYSTVSHMGFILLAFMAGAVGFAAGLYYAITYALMAAAGPGVILVLSGDGNECENISDLAGL  
NOHRVWLAFILMLLVMSMAGIPLMGFYAKFGVIMALLKOGYVWLVSFAVVMSLVGAFYFLRVVKVMYFDESGRARPAAGGNNAKSLLSVNALLLVLWGTMPOTVLDWCAKALEXTL

**SEQ ID 6785**

ATGACTTTCGCCCTATTGGTCGATTCGCTGCCCTATTGCGCGCTTTTGTGTGGGGCGATGCGCAAAAAGCGGGCGGATTCCGGTTTAAAGACAACCAATCTCGCGGTTTCTCGG  
CACATACGCAAGCGCGAGCCGCCCGTGGCCACGCCGCGCAGCAAAACGGTTTGAAGCCCTTTGCAACCGTTTGCGCCCGCGGTTTTCGACGGCACACGCAACCGGCAATGCGGACAAGCAAC  
CGTCAACACGCTTGGCGGATTTGTCATCTCTGCTCCGCCCTCGCCTTTATCTGGTGTACATCGCAGACAAAGCAGCATTGGCTCGCTGATGTGGGCGGGCGGATTTCCTGCAACCGTCGGA  
CTGTTTGTGCGCGCTGCT

SEQ ID 6786

MTFAFYWCILLIACLLPLFCAAYAKKAGGFRFDNHNPRGFLAHTQGAARAHAHQNGFEAFAPFAAAVLTAHATGNAGQATVNTLAGLFIILFRLAFIWCYTADKAALRLSLNWAGGFACTVG  
LFAVAA

SEQ ID 6787

TTGAAACAGATGCCGCTGAAAACACGAACGTCAATTTTTCAGACGGTATTGAAAACAAATCATCGAAAATCGGAGAATTTCATGTCTTCAGGA

SEQ ID 6788

LRKOMPSENTNUNFSDGIENKSSKIGEFPCLODS

**SEQ ID 6789**

TTCTTATCTGCAGCTGCAGCAGCGGCTTCAAAATCCAACCTCTTGACCGTCAACCAAGCTTACATAAGCTTTTTTAAATCGCTGGCGGACCCAAAATACGACCAAAACGCTTAGTGTTC  
CCTTTAGTGGTTAACGGTAGTTACAGAAGCAACTGGAACACCGAACAGCAGCTCGCAGCAGCAGCTTTGATTCAGGTTTGGTTGCATTTGCCAAGACTTTAAACGTCATTTGGTTGCATTTT  
CAGCCAAACAGTGTGCTTTTTTCAGAAAACGACAGGCACCAAGATTACTTGAGTCAAAACGTTGTTGATTCATACCCAT

**SEQ ID 6790**

FLICSCSSGFIQLLTVNQAYISFFNLAATQNTTKTLSFAPSGNGSYRSNLNTEQQLDSSFDPRFGCICQDPKRHLVAFPSQYVAFPRNDRHQDYLSQTLLETH

**SEQ ID 6791**

TTGGGAATAAGTAAAGAAGGGGGGAGAGTATTCATTCCTTCCTTCAGACGACTTCCTAAAACGCTGTCTGTAAAGACCAACCCATACAACATATATTTTTATTTTAAACCAAGGTTAACCA  
CTATGTTTTCCTCAACTACTACTACGCTGGCAAATATGATACCCATCGCCGAGCGGTGCTGGTTTGGGCGACCGGTAAAGACAGCCGCTGGCGCGGTGCTCTGCCTCATGGG  
AGCGCTTCGCGGTTCTTCGTGAACGCTGCCTCTTCATCCGGTTTCGACGGTTTGAGCGCGCGGCTCAATTTACCGAGTTCACAGATGGATGTTCCGCGCTTCGAAAACTCAACTACGCAAT  
GGCGTGAGACGCTTTACAGTGCCTTTATCATCTTGAACTGGCTTTATACGCTGCTGGTGGTATTTGGCGGATGATTCAGGAAGCTCCGCGCGAGTATATGCGGCGCAITTCCTGA  
TGATGTCGGGTTTGATTAAACGGCGCGTTTGGCGCGCAGGATGCGATTCGTGTTTATGTGTTCTTCGAGGGTATGCTGATTCCGCTGTACCTGATTATCGGTATATGCGGCGCGCGCGCG  
CGTCTATGCGTTCGGTCAAGCTGTTCTCTATACGCTGACGGGTTGCTCTTGATGTGGTTGCCATGGTTTACCTGTACTATCAGACAGCGAGCTTCTCTATTGTGCGATTTCCAAAACATC  
AAACAGCATTCCTGTTGGGCGTACAACAGCTTTGTGTTGTAGCGTCTTCCTGTTCATTTCGCGCTAAGAGTGGCGATGTTCCCGCTACACATCTGGCTGGCGGATGGCCACGTTGAAGCGCGCA  
CGGCGGTTTCGATGGGTGTGGCGGCAATTACGCTGAAACTGGGTGCTGATGGTTCTTCGCGCTTTATCTCCGCGATTCGCGGAGCGGCTCGCTATTTGCCCCGTAATCATCGTATT  
GAGCCTGATTCGCGTAAATTATATATTCGATATGCTGTGGCCCTGGTGCAACAGCATGAAGAAACTGTGGCGCATTTCTGCTCATCAGCCATATGGGTTTGAACGCTGGGATGTTTGTGTT  
GTTGACGGGCAGTTGGACGACTGGCGGTTGAAAGCGCGGCTCATTCAGATGATTTTCGACGCGCTTCGTGTCGGCGCGCATGTTTATGTGCATCGGCGTGATGTACGACCGCTGCACACGC  
GCAATATTTCGCGATTAACGCGCGCTGTGCAATGTGATGCCAAAGTTTGGCGCGTTATGATGTTGTTGCGTATGGCGGAACGCGCGGCTGCTGCGCATTCGCGCTTCGTGGCGGAGTTTAT  
GGTGGTTATGGGCGCGGTCAAAGTGAATTTTCGTTGGGTGGCGCGCTGGCGGCTATGACGCTGATTTACGGCGCGCTTTATACCTGTGGATGTACAAGCGCGTGAATTTTCGGCGCGATTAC  
AATCTGCACGCTTCCGGAATGAAGACATCAATTTGGCGCGAGTTTGCGATTCTGCGGTTTGGCGGTGCTGTTTGGGATGGGCTGTATCCGAACGCATTTATCGAAGTGGTGATC  
AGGCGCGAACCATGCTTTGTTGCCATGTGGCGCAAGCAAGATT

SEQ ID 6792

LGISKEGGRVFPSPRRLEPKTLSVKTNPYNTIFYFNHRLTTMFSNYLLSLAIWPIAAGVLVLATGKDSRAPLARVLAFMGALAGLVLTPLPFTGFDRLSGGYQPTFEHENTPILKINYAL  
GVGDISVLFIILNAFTITLVLVLAGNEVIQRRPAQYMAAFIMMSGILINGAPAAQDAILPYVPFEGMLIPLYLIIGVWGGRPRVYASVKLFYLTLTGSLMLLVAMVLYIYQGSFSIVDQNI  
KQIPLGVQQLLEFAVFLSPFAVKVPMFVHTWLPDAHVEAPTGGSNVLAATTIKLGAYGFLRFILPIMPDAARYFAPVITVLVSLIAVIYIGMVALVQTMKKLVAYSSISHMGFVTLGMFLF  
VDQLDDWALKGAVIQHISHGFVASAMPNCI GVMYDRLHTRLNADLDGGVNVNKPFAFPMKPLFGMANGLPATSGFVGFMVNVKGAVNVFVWGALAAHTLTLYGASTLHMYKRVIPGAH  
NPHVAAEMDINCEFAVITLAVLAVAVLNGLYPNVIEVHQAANDLALHVAOSKI

**SEQ ID 6793**

ATGTCCTTCAGGACTCTGTAACAGCGGGCGTATATCGTTGCCGCAATTTTATTATCATCTTCTCACTGGCGGGCTGTGCTAAACAGGAAACCGCCAAACGGGGCTGCTATTCCGGTATCGCCGGTA  
TGCGCGGTGCCCCCTCTTCGTAAACGGCTCTTTTCGCAACAATACCCAAGGCTGGGCTGGATTATCATCGCCATGCTCATCGGCGCGGCAATCGGCATCCCAAAGCCAAAAAGTAGAAATGAC  
CGAAATGCCCGGAACGTATTGCACTTTTCGCACAGCTTCGTGCGGTTGGCAGCGCTTTTGGTCGCGTTCAACAGCTACATCGAGCGGGCAACGTTTCGCACGATATGCAACACCTTCCATCTG  
GTGGAAGTCTATTTGGGCATTTTTCATCGGCGCGGTAAACCTTTACCGGCTCACTGGCGGCATTCGGCAAACTCAACGGCAAAATCAGCAGCAGCCCGCTGCACCTGCCCGCCAAACACAAGC  
TCAACAGCTTGGCGCTCGCCGGTATCGCTTGTGTGTGTCGTCGTGATTTTGTCGCGATTTGACGGCATGACGGCTGACCTCTTGATATTGACCTGATCGCCCTCGCATCTCGGCTCAACCTTGGT  
TGCCCTCATCTGGCGGGCGGGATATGCGCGTGGTGTGCTATCTATGCTCAACTCTTACTCGGCTGGGCGCGCACGGCGGACGGCTTTATGCTCTCTCAAAGCTGCTCATCTGTTTACCGCGCG  
CTGGTCGGCTCAAGCGGCGCAATCTGTCTACATTTATGTGCAAAAGCCATGAATCGGTGCTTTGTTTCCGTGATTGCGCGGCGGTTTCGGCAGCGACAGCGGCATATGCTCTTCCGCGAGCC  
AAGAGATAGAGGAATACCGAGAAGTCAAAGCTGCGGATGTTGCCGAAATGCTGAAAGCGCAAGCAGCGCTATTATCACCCCGGGCTACGGCATGGCAGTGGCGCAGGCACAATACCCGCT  
TGCCGAAATCACCGAGCTTTTGCCTAAAAACGGCATGGAAGTACGCTTCGGCATTCACCCCGCTCGCGCGCGCTGCCCGGTCAATGATATGCTGCTCGCGAGGCCAAGTCCCGTAC  
GACATTTGTTTGGAAATGGACGAAATCAACGACGACTTCCCCGAAACCGATGTGGTCTTTGGTGATTGTTGCGCAACGATACCGTCAACCTTGCGCCCAAAACCGATCCGAACAGCCCGATTG  
CAGGATGACCGGTTTGAAGAATGGAAAGCAAGAAGTGTGCTGTATTCAAAACCGCTCGATGAACACCGCTACGCAAGCGCTACGCAAGCGCTACAAACCCGCTGTTCTTCAACGAAACAGCGTGATGTG  
TTTTCGGCGACGCAAAACCACTGTCGGGATTTTGGCGGAATGAAAAA

SEQ ID 6794

MSSGLVTAAYIAAILFIPSLAGLSKQETAKGCGSYGIAGMAVALFVTVPSDNTHGLWIIIAMLIGAAGIHKAKKVEETPELIALHSHFVGLAAVLVGFNSYIEPGNVSHDMHTIHL  
 VEYVLGIPIGAVTFTGSLAAPGKLGKISSPQLPAKHKLNALALAVSFVLLLVFVGIDGSGFILLDTLIALAFCHLVAISIGGADMVTVVSMINSYSGWAAAAAGFMLSNDLLIVTGA  
 LVGSSGAILSYIMCKAMNRSFVSVIAGGFGSDGSISSGSGQEI EEEYEVKAADVAEMLKGASSVIITPGYHMAVAQAQYPAEITELLRFNGIEVRFGIHPVAGRLPGHMNVLLAEAKVPY  
 DIVLEMDIENDDPETDVLVIGANDTVNPAQTDPNPSIAGMPVLEWKAKEVVVFKRSMPTGYAGVONPLFFNENSMVCPGDAKKTVDGLIAELAKK

**SEQ ID 6795**

TACCCATTGCTCCTCTAAATTGTGCAACCGCATCTTTAGTGATGATTACTTTTTTATAACGCAGCAAGCTGTAAGGATCAACTTGTGTAGCTTCCAAAACCAATACGTTTGGCAAGTTGCGT  
GAAGCCAACTAAACATCTCTGTCGACGCCGTTTGGTTACAAACAGCACATTGCTCCAGAGCCAAATTTTTTACTTGTTCGGCAAAACTTTGGTTTGGGAGTTTCGGCACTCAACGCCTCAA  
TCACAAACAAACGCTCGTCACGCGCCAAATTGGGACAGGATAGTCGCCATACGGGACGGTACATTTTACGGTTTACTTTTTGAGTGAAGTTTTCTGTGGGTTTGTTCGGGAACGCGCGACC  
GCCTTTACGCCACGCGGAGAAGAAGTCATACCGGAACGGGCGGGCGGTACCTTTTTGAGCCATGGTTTTTGGTTGAGTGTTTTACTTCGGCACGGGTTTTTGTAGCACGGTTACCA  
GACGGGGCTTTGCCAAGTAGGCATTTACAGCTGGTGAAACCAACGCTTCATTTGTATTTCGGGGCAACAAAGCATCAGAAACAGACAGGCTGCCTGAAACTTGTCTTTAGCGTCAATTA  
CTTCTGATTTCCAT

SEQ ID 6796

YPLL<sup>LL</sup>LCNRI<sup>FS</sup>DDY<sup>FF</sup>ITQ<sup>Q</sup>AVRI<sup>NL</sup>SPQN<sup>QV</sup>YV<sup>VQ</sup>VA<sup>^</sup>SQV<sup>NL</sup>VE<sup>FP</sup>GY<sup>KQ</sup>HL<sup>LS</sup>Q<sup>S</sup>I<sup>Y</sup>FL<sup>PK</sup>NG<sup>FG</sup>SG<sup>FS</sup>Q<sup>RL</sup>NH<sup>KQ</sup>TL<sup>VT</sup>RL<sup>Q</sup>G<sup>D</sup>SR<sup>HT</sup>GT<sup>VH</sup>FT<sup>VY</sup>FL<sup>SE</sup>V<sup>F</sup>VG<sup>FV</sup>RR<sup>ER</sup>AT<sup>^</sup>  
AFT<sup>PE</sup>ORRR<sup>SH</sup>TG<sup>TA</sup>AG<sup>TL</sup>TE<sup>WF</sup>GG<sup>^</sup>V<sup>F</sup>Y<sup>FG</sup>TG<sup>LS</sup>TV<sup>TR</sup>AG<sup>VC</sup>GI<sup>YQ</sup>LV<sup>NR</sup>FI<sup>TV</sup>FA<sup>GS</sup>BI<sup>EN</sup>RO<sup>AA</sup>^NL<sup>FS</sup>SE<sup>VN</sup>Y<sup>PO</sup>PE<sup>^</sup>

SEQ ID 6797

TTGCAAGAGTGTAAATTTATTTTGGACAAGATTTCGGATTGTCTAAAAAAGAGGCTATTTCGGAAGTGTGAAATGGCTCCGTCCCATTTGAAATTCACACTGATGGTAGCTCAAGGCA  
TTCAGGGTTTTCATCTAAAGCTGTATTTTGGAGAATGATAAGAATGAATATTATGCTTTAATCGGTTCTTCAAATTTGACTCATGCTGCGTTTAATAGCAATTTATGAAGCAAAATTTTT  
GACTAAAAATTTCCGAGCAGGATTTTATAAAGTCAAATCTTGGCTGATGAAATTCGATGAAATCTATCCCGGTATCGGAAGATTGGCTTGAGGAGTATCAGGAAGCTGAAATTAACATAT  
AAGAAATCACTGTGTAGACAACTAGTGATGGATAAGTTATTTATGAGAGTGCCTAAATTTAATCAAGAACTGATTCGCGCACGGAGAAACGAGATGAGAAACCATCAAACTGTGTGTAATC  
AATTAATAAAATCTTTATTAAGCAATGTGCAGCAGGAAAAATAGACATAATGATTTTATGCGGAATTTAATAAATTTATGGTCTTGGAAAAAGCGAAATTAAGGAGAAGGGGTAGGCAATFCG  
TTTTCAAGATAAAACGTGGAAGGACGGGTAACTTCTCAGATTTTAGAAAAATTATGCATTGCCATCCAACTAGTTTTCGATGCTCCACTTACTGAGAGAGATAATGTGGTTGCCAAGCAA  
ATTGATTTGGCTAAAGAATGTGGGGTTTCCACTCGTGGTTCAGTTTCTGAAATGCTTTGTCAAGAAATCCAGATAGATATCTGTTTAAATGCTCCCAATTAATAAAATTTTATAGAG  
AAAAATAAATTAAGTCTGCAAAAGGAGCAAGCAAGGAGTCCAAATTTATGATTTTAAGTATGAAGTTAAGAGTTTACTAGCTATGCAGTCAAGAAATAAAAGATTTTGGCTGAATTAGATGT  
TTTAGTACAGGCAGATATCGCAATCGTACAGATATTGATTTGGGAA

**SEQ ID 6798**

EQ ID 8798  
LQEPFKIPGQDPGLSKKRAIRKVLKWLPSHLKPTLMVAQIGCFHPKAVPWKNDKNEYALIGSSNLTAAFNNSYEAANILTKISEQDFIKVKSNADEIAMKSIPIVSEDWLEKYQEAETNY  
KKS2TVRQSVMDKLFMFMPIYNNQBELLAARRKQMRNHQTVCNQLKNLTKQCAAGKIDNNDYGFENKLSNWSKSENKGEVGNRPQDKTWKRTGKSSDFKLCIAIQSVFDAPLTRDNVVAQI  
TDMKFCQGVSTRSVSFSEMLCOEYEDRYPVLNAPTKPKPLEENKPKSAGASEGSKYIDLSMKLRALLAMQSEITKDIAELDVLVQAEYRNRTDIDME

**SEQ ID 6799**

CGACCACTACTTTCACGCTGGGAGCAACTACAACATCGCTGTGTGACCGCACCCGGGAACAGCACCCCTTAAACCAACAGCAGTTGGCGTCTGCATCAACACGGGACAACTTCCAAATTTTGAACA  
GTTGCTTTTGGTGTGCGGTATTGGCCGGGCATGCGCTTACCGGGGAACACGCGACCCGGGTCTTGGCGCATACCGATAGAGGCTGGAAACCGGGTGAGAACGGGAGTTACCGTGGGAAGTAC  
GTTGGGCACCGAAGTATACAGCTTGATCGTGC CGGGAACAACTTTACCTTTAGAGGTACCGGTATACATCGACCAAGTTGACCGACTTCAAACATAGAAACGGTGATTTTCGTCACCGGCTTT  
CAATTACAGCCAGTFTTTCTTCAGTCAAAGCAAATCAATCAAACCGCAGCCGGCTTAAACACAGTTCGCTTTCGAAAGTGCCGGTTCGGCTTTGTTGACACCAATGGCTTTTCTTCGACCA  
AAGGTAACCTTGAACGGCGGTATAGCGGTGACATCTTTGGATTTTTACCTTTGCGTGAACCGGGTTGCGACCATATACCAAAACCGGTTACCGGTAACAGAACAGAAACCGTCTGTGCAACACGCGGG  
TCAATACCAACTTTGCGCTCAACACAGACCTAAGTCTATGATTATTTTCTTTTAAAGTAAAGGGACAGGCTGCGATTGGGCTGTCTTTTCAGACAA

**SEQ ID 6800**

RTYTHAGTINIAVDRTNRNSTLNQQQLAFCINFDFQFLNSCGFVAVLAGHALTGEHATVRLRHDRAMNAVRTGTVVGSTLGTETVMTFDRAGETFTFRTGTYIDQLDTPKERNQDFVTGF  
QFSQFFPSQSKLNQATGCFMTCCKVSGFGFVDITGFFLTAKNLNGLLAIVSIFGFYLCNAVGRHIQNGYRNRNTLLVEHAGHTNFAISQRT\*SDHYFPFKVKVQAAIGLSFRQ

**SEQ ID 6801**

TGTGTTGTGTTTCGTTGATTTTGTGTGTCAGTTTCAGATGTGGGTGCTTATCCGGACGGGTGCTGTGAAAAATGTTTGCCCCAATGCAAAAAAATCACTGCAAACCTTCACAAACGGGGCTGGTAG  
 TGAATTTTTTCAAATCAACAGAT

**SEQ ID 6802**

LFVSLILCQFQMWVLIRTGRLKNFAPMOKNHCKPSQTGLVVIFSNQTD

**SEQ ID 6803**

SEQ ID 3686  
ATGTTACCCCAACAGGCGTGAAATAGCCAAATGCAAAATTATCTGTTTCTAAAATTTTTTAGGCAATCTCAACAAATATAGAGGAGTCAAAAAGGGATGACACAGTTAATTTTTACATTTCAGAT  
ACACCAAA

**SEQ ID 6804**

MVPNRREIANMOIICFLNFLGNLNKYRGVKRDDTVIFTFPRYTK

**SEQ ID 6805**

TTGGCCCTGCTTTTCAGACAAAGTTAAACTTGGCAAAAATGTACCAAGCTTGACATTATATCCGACAAGTCAAGAAATATCAACAGAAATATCAGAAATATCTTCAATATGCCGCTCTGAAG  
CGTTT

**SEQ ID 6806**

LACLSDKVKLGKNVPSLTLYPTSORNINRNIRNIFNMPSEAF

**SEQ ID 6807**

ATGAATATTTTTATTATTAGACGGCGCGCAAGCGTTCGGACATTCTCACGGCGGTGTAAACCAACAGCTTCACAAAAAAGCGAAAGAAGTTTGTACCGCGCTCGGCACAATGTTCAAGAAA  
CCGTGATTGATGCCCGCTATGATGTTGAGGCGGAANTCGAAAAATTCGTTTGGATGATGCTGTGATTTTGGCAGATGCCGGGCTGGTGGATGACAGAGCCTTGGACAGTGAAAAATATATAT  
GGAACGAAGTCTTTACCGCGCGGACACGGCAAACTCTACCAAAAGCGACGGCAGACACCGCGTCAATCCGACTGAGGGCTACGGCACAGCGCGCTGTTGCAAGGCAAAAAACATATGCTTTCA  
CTGACTTGAATGCCCGGATTTGAAGCGTTTACCCCGGAAGCGCATTTCTTTGAAGGCAAGAGCGCTTGTGATGTTTGTATATGACCTTCCACAAAGCCAAACAGATTCATCGGCTTGAGCGCCGCT  
TGCACATATCTGCTACCAAGCATCTGTTTAAAAATCCCGCAAGTGAAAAAATACTTGCAGATPATCAGGCACATATGCAAAAAAGTGTTCGCG

**SEQ ID 6808**

MTLLLDGGKAGPHSGHGLNHTLHKKAKEVLTALGHNVQETVTDAGYDVEAEIKKPVMDAVIWMQMPGWNHHEPWTVKKYNDVEVTTGGHGKLYQSDGRHRVNPTEGYGTGGLLQGGKHMLS  
LITWNAPIEAFTRGDDPFECKGVDVLYMHFKANEFIGLSRLPTPLCNDVVKNPQVERYLADYQAHLEKVPFG

**SEQ ID 6809**

ATGAAACCAATTCAGAGAAGACTGACCGTATTTGTGTTCAAGTGTGGAAAAGCGGCAGCTTCAGCCGTGCGGCGGAGCAGTTGGAGATGGCAAAATTCGCCGTAAAGCCGATCGTCAAAACGGC  
TGGAGGAAAAGTTGGCGGTGAACCTGCTCAACCCGACCCACGCGCAACTCAATCTGACGGAAGAAGGCGCGCAATATTTCCGCCCGCGCAGAGAATCTCTGCAAGAAATGGCAGCGCGGA  
AACCGAAATGCTGGCAGTGACGAAGTACCGCAAGCGGTGTGTCGCGTGGATTCCGCGATCCGATGGTGTGCAATCTGCTGGCGCGCTGGCAGCAAAAATTCACGAACGCTATCCGCAT  
ATCCGACTTTCGCTCGTTCTTCCGAAGGCTATATCAATCTGATTGAACGCAAAAGTCGATATTGCCCTTACGGGCGGAGAATTGGACGATTCCGGGCTGCGTCAGCCCATCTGTATTGACA  
GCCACTTCCGCGTAGTCGCCAGTCTGAAATATTTAGCAAAAACAGCGCAGCCCAATCTGCAGAAGATCTTGCCAACCATCAATGTTTAGGCTCTCACAGAACCCGGTCTCTTAATACATG  
GGCGGTTTTAGATGCGCAGGGAAATCCCTATAAAATTTACCCGACACTTTACCGCCAGCAGCGGTGAAATCTTACGCTCGTTGTGCCCTTTCAAGTGTGGCGGTATTCGCTTGTATCAGATTTT  
TTGGTTGACAACGACATTTACTGGAAGGAAAGTTAATTTCCCTATTTCCGCCGAACAAACCTCCAATAAAAACACACCCCTTTAATGTCTGTTTATTACAGCGATAAAGCCGCTCAACCTCCGCTTAC  
CGGTATTTTGGGATTTTCTAGTGAAGGACTGGGAAAAAATATGAATAGAACGAATACCAA

**SEQ ID 6810**

SEQ ID 6810

MKPNSELIVFVQVVEGSGFSRAAEQLEKANSVSRIVKRLLEKLGVLNLNRTTRQLNLTEBGAQYFRRARQLQEMAAETELVAHEVFPQGVLRVDSAMPVHLHLAPLAAKFNERYPH  
IRLSLVSSSEGVNLIIRKVDIALRAGELDDSGLRARHLFDSHFRVVASPEYLAKHGTPQSAEDLANHQCLGPTPEGSLNTWAVILDAQGNPYKISPHFTASSGELIASLCLSCGCIACLSDF  
LVNDNITEGKLIPLFAEOTSNTKTHPPNAVYYSKAVNLRRLRVFLDFLVKELGKNMNRNTTK

**SEQ ID 6811**

ATGACAGCATATGACTTATATTTTGATAATTGCCCTTGTCCGTTGGCAGGCTCGCTGATTGCGGGTTTGTTCGGCAACAAAATCGGGCGTGCCGCGCGCATACGGTTACGATACTCGGTG  
TCGCTGTATCTGCCCGTGTCTCGGCTTATGTGCTGTGGGGATTCCTCAATGCGACGCGTACCAAGTTTGACGAAAACGCTCTATACCTGGCTGACAAATGGCGCGCTTGGAATTTTCCGTCGG  
CTTCTTGGTCGATACGATGACGGCGGATGATGATGGTCGTGGTAAACGGGCGTGTGTTGATGTCGCATATCTATACCATCGGTTATATGACGATGAAAAGATCGCGTACCAACGCTTCTCG  
AGCTAATATTTCTTGTGTTACTTTTCAGCATGTGTGATGTGATTATGACGAAACAACTTCTCCGACGCTTTCTGTTGGGAAGAGCGGGGCTGGTGTCATCTGTACGTGCTTCTCAATT  
TCCGATCTCCGAGCGGCACATTTGCCAAGCTTGAAGAGCCTTTTATGATCAACCGGTGTCGCGGCTTCTCGGCTTTTGTCTCGGTATCGGCTTGGTCTTGGCTATTTTCGGCGGCGCCTGCGTTA  
TCAGGACGTAATTCGCCCTATCTGCCCAACGTACAAAATGCCACTATCCAGCTTTTCCCGGCGTGGAATGGTCTTTGATTACCGTAACTGTTTGTCTCTGTTTGTCTCGGTGCGATGGGTAAA  
TCGCGACAATTTCCCGCTGACAGCTGTGGCTGCCGTGATTTCGATGGGAAGCGCGACTCCGATTTCTGCAATGATTACGCGCGGACGATGGTATACCGCGGTTTGTGTTATGGTGTGCGGTATGT  
CGCGGATTTATGAGATGAGCAGCACCGCGCTATTTGGTGCTCAATATGGTAATCGGCGCGATTACCGCCCTGTTTATGGGCTTCTTGGGTGTGATTCAAAACGACATCAATGCGGTGGTGTGGTGA  
TTCTACGCTGTGCGCACTGGGCTACATGACCTGTGGCTGTGGCGCGCTGTGGCGCTATTCTGTGGGATGTTCCAGCTATGACCAACGCGCTCTTTAAAGCCTCTGCTGTTCTTGGCGCGCGGG  
AGTCAGCATATTCGATGTGACCAAGCATCAAGATATGGGCCATATGGGCAACCTGAAAATAATACATGCCGATTAATTGGCTGACTATGCTGATCGGCAATTTGTCTCTGATCGGTACGCCGT  
TCTTCTCCGGCTTCTACTCCTCAAAGATTTCGATTATCGAAGCAGTGAATAACAGCACCTCGCCGGCAGCGCGTGTGCTTATTTTCCGCTCTCGCCAGCGGTGTGTTACGCCGTTTACCG  
GTTTCGCCCAATACTTTATGGTGTTCACGCGGAAGAAAATGGCGAGCTTCCCGAACACCAATTTCGAGCGCCATGGTGTGAAGAACTACCGGCTTGGGCAAAAACGCAATTCGCGACGA  
AGCCCGCTGGTGTCTTACCTTCCGCGCTGATTCTGCTTGGGATTCGGTCCGTATCTGCTACATCGGCTACGACCCATCGAAGCCATGCTCTTCAAAGACCGTGATTTTCGCTCAAG  
CGGACGCGCATCCGACCATGACATCATGAAAGAAGAGTTCCACAGCGCATTTGGCAATGTGCGACAGCTGACATGCGCTTGTGTTTGTGATTTGGCGGCTGGCGGTGTGGCGCGCGTG  
CGCTTTTGTACGTGCAACTCGCCGACCTTGCSCCGCTAAAATCGCGAGGCGTTCGCTCCGGTTTACGTTTGTGTTGAAAACAAATACTACCTCGACGCGCTTGATTTTCAACGCTTTCGCCAAA



GGCACGCGCGCATTTGGGAACTTCTTCTGGAAAGTCGGGATACGCCATTATCGACAAACGGCATCGTCAACGGCTCCGCCAACTGGTCGCGCGGATTCGGCTCAGGTACGCAAGGCC  
AAACCGGCTTTATCTACACCTACGCCGCGCTATGGTGTTCGGGTATTTGCTCTGCTGGCATGACCTTCTGGGCTTGTTCAGA

## SEQ ID 6812

MNDMTLYLIALVPLAGSLIAGLFGNKIGRAGAHTVTILGVAVSAVLSAYVLWGFINGSRKTFDENVTYTWLTMGGLDFSVGLVDITMTAMMVVVTVGSLMVHLYITIGYHDEKVGXQRF  
SYISLFTFSMLLMSNNPIQLFPWEAVGLVSYLLIGFYFKRPSATFANLKAFLINRVGDFGLLIGLVLAYFGGSLRYQDVFAVLPVNVQATIQLPFGVWVSLITVTCLLLPVGANGK  
SAQFPLHVLVPSMEGPTPISALIHAAVTAGLFWVRMSPIYMSSTALSVIMVIGAITALFMGLVQNDIKRVVAYSTLSQLGYMTVALGASAYSVMFVMTHTAFFKALLFLAAG  
SALIGMHQDHRHMGNLKKYMPITWLTMLIGNLSLIGTPPFGSPYKDSIIIRAVKYSTLPGSGVAYFAVLASVFTAFYAFRQYFMVPHGEEKWRSLEPHSDGHGEEHGLKNDNPHB  
SPLVVTLPILLIAPSIVTIGYLAIEPMLYGDFFKDVIFVNADAHPTMHIMKEZFHGALAMVSHSLTSPVLYLAAAGVAAANLLYVKLPHLPKALQAQAFRPVYVLFENKYLDALYFNVFAK  
GTRALGNFPWKVGTALIDNGIVNGSARLVGALAAQVRAQTGFITYTAAAMVPGVLLGLMTFWGLFR

## SEQ ID 6813

TTGGCGGCGCGGTATCAGGTATTCGCATAGGCAACCGAATCGTCGCGCTTTTCTTTTGAACGAACCTCGATTTTGCAATCGCTCGGGGTCTTCTACGAAGGCTATCAGGTTGTGCCGTGT  
TTCTATCAGCGCGCTTCGCGGACGACGTTTCGCCCTCGCGCTTCACGCGTTCGCGAGCTTCGTAGGCATCGTCCACTTCAACCGCGATGTGTCCGTAGGCGTCGCCAAGTCGTATCGTT  
TCGTATCCGAGTTGTGCGTCAGTTCGAAACCGTCTGTCTCGGTTTCGTCGCCCTAACCGACGAGGCAAGGGTAAATCTGCCCTCGGGATAGTCTTTTCGCGGAGCAGTTTCATACCCAA  
AACGTTTGTGTAGGAATCGAGGGATTTTTCGAGATTGCCACGCGGAGCTA

## SEQ ID 6814

LAAVSGIRIGNRIVAFLNLDLPASGVVFYEGYHCAVPHQAGFADDVSALPLHAFAGFVGIVHFNDRVSVGVAVQVVSFRIPVVRQFQNRVAVFVAITDEGKKSAPGIVPSAEQPHQ  
NVLVGIEGFPFIAHAEL

## SEQ ID 6815

ATGAGCATCGAACACACTCTCCGACACACGACGCGGAAACCGGTCAAAACCATGCGGACGCGCTTCGCGCGATTTGACCGCTGCTCACTCCCTCGCGAAATCTCGAACTGCTTTTG  
AACAAATCGAAACGCGACACCGCTCGAAGATCGCGCTCGCGGACAACTGACCGAGTGCACCGTCTCTTGGCGGAGTGCACCGTCCGCGACGTCGCGGACGCTCTTGGAGTCCCTGCC  
GCCGCGGACACCAATATCTTTGGCTTCGCTCAAAACCGAAGACGCGGCAAGTATGCTGGAAGTATCCGACGCGGTGCGAGAAACGCTGATGAGTCAATGGACAAAGGACGAATTG  
TTGGCGGCGGTGATGATTTGGATGCGGACGAATTCGCGGAGCTGGCAGACGATTTGCCGCAACAGTGGTTATGAAGCCTTACAGACGCGGATGAGGAAGAGCGGCCCAAGTCAAGG  
CGCAATGCTGTATGAAGACAACCAAGTCGGTCCGATTATGGAATTCGAGTTTGGTCAGATCCGCGCGGATGTCGCTCGCAAGTGGTGTCTGCTATCTGCGCGCTTCGACAGCTGCC  
CGACCATACCGCAAGATTTTGTGCTGATGAAAACGAGCTGCTGAGGCGGTCTGCCCATCCGCAAACTTTTGGTCGCGGATCCGCAAGATTTGGTGGAAAACGCTGATGGCGAAAGAT  
GTCTGCGCTTCCCGCGGAGGACGACGCTGGAAAGACGCGCGGCGGTTCGAAACGCTACGACTTGGTTACCGCGCGCTGCTGATGAAAACAAAGCTCATCGCGAGGATTCACATG  
ACGAGATGCTGAGCTGATCCGCAAGAAATCCGAAGCGGATATGTTGAACATGGCAGGTTTGCAGGAAGAGGAACGCTGTTCCGCCCCGTCTTGGATTCCTGCAAAAACCGCTGGAATG  
GCTCGCGCTCAACTCTGACACGCTTCTCGCGACGCGGTGATCGCGCGTTCGAAGCAGTATCGAAAAATCCTGCACTCGCGCGCTGATGCCATCTGCGCGGATCGCGGT  
AACTCGGCAACAGACGATTACCATGATGTCGCGCGGATGGCGAGTGCAGGATATCGAGCGGGAAGGCTGTTGAAAAAGAGTCCGCGTCCCTTGGTCAACCGCATTA  
TTTGGGAGCGGTGATGGAGCGGTTCGTCGCTGCTTTACCGGACGCTCGGCATCGGTTTGGTCATGTTGCGCGGATGACGCTCAACCTCTCTGCGCGGCAACCGTCCGCTATGAT  
TCCGCTGTAATGAAAAATTCGACGCGGATCCCGCGCTGGGAGCTCGGTGCTGATACCGCGTTACCGACTCCGCGGCTTCCCTCAITTTCTTGAGTCTCGCCACCTGTCTCTGCTT

## SEQ ID 6816

MSIEHTPTTHDGETQNHARPSADPDRVHSLCEILEPAFEQIENGTFLEDAFLDKLTELTVLLARLHPADVADLVLESPPFRERNIVLLVKPEDDGEVLLLEVSDAVRETLIESHDKDEL  
LAAVDLDDADELAELADDLPHQVVEALQTRDEEBRAQVKAAMSYEDNQVGAIMDFELVSIIRADVACEVVLRYLRFPDLSLPDHTDKIPVVDENDVLQGLPIRKLVLVADPEDLVENVHARD  
VVRFAEDDVEEAQAFERYDLVTAPVVDENKLLIGRITIDEMVDVIRESEADMLNMAQLQEEEDLPFVLDSVKNRMWMLAVNLCTAFPLASRVIGAFEGSIEKIVLAAALHPVAGIGG  
NSGQITIMIVRAMAQQLTDMQAGRLKKEVGVALVNGIITWTVGAVSWLLYGLSIGLIVMAAMTLLNLLAATVGVLIIPVMEKFRGDPALGSSVLITAVTDSGGFLIFLSLATIFLL

## SEQ ID 6817

ATGTCGCGCGTCTGTAACAACTCTCCATCCATTACGCCAAACACTTTTGAAGGAAATATCATGAAATTTATTAACACCTGCGTAAATACGCGCAAACTGGCTGTGTGAACAG  
CGCGCCGCTGCTTTGGCGGACAGGCAACGACGCTTGCCTGAAACGCGCAAAACGCTTTTGAAGCGCAAAAGCGGACGCTATGGAAGCGGTTGGATTGTAGTGGCGTTTTCGC  
CGCGCTTTTGTATTTTCCATCGTTAAGAGGCTGATGAAG

## SEQ ID 6818

MFGRLEKNSPSTAKHPLKENIMKFINTCRKYAKLAVVTAAPLALAAQANAALPETAKNALEAAKADGMEAGWIVGVFAALPVFSIVKRVHK

## SEQ ID 6819

TTGGCTCGCAATTCAGGCAAAACGATGAAGATTACCTCAAAATCTTATGGGTTTGGCTTAAAGACGCGCGGAGACCGAAATTCCTTATCCGAGACCTTTACAAAACCGATAAAT  
TCAAAATTAATAATAACCAAT

## SEQ ID 6820

LRRQFRQNDQEDYQNSYGVGVKDAKTEIAYPETPKPIFKIITN

## SEQ ID 6821

CGCGTATGCACTTCTCCGACAAACGGGATGACGTGCGGTCTCTGCAAGATCTTAAACGCGCGCTCCAAATCATGCGGTTCTTCCAAATCAATCTTTGTTGTTAAAAATAGTGG  
ATTAAATTTAAATCAGGACAAAGCGACGAAGCCGACAGTACAAATAGTACGCAAGCGGAGGCAA

## SEQ ID 6822

RRMHLSPNRRDVRVLQDLNRPLQIMPFIQIFVV\*NIVD\*I\*IRTKRRSRBQYK\*YKARQ

## SEQ ID 6823

ATGATTACTTTGACGCATTATCGGTATTTGGCGCTCTCTGTTGCGGTATCAGCGGATGGGCATCTTTATGAACCGCAAAACGCTGCTGTTATGCTGATGTCATGAGCTGATGCTTT  
TGGCGGTGAACCTCACTTTATCGCTTCTCGCAACATTTGGCGGATATCTCCGACAAATTTTCGTATTTCTGATTTGACCGTTCGCCGCTGCCGATCTGCCATCGGTTTGGCGATTAT  
GGTCTGCTGTTACCGCAACGACAAACGATTAAATGTTCCGATTTGGACGAGTTGAAGGG

## SEQ ID 6824

HTTLTHYLVGLALLFGISAMGIFMNRKNVLVLMSEIEMLLAVNPNFIAPSQHLGTAGQIFVFFVLTVAAEPSAIGLAIMVLVYRNQITINVADLDELKG

## SEQ ID 6825

TTTACTTGAGAAATAAACATCATCCATCTTAGAATCAGATGGATGCTTCTGCCCAAAACCAAGCCGATTTACTTTTTCGCGGGGCAAGCTTAGGAAAGTTATGGATAAAAAATATC  
CTGTTTGTCTCAATAAAATGCCCTCGAAATTTCTTGAAGCACA

## SEQ ID 6826

PT\*E\*NIHP\*NDASAQTKPDSTFFRGASLRKVMKXKYPVLPFKKRLKILEAQ

## SEQ ID 6827

TTGAGGTAATCTTCATCGTTTTCGCTGAATTCGCCAGCAAGCGATTATCGCGGTTGTGTTTGGCGGTTGATTGCGAGCTTGCCTCAATCTCAAAATTTCTAAATACCAATGAAAT  
TCAATATTTTA

## SEQ ID 6828

LRVIPVLPELPTQSDLSAVVFERLIAACPISNISKYQLKFNIL



**SEQ ID 6829**

SEQ ID 6829  
ATGACATTTTTCGGTGATCTGTTCTATATCTCTGCGCCATCGTTTGATACGGTGCGGTTCGTACCGTTACCGCCAAAAACCTGTCCATGCGCGCTTTGCATCTGGTGCTGACCTTCTGCG  
TAGCGCGCATGATTTTGGATGCTGATGACAGGCGGAGTTTTGGGGCGTGACGCTGTTGGTGGTTTACGTCGGCGCCGTAATGGTGTGTGTTCTGTGTCGTGATGATGCTGAATATCGACAT  
CGAGGAAATGCGCGCGCGTTCCTGCGCGCACGCGCTCTGCGCGGTGGTGGTGGTACGTTGTTGGCGGTTGCCCTGATCTCTGATTTCTGGTCAACCCGGAATACCGACTGGCGGCATCTTGGT  
CTGATGAAGACATTTCCGGCGGATACAAACATATCCGCGATTTGGGCAGCCGATTTATATCCGACTACCTCTGTTGCGGTTTGAATTTGAATTCGGGAGGATATGCTGCTTTGGGACATGGGGCGG  
CGATTCGATTTGGTTCACCGCAACCAACCAATCCGAACGATGATGATCCAGCCCAAGTTAAAGTACGCGCCGATGCGCTGCTGTTGAAATGGAAGCGGTCAAAACCGCA  
AGTCGAATCTCCGACGAAGACGAAGTTTCAGACGCCCTCAAGACGGAAGGGGAGGSCAAAGCA

**SEQ ID 6830**

SEQ ID 6830

MTFSVILFYLLAAIIVLYGAVRTVTAKNPVHAALHLVLTFCSVAMTWMLMQAEFLGVTLVVVVVGAVMVLFLFVVMNLNIDIEEMRAGFWRHAPVAGVVGTTLLAVALILILVNPKTDLAAG  
LHKDIPADYNNIRDLGSRITVTDVLLPFLEAAVLLILGMVAALALVHRKTTNPKRMDDPAQVKVRADQGRMLRVKMEAVKPQVESAESESEVSDGLKTEGEGA

**SEQ ID 6831**

SEQ ID 6831  
ATGGATGCTCTCTGCCAAACCAAGCCCGATTCTACCTTTTTTCGGGGGGCAAGCCTTAGGAAAGTTATGGATAAAAAATATCTGTTTTGTTCACATAAAAAATGCCGCTGAAAAATCTTGA  
AGGCACAAATAAAGCTGATTTACCGACCGCACTGTTTTTTGATTTGTGTTTTGCCCT

**SEQ ID 6832**

MDASATKPDSTPFRGASLRKVMDDKYPVLFTKKCRLLKILEAQNKPISTPALFFDFVVL

**SEQ ID 6833**

SEQ ID 6833

TTGAGGGGAACATAATATGGCTAACTTAGTAAAAACCTTTCGCTTGGCGAACTGGTCAAAGGCATGGCGCTAACGCTCAAAAACCTTTTGTGCCCGCAAGACACAATTTATTTTCCCGAAG  
AGAAAAACCGCGCAATCCGTGCGTTTCCGGGTCTGCAACGCGCAACGCCGTTATCCGAACGGAGAGGAACGCTGCATCGCTGTAAATTTGTGCGAGCGCGTGTGTCCGGCAATGGCGCATCAA  
CATCGAATCGGAAGAACCGGAAGACGGCACCCGCCACCAAGCGTTACGACATCGACCTGACCAAGTGCACTCTTCGCGGTTCTCGCAAGAGCGCTGCGCGACGATGCGATTGTGAGAA  
ACCCATATTTTGAATACCACGGCGAGAAAAAGGCGCATTGCATATGACCAAGCCCATCTCTTGGCAATCGGCGACAATAACGAAGCCGAAATGCCCAACCGCGCTGACGGCGC  
CGTACCGC

**SEQ ID 6834**

SEQ ID 6834  
LREHNMANLVKTFLLGELVKMGVTLKNFPAKRDITYFPPEKTPQSVRFGLHAQRRYPNGEERCIA CKLCEAVCPAMAINIESKEREDGTRRTKRYDIDLTKCIPCGPCEEACPTDAIVE  
THIFEYHGEKKGDLDHMTKPIILLAGDKYEABIAKRAADAPTR

**SEQ ID 6835**

SEQ ID 6835  
TTGAGGCACAAAATAAGCCGATTTCACCGACCGCACTGTTTTTGATTGTGTTTGCCCTAAATCTGTTTGCCGCCGATATTTTCAGACGGCATAACA

**SEQ ID 6836**

LRHKISRFRPHCFLILFCLKSVCRRIFSDGIT

**SEQ ID 6837**

SEQ ID 6837  
ATGCAGCAATTATTGATTTC AATCCTTGAAGATT TAAATAATACATCTACGGATATTATCGCCTCTGCCGTTATCTCAACCGACGGATTGCCGATGGCGACAATGCTTCCTTCACATTTGA  
ATTCCGACAGGGTAGGGCGGATTTCCTGCCACTTTGCTTGCTTTGGGGAGTCGCTCGGTGCAGGAACCTCGCCTCGCGGGAATTGGAAACAAGTGATGTTAAAGGAAAATCAGGCCTATATCCT  
TTTAAGTCAGGCGGGTAAAGATGCCGTGTTGCTGCTGGTGGCAAAAGAAACCGGCAGACTTGGTTTAAATCCTATTGGATGCCAAACGTCGCGGCAAGGCATATTGCGGAAGCCATA

**SEQ ID 6838**

SEQ ID 6838  
MOOILLSTILEDLWNTSTDIITASAVISTDGLPMATMLPSHLNSDRVGAISATLLAIGSRSVORLACGLEQVMKKGKSGYILLSQAGKDAVLVLVAKETGRIGLITLLDAKRAARHIAEAY

**SEQ ID 6839**

CCGACCGCACGTGTTTTTGATTGTTGTTGTTTGCCTTAAATCTGTTTGCCGCCGATATTTTCAGACGGCATAACATAAAAAATCCCCAA

**SEQ ID 6840**

PTALFFDFVLP\*ICLPPIFRRHNINPQ

**SEQ ID 6841**

SEQ ID 6841

ATGCGGCGAGAAATGGGTAGCAGTGTGAAAGCTGCTCGCGGGCGGACACCGCGGACATCGATACCGCTTTGAAACCTGTTGTACCGCTTTGCAAAAACCTCGAATTCCTCTATGGCGATGAAAAAG  
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CCATCATGAGTCGGCGGAAGAGTGTGGGGTTGTTGCGCGCAGAAAGTCGACAGATGGAAGAAAGAAATACCGGCTGCTGATTAGGAACAACCTGTATATCAACAATAACCGCTTGGCGGCGTTTCG  
GATCCTTCCGGTCAGAGCGCAATTGACATTTTCCCAATGTATATCGGTTCAACAAATTAATTTGGTATCGCGCGGCAATCCCGAATTTGAGCAANGAGGCATTTGTACTTTGTGTAAGGA  
TTTATATACCGCGGTTCAGCAACCGCTG

**SEQ ID 6842**

SEQ ID 6842  
MRTKWSAVRSCSRADTADITDNLNLYRLQKLEFLYDGENGSDGINLSDQLPLMLBQLSGSGKALLVDRNGLYLANANFHHESAEEGLLLAAEVAQMEKKYRLIRNLYITNNWGVCDPSGOSLELFFFLPYIGSGTKFILVIAGIPDLSKEAFVTLVRILYRRYSNRV

SEQ ID 6843

SEQ ID 6843

TTGATTATGTCAGGAATGGTTCCAAAACCTCTTTGCCGCAACGCTCGGTCTGGGCGAATTGGGCATCACCGTAGGCTTGGTGGTATCCGTCATCGTCAAAATCGTGATTATCCTGATTCCGC  
TGATTCTGACCGCTGCGCTTACCTGACGATTTTCGAAACGTAAAGTCATCGGCTTTATGCAGCTTCGCGTCGGCCCCGAACGTAAACGGCCCCGCGGGTCTGTAATCAGCGGTTTGGCGACGTGT  
CAAACTCTTGTTTAAAGAGGTTAACCCGTCCGAAGCTGTCAAAACAAAGCCTTATCTACATCGGCCGATTATGTGCGCTGCGCCCGCTCTTCGCGGGCGTGGCGGGTGATTCCGTTTAAAGAA  
GAATGGGTGCTGACCAATATCAATATCGGCTTTTGTACATCTCTGATGATTACCTCGCTGTCGGTTTACGGCGGTGATTATCGCGGGCTGGGCTTCCAACTCCAATAATCTGTTCTTGGGT  
CAATCGGTGCTTCGCGCAAGCATTTCTTACGAGATTGCCATGAGTGCCGCGCTGGTGTGCGCTTGTGATTGGTATGGGTACGGGCAGCATGAACCTCTCCGAGCATCTGTCGGCGGACAGCAAAAG  
CATCGCGGGCGGTTCTGTGTTCTCGTGAAGCTGGCTGCGGCTGTTCCCAATCTTCATCTCTCTCTGATTTCGCGGCTTTCGCGAAACCACTCCGCGACCCGTTTGTGACGTGGCAGAGGGCGAG  
TCTGAATAGCTGTTGCGCGGACACCACTCGTAATCTCGGCTGTTGCAATCTGCGCGGTGTCTCTCTTCGCGCAATACATTTTCATGATTCTGATTGCCGCGCTGACATCGCTGATGTTCTCGGCG  
GCTGGTGTGTCACCGTTTCGCGCAAGCTGGGCGATTCTCGGTACGCCCTCCGCAATCTCGGATGTTCTGTGAAATGGCGCGGTGCTGACTGGTATCTGTGGAATCTGTGCAACCTTCCCAAG  
CTACCGCTTACGACCAATCATCGCTTTGGGCTGGAAGTGCTGATTCCGATCGGCTTCGCTACATCTGGTGTGGCGGTGGATGATTTCACCGCTGAATTTGTGGAAA

SEQ ID 6844

SEQ ID 6844

LIMQEFQNLFAATLGLGLDGLGTVGLVVSIVIKIVILIPILITVAYLTPTPERKVGTFMQLRVGPNVTGPRGLIQPFADVKLLFKEVTRPKLSNKALFYTGIPMSLAPSFAAMAVIPFNE  
EWVLWNINIGLLYILMITSLVGVGVLIGAWASNSKYSPLGAMRASQSTSYEIAMSAALVCVVMVSGSMNFSDIVAAQAKGIAGGSVFSWNWLPPLFPITIVYLI.SAVAETNRAPFDVAGE  
SEVAGHVIGSGPAPALFPLFAEYIPMILIAALTSIMFLGGWLSPPQSGWIGVTPSAPFMFVKMAAVLYWYLWIRATTPRYRYDQIMRLGHWKVLPIPIGFATTVVLGVMMISPLNWK

**SEQ ID 6845**

SEQ ID 6845  
TTGGACCTTTAATTTCTACATCAACCCGCGCGCAAATCCAGCTTCATCAGCGCATCGGTAGTTTTATCGGTCCAATCCAGATGTCCATCAGCGCGAAATGGGTGCGGATTCCAAATTGT  
TCACGGGAAGTTTGTTCACGTCGGGAGAACGCAAAATGTTGAAACGCTCGAATTTTGGTCGGCAAGGAATCGGGCTTTTACAAACAGCACCGGTACGTTTTCAGTTTCAACGATTTCCT  
GTGCAGAACGGTCAATCAGGGCGTAATCATTAAGCTTTCAGGCGGATACGGATTTTGTGGTTTGGCAT

**SEQ ID 6846**

SEQ ID 6846  
LDNFNYITNGROIOLHQRIGSGFIGPIHNDVHQMQMGADFQLFTGSPVHVRRRTQNVEFLDFGRQRNRAFYNSTGTPCSFNDFLCRTVNGVILISFOADTFLVCH

## SEQ ID 6847

TTGCTTGGGATTTTCGACAGTCCGAATTATTGGACTTTAATTTCTACATCAACACCGCCGGCAAATCCAGCTTCATCAGCGCATCGGTAGTTTATCGGTCCAATCCACGATGCCATC  
AGCGCAAATGGGTCCGATTTTCAATTTGTTACGGGAAGTTTGTTCACGTGCGGAGAACGCAAAATGTTGAAACGCTCGATTTTGGTCCGCAAGGAATCGGCCCTTTTACAACAGCAC  
CGGTACGTTTTCAGTTTCAACGATTTCTTGTGCAAGACGGTCAATCAGGCGGTATCATAGCTTTTCAAGCGGATACGATTTTGTGTTTGCATTTATCAATATCTTCAAT

## SEQ ID 6848

LLGDFRQSELLDFNYINTGRQIQLHQRIGSFIGPIHDVHQAMGADPQLFTGSFVHVRTQNVETLDFGRQRNRAFYNSTGTFCFNDFLCRTVNVQVLIISFQADTDFLVCHLSISFN

## SEQ ID 6849

TTGGATGAGGATACCAAGTCCATTATATAGTACGCCCGGTGAGAACCGTTCAACTTTATGTTGGGAAATCTTAAGCCAAGGAGTATGGGTTTGGTATTCCTTTAGATAATGCCGAA  
CCAACCTGTTGAAGATTGGAATCTTTTACATTCGTTTCGAGGGCTGCTGGAGAGGCGATCGTCTGTTGCGGTATTAACAGATGGATATACGCTCTCAGCCCGGTATCGACGTGA  
TCACAAATATCTTGCACAAACATAATCTTAATGTTCCGCTTTTGAATTTGATGCCCGCTAAGGAAGATGACGTAAACAAATTTGGTTAGCGCAATGTTATTTCTATTTGATCCGGACGAG  
GTT

## SEQ ID 6850

LDIEDTKVHLVSTPQERFNPFWELLSQSGMGLVLLLDNARTNSLKLEFFLHSPRGLLEKASVVVGIITKDIRSQPGIDVYHKYLAHNLNVFVFEIDARKEDVKQLVLSAMLSIDPGLB  
V

## SEQ ID 6851

ATGTTACAAATCGAAATCGACGGCAACAGGTATCTGTGGAGCAGGGCGCGACGGTAATTGAAGCCGCGCACAGCTCGGTACTTATATTCGCGATTTCTGTACCACAAAAAGCTCTCTA  
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GGCGCAGGAAGCGGTATGGAATTCCTGCTCATCAACATCCGCTTGATTGTCGACCTGCGACGAGGCGCGCAATGCCAGTTGCGAGATTGGCGGTGGGTACGGCAAAACACCAAGC  
CGTTATACCGAAGAAACCGTTCCGTCGTGGCAAGGACATGGGTCTTTGGTTTCCGCGGAGGAATGAGCCGCTGTATCCACTGTACCCGCTGCGTACGTTTACCGGAAGAAATCGCG  
GTTTGCAGGAATTTGCGATGTTGAATCGTGTGAACACTCCGAAATCATGCCCTTTATCGGCAAGCGGTGAAACCGAGCTGTGGGCAACGTCATCGATTGTTGTTCCGTCGGCGCAAT  
GACGAGCAACCGTTCCGCTTCAACGCGGTACTTGGGAATGAACCGCGCAAATCGTTTTCGCGCACGACGCTTTGGGCGAGCAACCTGATTGTTACAAACAAAGACCAATACCGTCCG  
CGGTGTTGCGGTGGAAGAACGATCAACGAATGCTGGCTGTCGACCGCGGACCGCTTTTGCCTACGAAGGCTGTATACGAAGCGCGTCTGAAATATCCGAAATCAACAGGGTG  
CGGATGGATGCGATGGATTGGAAGAACCGGTGGAATATGTCGCGACGCGATTGAATGTATGCGCAAGACGCAACCAACCAAGTCCGCGTTTGGGCTAATCCGATGAATACGGT  
TGAAGAGCTGTATCTGGCAAAAAATTTGCCGACCGCTTGGGTGTTAAAACTTTGCAACCCGTTTGGCGCAACAGCAACAAACGCTTTTACAGCGGCTTAAAGGTGCGCAATGTTGGGA  
CAAGATTGTAATCTTTGGCTGACCAACGATGCCGTATTTGGTATGCTGCGTGCAGACTTCCGCAAGGAAGACGCGCTCTGACCGCGCGCTGCGCGCGCGCGCAAGACCGTATGGCCTGA  
CGTATTTGGCGCGCAGTAAGAGAATTTGTTATGCGCTTCTGTCTCAAGAACCGCACATCCGACGAGTGGCGAGCGCTGTGAAACCTGTCTGCGGATGCGGAACATCGCGTTAC  
CGCCAGCTGAAACCGCTGAAAGACGCGGTGATTGTTGGTGGGAAGTCAAAACCATCTGATTACGCGCGCAATTTATGCCCGCGCGCAAGAGTTGGCGGACGCGACCGCGCGAGTG  
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AGCCTGAAATCGATACGGTTGACGGTGCAAAAGCGGTAGCCGCTGAAACAGGCGAAAGCGGTATGGCGTTTACGCGCTTGTGTCAGGAAACGCTGCGACGTGTGCGAGCTATTGCT  
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GGGAGGGCGTTCAGACGGCTCAACCGGCTGTCGCGCGCGTGGTATTTATCATACTGATTCTATCGTGGCGCTTCCGCAACCGTTGCAAGAACCGGATGCGCGCGTGGC  
TGCCGCGCGTGTGAATCGGAACATTTGCGACGCTTGGGCTGCAAGACGGAACAAACCGCTGTGCCCAACAAACCGGTGCAAGCGTATCGGTGCGCTCAAGCGGATGCCGCTTGGCT  
GAAACCGTGGTCACTGCGCTGCATACCGAAATGCCCGCTGGGTGCGTGTGATGGGCAATTTGAATGCGCGGAGCT

## SEQ ID 6852

MLQIEIDGKQSVSEQGATVIEAAHKLGTVPHPCYHKLISIAANCRMLVDVEKAPKPLPACATPVTGDMIVRTHSAKAREAQSVMEFLLINHPDCTDQGGEQQLDLAVGYGKTS  
RYTEERSVVGKDMGPIVSAEEMSRCHICTRCVPTETIAGLQEIAMVNRGEHSEIMPFIGKAVETELSGNVIDLCPVGAITSKPPFRNARTWELNRRKSVSAHDALGSLNLIQVTKDHTVR  
RVLPLENEAINECWLSRDRFAYEGLYHESRLKNFKIKQGGEMDWDWKTALYEVRSALIECIADGNQNVGVWNPMTVEELYLAKKFPADGLGVKNFATRLRQDQKRLSDGLKAGNIG  
QSIESTLNDNDAVLVVGANLRKEQPLLARLRAAKDRMALSVLGSKSELPFPLLSQEAHPDEWAGRLKNLSADAHAHVASLKNAEAAVILGAEVNHPDYAAIYAAQELADATGAV  
LGILPQAAANSVGADVLGVNSGESVAEMANTPKQAVLLNVEPEIDTVDGAKAVALKQAKSVMAPTFPVSETLLDVCVLLPIAPPTETSSGSFINMEGRLOSPHGVVQGFQDSRPMKVL  
VLGNLFDLKGPEYHDTAAILKDALDARSLSKLDNRSTWAGBEVQTASNRLVRVGGVGIYHTDSIVRRSAPLQETSHAAPVPAARVNENTLARLGLQDGTAVAKQNGASVSVAVKADAGLP  
ENVVHLPIHTENAALGALMGIIELAGA

## SEQ ID 6853

TTGCCATTATCAATATCTTCAATTAAGCGATAACAGAGAAACACGCGCGCAACCGTACGCGCGCTTCCGGAATCGCAAGCGCAGACCTTCTTCATAGCGATAGCGCAATC  
AGTCTACAGTAATGGTTACGTTCTACCCCGCATPACATTTCCACACCTTTTCCAAAGTAACCGCGCGGTTACGTCAGTGTACGGAAGTAGAATTGGGACGCTAGTTGGCGAAAA  
ACGGGGTATGGCGCGCGCTCTCTTGTCTCAATACGTACACTTCTGCTTTGAACCTGGTGTGAGGAGTGATAGTACCGGTTGGCAATACCTGACCGGTTTACGCTTACGCTT  
GATACCGCGCAGCAATACGCTACGTTGTGCGCGCGCTGACCTTCTGTCAGCAGATTGCGGAACATTTCAACGCGGTACAGGTGGTTTTGGGTTTCTTACAGCCGACGATTTCAATC  
TCGTACCAACGTCGATGATACCTCGCTTACACGCGCGGTGACTACGCTACCGCGCGGAAATGGAGAACACGCTTCTCGA

## SEQ ID 6854

LPPINILQLSDNRNHAGTHGTAAPANRKAQTFPHSDRRNQFYSNGYVLTTRHYHFHTFFQSNRAGYVSGTEVELGTVVGEKRGMAAALFPAQYVHFCFELGVRSDSSTRFGQYLTAIFYVFTF  
GTAQYAYVVARLTFVQQAEPHFNAGTGGFLGFPQTDFFNLVTNVDDTSLYTAGDYGTAGKWRTRLR

## SEQ ID 6855

TTGATAAATAATTTTATGAGATCGTCTGAAAAATGGGCTTCAGACGGCTTTTGAATTTCAFTGACAATCAATACTGTTTAAACGTTTACTGCCACCTTGGCGTCAATCCCGCACAG  
CGGGAATCCATTTTGAATTTCCGCAACTGCTTTTCAATATCGGGTCTG

## SEQ ID 6856

LINNFLWRSSKHWASDGLLSFDINQYCLKRLPPCRHSRTGGNPFEPFQRLLPKYRL

## SEQ ID 6857

ATGAATAAAACCAATCCTCTGACCTTCATGATCAAACTAGCAACAAATCTAAGCGTTTCCATATCTTTCAAAAAAGACTAGAAAT

## SEQ ID 6858

MKNQSSDLHDQILQNLRFPHIQRRLIEI

## SEQ ID 6859

AGCGATAACAGAAAGAACACGCGCGCACCCAGGTACGCGCGCTTCCGGAATCGCAAGCGCAGACCTTCTTCATAGCGATAGCGCAATCAGTCTTACAGTAATGGTTACGTTCTCA  
CCCGCATTTACCATTTCCACACCTTTTCCAAAGTAACCGCGCGGTACGTCAGTGTACGGAAGTAGAATTGGGACGCTAGTTGGCGAAAAACGGGTATGGCGCGCGCTCTTCTT  
TGCTCAATACGTACACTTCTGCTTTGAACCTGGTGTGAGGAGTGATAGTACCGGTTTGGCAATACCTGACCGCGTCTACGTTTACGTTTGGTACCGCGCAGCAATACCGCTACGTT  
GTGCGCGCGCTGACCTTGTGTCAGCAGTTCGCGAACAT

## SEQ ID 6860

SUNRRNHAGTHGTAAPANRKAQTFPHSDRRNQFYSNGYVLTTRHYHFHTFFQSNRAGYVSGTEVELGTVVGEKRGMAAALFPAQYVHFCFELGVRSDSSTRFGQYLTAIFYVFTF  
VARLTFVQQAEPH

## SEQ ID 6861

TTGACCAAGGCATCCGTCACCTTAACGCTGTGTATAAAGTGATGCCCTTAAACCTCAATGATATCTGAATTATCTTGGCGCAACCTATACAAACCGGTTTTTGTGCGGTAGATTGAAAA  
CGGTTTTCACCAAGGCATCCGTCATGCGGATGAAATATAATCGGGGCCGATTCTGCTTCTGATAGTGAAATGATGAAAAAGCGGAAAAATACGACACCATCCCAATCCCACTG  
CGCGGCCCTCTCGAAAGCATGATGAAAACTGTTGGGCAGC

## SEQ ID 6862

LTKASVNLNLYKVMPLNLDILNLYLAATYTTGFLSVDLKTVSQAYSMDKINIGADSASDSEMMKAEKIFTFPSQSQSRLQLRLMKLLGS

## SEQ ID 6863

GTGGTTTTTGGGTTCTTTCAGACCGAGGATTTCAATCTCGTCACCAACGCTGGATGATACCTCGCTTACACGGCCGGTGACTACGGTACCGCGCCGGAATAAGAGAACAGCTCTCG  
ATAGGCAGCAGGAATGTTTGTCCACGGCAGCTCGGAGTCGGGATGTAGCTGTCCAAATGCGGTAGCCAGTTCGAAGATTTTTCTTCGTAAGCGGCATCGCCTTCCAGGCTTTCAGTG  
CGGAACCTTGTACGATCGGCGAGTCGTCCCGGGGAAGTCGTAGCTGGACAGCAGGTCGCGGATTTCACTTTCAACAGTTCCACAGCTCGGCATCGTCGACCATGTGCGATTGTTTCAT  
GAACACGATGATGAAGTACGCCCTACTTGACGGGCCAGCAGGATGTGTTCCGGGTTTCGGCATAGGGCCGTCGGCAGCAGAACATACAGGATTGACCCGTCATTTGTGCGCGCCG  
GTAATCATGTTTTTAACGTAGTCGCGGTGACCCGACAGTCTACGTGTGCGTGTAGTGGCGGTTTCGGTTTCGTAATCTACGTGCGAGGTGTTAATGGTAATACCGCGTCTTTTCTTCGG  
GTGCGTTGTGTAATTTGCTAGCTTAAGCTTTTCAGCGCCGCCGAATTTTTTAGC

## SEQ ID 6864

VFWVSRPTISISSPTWMPRSTRPVTVPRPENGHEVDRQQEWVHGTGLGSRDVAVQCSQFEDFFVSGIAPQGFQCGTLYDRAVVAGEVAGQVADFFHNFQQLGIVDHFVAFVH  
EHDVRYAYLGTQQDVFAGLRHRAVGSRTYQDCTVHLCGAGNHVFNVVGVTIRTVYVVCVAGFGFVYVVRGVNGNTACFFFGCVVDLVVSFCSAAEFFS

## SEQ ID 6865

GTGGGAGGGTGTAAATGTTGGAAGCTAAAAATTTTATCTATACGTTGACCAACAAAGGTAAAGTACGACACTCAATACGCTTTTATCAGATTGTGCGGAAATTTTCTAAATTTT  
TAGCTTTTTTGAAGATATGGAACCGCTTAGATTGTTGTCAGTATTGATCATGAAGTCAGAGGATTGTTTTTATTATCTGTTGATAATGAATACAGGTTAGGAGAAATTTATA  
CAAACTTTATTCGCATAATTTGTGATTTTATTTGCGCAGCTAAGGACACGGGGTGGTATTGCGATGCG

## SEQ ID 6866

VGRVVMVEAKIFILYGAANKGKSTTLNLFNQICRKFSLVFFERYENGLDFVAVFDHEGQRIGFYSSGDNIEYVRNLYKLYSHNCDPILARQGHGVVVMQ

## SEQ ID 6867

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GCGATCCCGGCGCAATTCGCGCCTGCGTCTGGCTTTGGAAAAAGCAGCCGAAACCAATATGCCAAAGCAATGTGCAACGCGCCATCGACAAAGGTACGGGTAACTTGAAGGCGGTGA  
ATACATCGAGTTGCGCTACGAAGGCTACGCGCATCGCGCGCGCAGCTTTGATGTTGAGTACGCTGACCGACAAACAAACCCGACCGTTTGGGACGTTACGCCACGATTTACCAAAAAACCGC  
GCAACTTGGGTACCGACGCGTGGCGGCTTCACTTGGTGCATCAGGCTATTGTTGTTATTCGAACCCGCGGTTGACGAAGACGAGCTGATGGAAGCGCGCTTTGGAAGCGCGTGGCGAAG  
ACGTGTTTACCAACGACGACGCTTCCATCGAAGTCATTACCGCGCAATGATTGGGGCGGCGTAAATCCGCTTTGGAGGCGCGAGGTTACAAATCCGTGACGCGCGAGCTTACGATGCG  
CGCCAAACGAACCGCACTCTCGCGCGAGATCGCGTCAAAATGCAAAAACGATTGACGCGCTGGAAGACTTGGACGACGTCGAAGACGTTTACACTTCCGCGGTATTGAATCTCGAC

## SEQ ID 6868

MAGHSKWANTQHKRQDAKRGKIFTRLIKEITVAARMGGDPGANPRLRLALEKAENNMKPNQVRAIDKGTGNLEGVYIELRYEGYIGGAALMVDCLTDNKTTRTVADVRHAFKNG  
GNLGTDCGAPNFVHQYLVEFPGVDELMBALEAGAEDVVTNDGSIIVITAPNDWAGVKSALBAAGYKSVGDVTVRAQNETELSGDDAVMKQLIDALEDLDVQDVTTSAVLWLD

## SEQ ID 6869

AACCTCGATTATTCGCGCTAAACGCTCTGCCATTGTTGTCAGCGGGGACAGTGCCAGAAAAAGACTTGGGATTGGAAGTGCAGTTGCGGCAACGGTACATACGCTCGCGCTGGAGCTGC  
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CGCGGTTTTCGCGCGCTTCTCTCGCCCTTAAGCAGCAGGGATTTCCTGCTACACGACATTGATCAGGTCAAGTTTCGGGAAACGCTGTCATATATCTGTCAGACGTTCAAGCTTCTCTC  
AGGTTTTCCCTCGCGCGCATAGGCTTCGTAAGCTTCTCGCCGACCATGCTCAAGTATGATGTTTGTCTGCTGATGCGCGCATAGGCTTTCGAGCGCGGACAGGAAATGCGCTTGTGCG  
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GGCTTACGCGCCATTTCAAGCTTCTGTCAGCCCAAAAAATCTGTTTCGCGCAGATCGACAAACCGCGCTTGTGATGTTTTCGCGCAATTCAAACAGGACGCGCGCGCTTTTCGCGG  
ACCGTATCGGGAGAAATCCAGCATTTGTCGCGGTATGTTGATGGCTTTGTCGTTTTCGCGCGCTGACGCTAAAGTTTTCGCGAGGTAAGGTTCAATCATACGATTGCGCGCGCGCTGCGA  
CGACTTCGCGCACTCCCTTTCGCGCGCGCGCTGTTGCGGTCGACAAAGCTCCAGGCTTTTATAAAATCCCGAAGGGATGCTTTTGTCTGCTTCAATACGTTTTCATATCCACGCG  
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## SEQ ID 6870

NFDFIRKRLFPVAGTVPKDLGFVAVAAATVHHALELPSDNRTHVIGFSPRIQAEFPQDAVHAVKVLAAADKLDGGLRFPFLALKQQLVHDDIDQVFKRLHISQTVQAPF  
RPSLRIGIFVKLLADHAQVCMVLLLDGGIGFDGREGIALSVFNQAHVAGAFVFGFELADIETRGIEIGLEBQRLGKFAIKLNLKLCIFLVVTKLGGNRPFPFVLVVDIBQVLS  
GTFRHLFTLQPKNLFGITDQTRALVLRQPKQDARALFADRIEHCPEVYVDFVFPALTVKFAEGKVQIIRLRPAVDDPRQLPCRAVAVDQSVQAFIKSRDAFCLLYGFHIA  
GGKPAHREEDGQKDNQDNPQFVVHIGFLKAVWQIRQH

## SEQ ID 6871

CCAACGTGGATGATACCTCGCTCTACACGGCCGGTGACTACGGTACCGCGCGGAAAAATGAGAACACGCTCTCGATAGGCAGCAGGAATGTTTTGTCCAAGGCACGCTCGGGAGTCGGG  
ATGTAGCTGTCCAATCGGTAGCCAGTTCGAAGATTTTTCTTCTGTAAGCGCATCGCTTCCAAAGCTTTTCAAGTGGCAACCTTGTACGATCGGCAACCTTGTACGATCGGCGGAACTGCTAGC  
TGGACAGCAGGTGCGGATTTCCATTTCAACAGTTTCCACAGCTCGGCATCGTCGACCATGTGCGCATTTGTTTCATGAACACGATGATGAAGGTACGCTACTTACGCGGCGAGCAGGAT  
GTGTTTCGCGGTTTTCGCGCATAGGGCCGTCGGCAGCAGAACATACAGGATGACCGCTCCATTTTGTGCGGCGCGGTAATCATGTTTTTAACTAGTTCGCGGTGACCCGACAGTCTACG  
TGTGCGTAGTGGCGGTTTTCGTTTCTGATTTCTACGTGCGAGGTGTTAATGTAATACCGCGTCTTTTCTTTCGCGTGTGTCGATTTGTCGTTAAGCTTTTTCAGCGCGCGCGAAAT  
TTTTAGCTAAAAATAGTAGTCAAAAGCAGCAGTCAAGGTGTTTTACCATGCTCAACGTGACCGGATGTTGCCAACGTTTACGTGCGGTTTGTACGTTGCAATTTTTCTTACGCT

## SEQ ID 6872

PTWMPRSTRPVTVPRPENGHEVDRQQEWVHGTGLGSRDVAVQCSQFEDFFVSGIAPQGFQCGTLYDRAVVAGEVAGQVADFFHNFQQLGIVDHFVAFVHEHDDVRYAYLGTQQD  
VFAGLRHRAVGSRTYQDCTVHLCGAGNHVFNVVGVTIRTVYVVCVAGFGFVYVVRGVNGNTACFFFGCVVDLVVSFCSAAEFFS\*NSSSQSSQGGFTMVNVTGDANVYVRFATFEFFLSH

## SEQ ID 6873

GTGGCAGTTTTCCATTGAGCGCGCAGGACAGGTTGATTATCCGATTTTTCCCGATACCTCGGTTACGTTGAAATCTTGGCCAAACCTGACCCGCTAGGCAATGTGCGCGGTCGATA  
CGCTTGTGCGCAITTTTGACCAAGGCATCCGTCACCT

## SEQ ID 6874

VAVPHLDGAGQVLDSDPSRYSVYVEILAKPDPVKGKAGVDTLVGIPOQGIQF

## SEQ ID 6875

ATGCGTATTTTACCAATCAGGCGTGATTTTTGACCAAGTGATACCGCAATCCCGATTGCTGGACATTGGACGAATACGTCAAAACGCGCGGCTATACCGCCCTGCGTAAAAATCTTGTGCG  
AAAAATCTTCGCAACCGATGTGATTGACGAAGTCAAAACCTCCGCTTTCGCGCGGCGCGCGGTCGCGGCTTCCGACCGGTTTGAATGGAGCTTTATGCCCCGTTCTTCCCGCGCA  
AAAAATATGCGTTTTCACACCGGACGAAGCGGAGCCGGTACATTTAAAGACCGGACATCATATGTTCAATCTCATGTCCTGATTGAAGGATGATCATTTCCCGGTTACGCGATGCGG  
CGCAAGCCCGCTACACTATATCCACGCGGAATTTTCGAAGGTTATCAACGCTTTGAAGCGCTTTGGAGCAGGCGGTCGCGCAGGCTTTTGGGTAAAAATATTTTGGGTTCCGATT

TTGAATTCGAACTCTTCGCCACCAACGGCTACGGCGCATATATTTGCCGCGAAGAAACCGCATTCCTTGAATCGTTGGAAGGCAAAAAAGGCCAGCGCGCTTCAAACCGCGTTCGCCGCTCGCTCGCGCTGTACGGCAACCGACCATCAACAATACCGAAACGTTCTCTCCGTCCTGTTATTTATTCGTCGACGGCGGACAGCGCTTTCGCGATAAAGGTATTCGGAATCGAGCGGTACCAAAATTTATTTGTATTTCCGCCATGTCGAGCGTCCGGGCACTATGAAGTGCCTTGGGCAAGCGCTTTCGCGAAGTCTTGAATAAGCGGGCGGTATCGCGCGCGTAAAAAC TCAAAGCGGTATTTCCCGCGGTTCTCCGCCCGGTATTCGCTGCCGACATTTATGATGACGACCAATATGACTATGACTCGATTTCCAAGCGCGCTCGATGCTCGGTTCGGCGCGAT TATCGTGATGGACGAAGACGTGTCATGCTCAAGCCCTCGAACGCTTAAGCTATTTCTACTACGACGAATCTTCGGGCAATGCACCCCTCGCGCAAGGTACCGCTGCTTTACCGC ATCGTCCGCGCATGCTAGAAAGCGCAAGCGCGCATGGAAGACTTGGATTGCTGCTGCTGCGCAACCAATGCGAGGCGGACCATCTGCGGCCCTTGCAGATCGCGCGCTTCCTCG TCCCGAGCTTTACCAAGCATTTCCGTGATGAGTTTCCGCTATACATCGAACACGGCGCGCATGAAAGAGCATAAGTGGGAGGCTGG

## SEQ ID 6876

MAIYQSGVIFDQVDITANPCDWITLDEYVKRGYTAIRKILSENIQTVDVIDEVTSLGRGRGAGFTPLKNSFMPRSFPGEKYVVCNTDEBEGPTFKDRDIIMFNPHALIEGMIITAGYAMG AKAGYNYIHGEIPEGYQRFBAALEQARAAGFLGKNILGSDFFELFAHHGYGAYICGEETALLESELEGKKGQPRFKPPFPASPGLYGKPTTINNTETFSVPPFIIRDGGQAFADKGPINAG GTKLFCISGHVERPQNYEVLPTGPPAEVLKMGAGNRGGKLLKAVIPGGSSAPVLPADIMQTRMDYDSISKAGSMLGSGAIIVMDEDVCMVKALERLSYFYDESCGCTPCREGTGLYR IVRRIVBGKGRMEDLLDLSDVGNQAGRTICALADAAVFPVRSFTFKHPRDFAHYIEHGGPKHEKKGW

## SEQ ID 6877

TTGTGGATCTCGAACCATTCGCTTGCTGCGCTCATTCGCCGCGAGCGGGAATCCATCTCAATGGTAAAGCAATGCTTATTAATTCAGAAACCGAATCTTACCGTGATTCGCCGCT GCGCGGAATGACGGCATTTCACTATTTCACTAGGGCGGATTCCT

## SEQ ID 6878

LLDLHLILVCRHSRAGGNPSSMVSNNILNSETESYRWIPACAGHTAPQYFSRAD

## SEQ ID 6879

GCCFTTACGGGCTTCAGTTACAGCAGCAGCTATGTTGGGCGAGAGCTTCAGATATTTCTTGAATCCATAGAGTAAGTAGCGCGCTTGGGTTCAGAACCGAGGTGCGTGCAGTAACCG AACATTCTGCCAGAGGTACTTCGGCAGGACTTTTACCGCGCATACCGTCATCCATACCAATACAAACCGCGAGCGGTTCAAGTCGCCCATTTACGTCGCCCATGTATTCCTT CCGGAGTTTCCACTTCAACTGCCATAATCGGCTCAAGCAGGCGAGGAGTGTGACGCAATACCTTCTTAAACGCTTGAGAGCAGGCAATCAAATGCCAATTTGGGAAGATCGCATC ATGTGTAAGAACCGAATACAGAGCGGATACGTACCTCACTACAGGATAGCGGCAACGATACCGTTAGGCAACGTATCGCGGATACCTTTATCGACAGACGGAATAAATTCGCGAGGAATC ACACCACTTTAATTTTCATCGATAAATCGTAACCTTACACACCGGTTCCATAGGTTCAATTCATACACGTCAGCGTATGACCTTTACACCGGATTTGTTTGCATGTTTGTATTC CAGCTTTAAGCGCTTTGCGGATAGTTTACGCTAAGCCACTTGAGGTGACCGGATTTTGTCTTCCACCGAATTCGCGTTTCATACGCTCAACAATAATTTCCAAGTCAGCTCACCCAT ACCGGAATAATAGTTTGCAGGATTTCTGCTGTGTAAGACGCGGAAGAGGCTTCTTTAGCCAAAGCGGTTACGCGGATACCCATTTCTCTTGTGCGGCTTTGGTTTTCGGCTCA ACGGCAATATGGAATACCGGCTCGGGGAATTCATACGTTTCAAGATAATCGGCGGCTTTCGCGACACAAGGTTTACCGGTAGTAACGCTTTCAGACCGATAGCGGCTGCGATGTCGC CAGCGGCTACTTCTCGATTTTCACTACGCTTTCGCGGAGTTCATTTGCACAAACGACCGATACGTTTCGCGAGTGCCTTTTACAGAAATTCAGTACGCTATCGCGGATTTTACTACGCTGA GTAAACGCGGATAAAGGTGAGCTGACGACGCTATTTGCTGTTCAACATTTTGAATGCCAATGACAGAAATTTCTCTTCATCGCTGCGCTTACGCGCTGCTGCGCTTCTTCAGGTGATGATTA ACACCTTGAACCGGAGGAATATCGGTAGGAGCTGGCAGCAATTCACAACCTGCTCCAAACATACGTTGAACACCTTTGTTTAAATGCAGAACCCGACAGCATAGGCTGAATTTTCGCTG CCAAAGTACGTTGACGCAACGCGCTTACGATTTCTTCTTCGCGCAGATCTTACCGCCCAAGTATTTGCTCCATCAGTTCTTCTGCTGCGCTTCGCGCTTCGCGCTTCAATCATATTTGACGCCA TCTTTCGCGAGTTTCGACCAATTCGCGCAGGAATTCGCCATAGGTAAAGGTTGTACCTTTATCGGCTTCATTCAGATGATAGATTTCAATTTTACAGAAATGCAGAACACCGGTAAGAACTG TCTTCGCGGCTTACCGGAATGACGATAGGTACGCGGTTTTCGCGCAACCGGTTTTCATTTGCTGACAAACCGGGAAGGTTGGCACCTTGGCGGTCCATTTTATGACAAACCGCAAGC GCGGAATTTGATATTTGTTGCGCTTTCGCGCATACGCTTTCAGATGCGGTTGAACACCGCCACCGCACAGTAACCATTTACCGCGCGTCCAATACAGCATAGAACGCTCTACCTCTAC GGTAAAGTCAACGTTGCCCGGGGTTGCTGATGATTTGAAGCGGTTGCTCGGGAATTTGTTTCCGCTACCGGACAGTAGGAAGTAACCGCAGCGGAGGTAAATGGAATACCGCGCTCTGCT TCTTGTTCATGTAGTGGTAGTACCGCCACCGCTATGCACTTTCGCCAGCTTGTGGGTCAACCGGTATAGAACAAATACGTTCTGCTGCTGCTGTTTACCGCATGATATGCGCGG AATACCATGTTTCGCGTACAGGCTGATCGGGCTTACGAGCCAT

## SEQ ID 6880

AFTGFSYSSSYVGRSPRIPLLELHRVSSAALGCRQVGRVTEHFQRYFGTDPFTADTVLIHTQYNTATAVQVAVYVAHVFPSPHFNFCHNRKQGRRLTHTFFKRLRSSQPKQJLGRVDI MVRTEYQDTTVNRYIAGNDTVQRIDATFIDRNRKFNHNTTFNFIIDKLVFTTFRHFHFNHNTVLTFTTGLPCMFVPSFNGPADSFTVSHLRCTDICHTEFAFHTVNNNPQVQLTH TGNNGITGFFVCTNAERRVFPQAVQGDTHLLVGFGRFLNGNDYRLGEFTFQDNRRFRTQGTGNSVFTDSGCDVASAYFPDFTVCGSHLHQITDTPASAPYRIQGIAGFYIA\* VNADKQLTDFVVOHFPEQCREFLFIAGLTAVGFPFSVRINTLNRNIGRSWQYNYCQHTLNTFFVKRTAQHRLNFAQSTLTQRAYDFFPQIPTAQVVPVHQPAGFGCGFNHILATP FGSFDPQGRNLAIGKCTFIIGFIIPDRPHFQQIDMTGKTVFRAYRNDRYGCAQTGPHLLDNEAEVGTALVHFIDKXQARNLVFVGLPPYGFRLRLNTAHTVNNHYRAVQYTHRTLYLY GKVNVRGVDVDEAVLGEFLFRHTGFPVGSNGSGNGNTALLLHFVVGSSRTVMHPAQLVQGTGIEQNTFCRGRFTRIDMGNTDVAVQADRGLTSH

## SEQ ID 6881

TTGCAGGTCAGTTGCAAGACTGTTCCCGATAACTCGCAATGGCGCGAAAAGGCTAAAGTAGGCATTTATGCTCTGATGTCGAGTTCCTCATTTTGGACGCGCGAGGACAGGTTGATTTATC CGATTTTCCCGATACCTCGGTTACGTTGAATCTTGGCCAAACCTGACCCG

## SEQ ID 6882

LQVSCRTVDNSNQWREKAKVGIMSCM#QFSIWTAQDRLIYIPFDTPPTLKSHPNLR

## SEQ ID 6883

TTGCAACTGACCTGCAAAATTTCTGCTTTTGCACAATTTCTCGAGTTTTCACACACTTTCTGTCAGCAAAAACCGTGTATCGAGGGGAAAACAATTAAGGACCGGCTTATTTCCATGCAAG ATAGCGATGCTCTGCTGTCTTTTCCGCAACCGCAACGCCCCCA

## SEQ ID 6884

LQLRCKPSSLNSSFYTLVSKTFCIEGRTIKDRLISMQSDVLPVLFRKPQRPQ

## SEQ ID 6885

ATGTTATCGCAAAATCCTTAAACAATGACATTGAGTTGGGGAATATCCGCGGACCAACCGGCTTCGCGCATCATGGGCGGTTGCGTATCGCCCAACCGAAAGGCTGGCTCG CCCCGAAACCATTCGCTTTTGTGCTGACTACATCGGCATCAGCGCGCGCAGGCATATGAAGTCGCCACTTTCTACAATAATGTAAGCACTTGAGCCTGTCGCGCAATACAACTGACCGT TTGTACCAACTGCGCTGCGCTCTGCGCGCGGTATGCGGACCGCGAATACCTCAAAACAAACTCGGTATCGGCTACGGCGAAACACGCGCCGAGCGCAATTTACCTTGTGCAAGGC GAATGCAATGGGCGGTCGCGCATGCCCGGTTATGCTGTTCAACAACACAGCATGTCAGCTTTATGACCGAAGAGGCGATTGAGAAGAACTGGCGGAGTTGGAG

## SEQ ID 6886

MLSASLKLQIDIELAKYPADQRRSALMGALRIAQTEKGLAPETIAFVADYIGTTPAQAYEATVFNMYDLEPVGKYKLTVCNTLPCALRGGMATGEYLKQKLGIGYGETTPDGKFTLVEG ECMGACGADPVLVNNHSMCSFTEBAIEKKLALE

## SEQ ID 6887

GAAACGGAAGTGAGAGAATGCTTTGTTGGCTTACGCATACGGTGACTTCTTACGTTTTTTCACGCAACCGCCACGGCTTTCGAGCGCATCAATCAACTGCTGCCAAACGCAATCC ATGGAATTTCTACCAACGTTTGGCGGCGCGTTCGCGAACCACGCAATGCCAAAGCGAGAGCGGCTGAAGGACGAACCTTCAACAGAACTTGTGATTTGACCACTTACAGCGCGCTT TCACTTCCAGATAGGTTTGGAGTTTGCAATGCTTCTGTTAAATCTTCGATTTGCTGCTTTGCGGTTTTTTTCTCAATCTGTTCCAAACGACCGTAACAGCATACGCTCGGCAACGATTT TTTACCTCAATCATCAATACGTTTCAATTTTGGTCAACTCGACCTACCGAATTTAGGATCTGCGCAGTACGTCGCGCTTGGGACTTCTCTACGCTCTGGCAT







**SEQ ID 6904**

VRGKKDVSGISQEKIGAIAGLV RADQGA KILKDKVSYETASKQYDRAIQ TSEK PANLIIDAL KLDYQHADIDRFAGHLWKL YQTLGNYGRQVKEH LG

**SEQ ID 6905**

GTGCGCTCATACCGGATGTCCTTGGATTGCGCGATCGGTCGCGGCCCTTTTCCAAATCATCGAAACCTCATAGGTAAACCCAGGCTGTATACCCCTAAACCCAGCATCCGCGCTCTTAAACCTGCCTGCGG  
TAGTGTGCCAAACGTTTGGTAAAGTTTCCACAAATGTCGCGCAAAAACGGTCTATGTCCGCGTGTTGGTAATCGAGTTTCAACGCATCGATAATCAGGTTTGCAGGTTTTCGGAAGTTTGGGA  
TGGCACGGTCGTATGTTTCGATGCGGTTTCGCTAGCTGACTTGTCTTTAAGGATTTTCGCACCTTGATCGCGCGGAGCCAGGCGCGGCAATCGCACCGGATTTCTCTTGGCTGAGTTCGCGGA  
CAGCTGCTTTTTCGCGCCGCAAAATCGCGGATGCGCTGACTTCTTCGGCTCCATAAGCCTTACCGCGGACATCGGAGAGCTGCGGTCGCGCAGAAACCGCTTCCGCGACGT  
TTTTCAACTCTCTGAGTGGCCCTATCCCAAACCTTCTTCCGCCAAGACGCGGATACGCAAAATGGTT

**SEQ ID 6906**

VPHTVDVFLVPLRPLFQIIEFMTQAVPLTQHPLNPLPAVVAQRLLVKFPQMSGKTVYVRVLVIEFORIDNQVCRFPFGLDGTVVLFRCRFVADVFVKDFRTLIGADQAGNRTDFLLADSG  
HVFFAFPHNRDALDFFGSIISLTDIRRGRCGSCRRRTAFRTYFNLLSALSQTFPQADADQHV

**SEQ ID 6907**

TATTTTATTGCAAGCAGACAGTCAAGCATAACGACAAGAAAAAGATGATTTTCTGTTTGCCGATAAATATTACCGACATCCCTCACAATCAGTCGGACGGCTGGAGAAAAATACTGTC  
AATACGCTTTTTCCTACTGCACAAACCAT

**SEQ ID 6908**

YFYCKQTVKHNDKKKDDFLVCR\*IFPTDI PHNQSDGWRKYCQYVFSILTNH

**SEQ ID 6909**

ATGGAAAAAGGTGCGCTGGAATGGGAATAGAAGGCGTTTTGAAAAAGGTTTCATCACCAACGACGCGGATACGGTGTTGAACCATATGCGGTACCGGTTTCATTGTGTGGCGGTACTTTGCGATTGGCGCTGCTGCGCGGTGGAATGATCATGTCGGGTATGCGCGGTTATGACCTTGAACGTTTCGGTATCATTTTCGGTCCGTCGCCACGTCAGGCCGACCTGATGATTGTGGCAGGTACGCTGACCAATAAAATGGCGCCAGCCCTGCGTCGCGGTACGACCAGCTFCGCGGACGCCGCGTGGGTATTGTCTATGGGTTCTGTGTGCCAACGGCGGGCGCTATTATCACTATTTCTATTCCGTTGTGCGCGGTGCCGACCGTGTGTGCGCGGTGACGTTTATGTCCGGGTTTTCGCGGACGCGAAGCTCTGATTTACGGCGCTGATTCAGCTCCCAACAAAAAATCAAGCGCATCTCCAATCCGCGCGTGACGAG

**SEQ ID 6910**

MEKRCAGMGTGVLKKGFIITTSADTVLNMHRTGSLVPVTFGLACCAVEIMHAGMARYDLDRFGIIFRPSRQADLTIVAGTLTNKMAPALRRVYDQLAEPRIWLSMGCANGGGYTHYSYS  
VVRGADRVVPVDVYVPGCPPTAEALTYGLIQLQKIKRTSTIARDE

SEQ ID 6911

ATGATTCGGACATGGGTCGATCAGACTTGGTCAATCGGTTTCAGACGGCAGCCAACTCGACTGGTCTTTGGAACGAAAGTGCCGAGACCGCATCCGCCGCCGTATCCGGCGCAAGAAGTCGATC  
CGCTTACGGAGTATCAGGTTTATAAGCAATTTCGGTTATCAGGGCAGGCTGCCGAATCTTTGGCTGCCATCTCGACGGCATTCCGGATGGTGAAGCGAAACCTGAGAACCTTATCCGCGA  
GCTGATCGATATCAATCTCGAAGTGGGGGATGTGCATGTTTGGCAGACAAATCTGCAAAAATACGGCAGACTGATTCCTTTCGAACTTTGGCAAAATATATCGAACAGGCATTACACGGA  
GATTCAAACCAATTTCGCTATCCGCGTCTTGGCGGAAGAAGGTTTGGGA

**SEQ ID 6912**

MTIRGSGIRIGQSVSDGTQLDWSWNEAETASAAVSAQEVDP LTEYQVYKQFGYQGAESLAATLDGIPDGEAKPENLIRELIDINLEVGDDVDVLADNLQKYGR LIPPELLAKYIEQALQR  
DSNHLRIEVLAREGLG

SEQ ID 6913

TTGTTAAACGGATTGGGTGTAACCATGTGTCGCGCTTATTTTCCGCTCTTTGTCTTTATCTCGTCGGCCTCGCGGCGGGCTACTGTTTATCTGCTCGGCACGATTTTGGGCCCGAAAC  
 GGCCTATGCCGAAAAAGACGCCCTTACAAATCGGTTTTGAATCCTTTGAAACGCAAGGATGAAGTTCGACGTGCGCTATTACCTCGTCGACATCTGTTTCATCCTCTTCGATTGGA  
 GGTGCGTTTATGCTGCGCTGGGCAGTCTGTTCAAGATTGGGCGCGTACGGCTTTTGGTCTATGCTGCTGTTTATCTGCTGCTGACGGTAGGCTTTGTTTACGAATGCAAAAAAGGT  
 GCGCTGGAATGGAA

SEQ ID 6914

LI<sup>1</sup>FDLGGT<sup>1</sup>HL<sup>1</sup>SA<sup>1</sup>Y<sup>1</sup>FFV<sup>1</sup>FF<sup>1</sup>IL<sup>1</sup>VGLAAGV<sup>1</sup>L<sup>1</sup>FIL<sup>1</sup>GLTIL<sup>1</sup>GPKRH<sup>1</sup>YAEK<sup>1</sup>DAPY<sup>1</sup>KCFES<sup>1</sup>FNARM<sup>1</sup>KFDV<sup>1</sup>RY<sup>1</sup>YLV<sup>1</sup>DI<sup>1</sup>L<sup>1</sup>IL<sup>1</sup>FDLE<sup>1</sup>VAF<sup>1</sup>ML<sup>1</sup>MAV<sup>1</sup>VFK<sup>1</sup>DLGAY<sup>1</sup>GF<sup>1</sup>WSML<sup>1</sup>V<sup>1</sup>FW<sup>1</sup>LV<sup>1</sup>GV<sup>1</sup>YEW<sup>1</sup>KRG<sup>1</sup>  
AL<sup>1</sup>EW<sup>1</sup>

SEQ ID 6915

ATGGGTACACCCAAATCCGTTAACAAAATTTCTACAATAATTTTCGTATTTTGTAGCGAATTTCAAAAACCATTAAGGTAAATATCGGCCAAACGCCCAAAAAAACCCATAAATACAATCA  
TGTTA

**SEQ ID 6916**

MVTPKSVNKISTIIISYFSEFQKPLKGKYRONAQKNPINTIEL

SEQ ID 6917

ATPACGTCTTTTTCCTACTGCACAAACCATCCCTCTGCGCTGTGCGAATAAAAGGGCGGCATATTGTCTGTTGTTCTTGTGTGAACGGAAATTTATTGGGGTGTAATACCTTCTCCACGACAGT

SEQ ID 6918

TRFPHTDKPSLA AVBRIKGGHIAVVLVVTETIYLGCKSPFPROFFMP\* SRAH

SEQ ID 6919

GTGCCAGAAAAGACATTGGGATTTGAAGTGGCAGTTGCGGCAACGGTACATCAGCTGCGCTGGAGCTGCCGTCCGATAACCGAAGCAGCATATGTCCGCATCGGCTTTCCAAGCCGGATCC  
AAATCGCTGAGTTTCAAACCGAGCAGGCGGTACACGCCGTTAAGGTGCGGCTTCCGGCGGACAAGCTGCAGCGGGCTTTGCGCGGCTTCTTTCTCGCCCTTAAGCAGCAGGGAATTTCTCGT  
ACACGACATTGATCAGGTCAAGTTGCGGAACGCTCTGCATATATCTCTGTACAGCGGTTCAAGCCCTTCTTCAGGTTTTCCTCGCGCGCATAGGCTTCGTAAAGCTTCTCGCCGACCATGTCT  
CAAGTATGCATGGTTTTCGTCTGATGGCGGCATAGGCTTTCGACGCGCGCAGGGAAGTTGCCCTTGTCGGTGTCTTAATGTCCGCCAAATCATGTGGCGCGGTGCATCTTTCTGTGGCT  
TTCAGTGCCTTTCCGCAATGTGAACCGCGCGCATCGAAATTTGGCATTTGACACGCGGCTTGGGCAAGTTCGCAATAAATCTGTGCAATCTCAAACTGATATGCTGTGTCTGTGATCA  
GAAGTTTGGGGGTTTCAACCGTTTPTCCCAATCCCTGCTCTCTGTTAGATATTTGAGCAGTGCTGTCTGTGGCTTACGCGCCATTTTACCCTCTTCGACGCCCAAAAAAATCTGTTTCGCG  
ACGATCGACCAAAACCCGCGCTTTGGTAGTTTTCGCCCAATTCAAACAGGACGCGCGCGCGCTTTTCGCCGACCGTATCGGGAGAATTCAGCATTTGTCGGGTGTATGTTGATGGCTTTGTGCG  
TTTTTCGCGCGCTGACGGTAAAGTTTCGCCAGGGTAAAGTTTCAAATCATACGATTTGCGGCGGGCGCTGCAGCACTTCCGCAACTCCCTTCGCGCGCGCGGCTCTGTTTCGGCTCGAACCAAG  
CGTCCAGGCTTTTATAAAAATCCCGAAGGGATGCTTTTTCGCTGCTTCAATACGGTTTTCATATCCACGCGGGCGGCAAAACCGCCATCTGTGAAGAAGACGGCAAAAGGATAATCCGACG  
CAGGATAATCCACAATCTGTTTGCCATATCGGCTTCTTCAAGAGCTGTTTGGCAGATTCGAGCAGCATTTTGTATCGGCGGTGACAGTCTTCTGTGCGCTCAAGCGCGCATCTTTCTTCAC  
TCTGCTACGACGCGCTTTTTCGCGCGCGCAAGGACAGCGCGCGCGCTTCAACAGGCGCAACATTCGACAGCAGATGCGCGACCAAAACCGCGCGCAACATACGACAATCAGCGCGCAGAT

SEQ ID 6920

SEQ ID 6920  
VPEKDLGFEVAAVATHHAALPESDNTRTHVHGIFPFSRIQIAEFQTEQAVHAVKVLGAADKLDGGLRGFFLALKQOGLVHVDIDQVKFGKRLHISCQTVQAFPRFSLRGIGFVKLLADHA  
QVCVTRALLDGGIGFGDGGREIALSVFNVAQNHVAGAGAFVVGPECLADIETRGTIEIGLEQRGLGKFAIKLNLKILCLFVVTKLGGFNRPFPPIVLLVDIEQVLSGFTRHPTVLQPOQKNLFG  
TIDQTRVLVVLROFKQDARALFADRIGRIEHCFFVYDGFVFAALTVKFAEKGVIIRLRPAVDDFROLCPAPAVAVDQSVQAPIKSRDAPCLIQYGFHAGGKPAHREZDGQKDNRO  
QDNPOFVVHIGFLKAVWQIRQHFVSAVQISVRSSAHFSSLPHAGGCFRRARTAAATGQTFTRTCRRQTRRTIRQSAAD

SEQ ID 6921

ATGCGCGCTGAAAGGTTTCAGACGGCATTTTGTGTGATGTCTGCTGTGCTGCGTATCAGTCCAGATTCAATACGGCGGAAGTGTAACCGTCTTGCAAGCTGCTCCAAAGCTCTCCAGCGCGTCA  
ATCAGTTTTTGCATTTTTCAGCGGCATCGTCGCCGAGAGATTCGGTTTCGTTTGGGCGCGCATCGTAACGTGCGCGTCAACCGGATTTGTAACCTGCCGCCCTCCAAAGCGGATTTTACGCCCG  
CCCAATCATTTTGGCGCGGTAAATGACTTCGATGGAACCGTCGTCGTGTGTAACCAAGTCTTCCGACC CGGCTTCCAAAGCGCGTCCCATCAGCTCGTCTTGTCTCAACGCCGGGTTCCAGATAC  
CAAATAGCCCTGATGCACGAAGTTGAACGCCACGCGACGGCTCGGTACCCAAAGTTGCCGCCGCTTTTGTGTAATCGTGTGCGTACCGTCCGCAAGCTCGCGGCTTTGTTGTGCGGTCAAGGAG  
TCCACCATCAAAAGCTCGCGCCGATCGCGATCGCTTCGTAGCGCACTCGAGTATGTCACCGTTTCCAGATTACCGGACCTTTGTGCAAGTGGCGGCTGCACATATGTCTTTTGGGCATAT  
TGTATTTTCGGCTGCTTTTTCACAAAGCTGACGACGCGCGGATTCGCCCGGAGATCGCGCGCGCCCATACGCGCGCGCAACGGTGATTTCTTTGAT

**SEQ ID 6922**

NPSPRRFRHHVYVCLLCVSVQIQYQSGSVNVLHVYVQVFRVQNFLLHFDGTIVAGEFGVLGARHNVAVNGVYTCRLQSGFYARPIIWRGNDFDGTVVVGNHVFTGQFSRFHQLVFNAGFEY  
QIALMHEVBERHAAVGTQVAIVPGKCAVYVRNGAGFVVGCAVHHOSCAADAVPAOLDVFAFOVTRTFVDGALHIVFGHIVFGCFQOSQTOARICAGIAAAHTRRNGDFFD

SEQ ID 6923

TTGCTTCGCGGCGCGCTGCCCTCGCGATTATGCGGACACCTTGGGATTTCGCGTCTCGGTGTTTCTTTACCGTGCTTCGCACGCATAAACCAAAGCATCAGCAATAACGCCAGTGCCAGACCGA  
TAATTAATGAGTTTTCACAAAGGAAACCCCGATACCGTAACGAGCGGATAGCTGAACGCCCGCAACGGCCAAATGTGTCGCTTTTATTAT

**SEQ ID 6924**

LLPGGCPCVLPTPWDLRFGVFLPCFARITKSISNTASARPIINEFSKGNPRYRNERIADRPQRPVIRFY

**SEQ ID 6925**

ATCATCAGCCGGAGTAAATTGTAATTAATGTTGCAGGGGCTTTAAATATCCGTTTCGTGTAAACCCGACCCAACTTCAGTCCAAGACCGCGCTAATAATTTTCACCGTACCCAACTT  
ACACCATAACGCCGTGAAGCCTGCTCTTCTCCACAGTATTATCAACATACCGCTAATACCCCGTACAACCTGCCAAGCCGACATAGCGTAAATAGCTGAACGTACCGCTCACCGAAATCG  
TTTTACTGTTGTAACTGTTTGCACAAATATCTGTCATGGTATTGTTTGGCGGCATCTCGGAAGATTTGGTGCTCGGCCATTTTTCATTAGACGCGCGCTGTAACTCAACACAATACCCGT  
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TCCCGGCCATTTCCAATATGCACACCGGAACCGCTGATGCTTAAGCGGGCAAGGTGAGGCTGCCATGTTAAACATCCGATCAACGCCGATTCGTACCTTATCCCGTTGGCGCGTTGG  
CAGCGCTGCTCTCCGATTTTATCATTTTCCGCGCGTTGATGACGATGTCCCGGTGAAGGGACCTGTTTAACTATCTGTTGTTTCACTAGTTCATTTGAACGAAGGATGGCCAGCTG  
CACCGTTCTCCGCTGACGGATATATTTCCCGTCAAGCTGCCGATATCCGCGGCAACACCTCTCTCGGCCGCTGCAACTGAACCAATGCCCTCAGATATTGTTTGTCTCAACAGCATC  
ACGCCAAATCAAAACGGGGATAAAACAAGATCGGGTCTTTCCGACAACAACCTCAGGTTATAGATGGCGCGCTCGAACAT

**SEQ ID 6926**

IITPSKIVN\*ACRGKYPFFVTRTQLQSKTAV\*YFHRTOYTTITP\*SLLFHLSIIKHTANTPVQLPSRHSVIAERTAHNRNFTVVTF\*COQIFVMVLFAAILERLGAAPFFIQTAIVQHNTK  
 ICRTITVIAQVPLFDKGPSPL\*TAIPITVAYFGMKRLFAKIGPIMHTGTADA\*AGKVIACHVKHPINAQFVPYPVGAQGAVFRFPYPPAVDDDDVP\*KGRIVYILCLFTVHLERRMPL  
 HRFRIIDIPCKLPHIGROHLLGPVOLNOCLTILFVFRQHHAQIKTGINKIGSFRQOOLTV\*IGRLKH

**SEQ ID 6927**

TGTGCTGCTCAGTATGCGTCGCTTACAGAAAGGATGGATATGGTGAACTAAACCGAATACAGTTTGGATTATATGCTTCTTCTTCTTACGCGGATATTAGAGCTTGGGTATAGAAGTCT  
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 CGCGTTTGTGTGATTTCCCTTTATCGGGCAGTGCTTTCTGTGGCGGGTATTGCGGATTTTGGATTTTGGGTGTCGCTGGTGTGTGACGGGTTTTCGGGCTTCGCCACCACGCGCGT  
 ATCTTTCATTACCTGTCTGCGGCTGTCAGGGGGTGATTTTCCCACTGTACACACTGTGGGTACGGATGCGCAACAAATTCGGACAGACAGTTTCCAATGTTTATTTTCGCCAACCGCGTTCGCG  
 CGAGTGCATTGGGTTCGGGCTTATTCGCGCTTGTGTACTTGTGATTTCTGTCCACCCAAACAGATTTTAACTGCTCATCTGTTTGATTCTCTGCTGCTGTCCTTTGTTTGTGTACACTGTTCGA  
 AAAAAGTCTCCGACTGAATGCAGTGTGCGTAGCAGTTTCCCTAATGTTGCGCATCTCTGTTTCTTACTGCGCGGATTTGCTCTTTTCAAAATATATGCTGCGCGCTCGCGATAGGTTGATTTGAA  
 AACAACACAGGCAATTTGTTGCGGTTTACCATAGAGATGGTGATAAAGTTTGTTTATGGTGGCGAATGTATACAGCGCGCATACATAACCGCATATATCTCAATAGTGTCAACCGCATCGCAACGCT  
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 AATCAATCCGGCATACTCCGATGCTTTATCGCGACGAGCCGCAATCGCACCGCTTTTGCAGGACAAACGTTTGAATTTGTAATGGATGACGGTAGGAATGGCTGCGTGCCTATCTGAT  
 GAAAAATTCGACCTGATTTTGTATGAATTCGACTTGGTACTGGCTGCTATTTCCACTAACTGTGTGAGTGCAGGAATTTTAAACAGGTGCAAGGCCACTTACCCCGGATGTTTGTGAA  
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 ACTGCTCAAGCAAGCCCTTTCCCGGTTGATTGTGCCGGAAGCGGACAGCAGTATTTAGCAGACAGCCGTCGTGACGACCAAAATGTTGCTCTCTGATGCTGATTCGGATGACG  
 GAACCTTCGCGTGGCGGGAAGTCACTTACTGACGATAATGTTGTAGAATACAAATACCGCAGAGGGATT

**SEQ ID 6928**

LLLQYGVCTERMEDMNTKPNPNTSLIYMLSFLSGLLSLGIEVLWVRMFSPAAQSVQPAFSFTLACFTIGIAGVAYFPKKRICRSRFVDIPFIOQCFLMAGIADPILILGAANLLTGFSGFVHHAG  
 IFITLSAUVRGLIPLFVHVGTDGNKSGRQVSNVYFANVAGSALGPVILGFVILDFSTQQTITLILCLISAAPLFCFTLFOKSLRLANAVSVAVSLMFGLMFLLEDPSVFNQIAGRFDRLIE  
 NKHGIVAVYHRRDGRVYVGANVYDGAINTDIFNSVNGITERAYLLPSLKSGLIRIFVVGSLTSGSWARVLSAIPEMQSMITVAETINPAYRSLIADEPQIAPLLQDKREVTIQLDGRKWLRRHP  
 EKFDDLIMNSTWYRAYSTNLLSABFLKQVQSHLTDPGIVMNTTHSPHAPATAVHSHIPYATVHVMVGSATPVVPFNKELKQLSRLIWPESGRHVDFDSTVDAAQKVVSRMLIRMT  
 EPSGAAEVITDDNMIGVEYKGRGI

**SEQ ID 6929**

CGGTATAGATCGCGCCGCTCGAACAATCGCGCGCTTGC CGCGCTTTTAGGAACTTCAGACGGCATTCGATCGCGAACCGCGCGGCACATCTCTCTGCAAAACGGCAGGAGGGCGAGGCTTTCCCTT  
TCAGACGCGCATCGCAGCCGACTACCGACGTTAATCGTTTCGACAGGCACGCCGATATCTCGGCAACGTCGCCGAAGCGATTAGGTATCCCATAAAAAGATATTTTTAGATTTCATCA  
ATTTCATAACAAATTCAAAATAAAATGCCCAGCAACGCCAT

**SEQ ID 6930**

RYRSAASNIAACRAFRNFRRHCIANRRHILCKROEGEAPFRRHRSPTTDVNRFRDRHADILGKRRRS\*VSHKDI FRFHQFHNKFK\*NAQQRH

**SEQ ID 6931**

TGGAAAAATGAGAAATATGAATTCGACCGCAGTAAAAACCTGAAAGGATTGTGCTGGTGTTTTTTCGCCCTTGGCTTCTGCGCCCTGATTTACAGGTCAGCTGGCAGAGGCTTCTATTCA  
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 CCGTPTTTCATCGCTGAAGTATCCATCGGTCTGTTCTGGTTTGGTAAGCAAGGCTCTGATTTCCGCCCTTGGGGCATCTTTTAGTTGAGGGCTGATTGCCCCATCATCGCTGCTGCCAATTTC  
 CTCCTATTGCTGCTCTCCACCTTTATGATGGGCGCGACCTTGCCCTTGCTGACCTGTTTTTTTAAACGGAAAAATACATAATGTTGGCGAGTCTATCGGTACCTTTATATTTTTCACACTT  
 TGGGTGCGGCATCGGATGCTGTCGCCCGCCGCCGAATTTTTCACGTCTTTTTTACCTCTTCCCAACCAATTGCGCTGACAGCCTGCCCTTAACCTCTTGATATGCTGCTCAGATGGCTCG  
 TACAGAAAGCATGGATTCGTTGAACAC

**SEQ ID 6932**

LKTIENNNSASKTKLKGSLVFFASGPGCALIQVSWQRIILFSGHIGDLSSTFVIIISVMVGLGVGAYPGGRIADRFPPSSIIPLFCIAEVSIGLFLGWSKGLISGLGHLLWEADLPITAAANF  
 LLLLLPTFMGGATLPLATCPFNRIKHNVGESIGTLFFPNTLGAALGSLAAAEFFVVPFTLSQTIALTACINLLIAASVWLRYKDGYGHEH

**SEQ ID 6933**

SEQ ID 69333  
ATGCCCGCAACACGCCATTTTCTCTTCGTATTGGCCGGCCATTATATGTTTCAGTAAGAATCAACTGTTTTAAAAAGAAATTATTGCTGTTTTAGAGGTATTGCATTGCCGCGTTGGCAGTATTCTG  
ATTCTTGGCGGCTGTTTTTGAAGAAAAATGCCGTCTGAAACTTCAGACGGCATCTTGCCCGGCAAAACGGCACTAAATAGAAAAAGTAGCTCTTCTCTATTCTCTCGCCGCCGAAACCGA

## SEQ ID 6934

NPSNAIFLVLPGHLCVSRNCFKRNYYCCFEVLHCLAVFDLADCFLEKMFSETSDGILPGQTALARNSAFSSISRRNR

## SEQ ID 6935

GTGCGTGTGCGCAAAAACAGATTTCAGCGAATTATTGGTTATTAAATGATTGTGCGATGTACGAAGCCGACTGGCTGAAAACTGCCTCAATCCTTTGATTTTATPGCGCGATGCGGA  
AAATTTTCCCTTTTCAACGACAAATTTGACT

## SEQ ID 6936

VPCCKNRFORIIGYLMICAMYADWLKNCNLPLIFIAAMRKIFLFDNLIT

## SEQ ID 6937

ATGAAGCCGCACAGCAGTTTGAACAGTGATACGCCCTTTGCGGGCTTACGAGTTTATTTCCCGGCTGCAGTTTGAGCAATGCGGTGATTTCTACGGCTAATACAAATGTTTACACAT

## SEQ ID 6938

MKPHSSLSNDTPFAGLEVYFPGLQFEQCGDFLRLIQGFTH

## SEQ ID 6939

TTGGTCGGCCTATGGAATCACTGACTGCCATAATAAACCGCGCATTCGGCAGGCTTTCCAAAAAGCATTAGCGATTATGACAGGCAGCGCTTAATCCAACAAAAATGACGATTAACT  
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GCCAAATCACAATATAGGCTTAAATTACCGACTTTATCCCAATGGCAGGCTTGTAGCCAAAGATTTTGAGCTTTTATGGTGTGAGGATTTAAGGTAATACAGACTTTGATACGCC  
GTTAGATGTACTCAACACCTTAAATATACAGCGCTTACCGCCAGAACAAAAAATTTGCAAGAAAAAATCTCAATGGATTATTTGCGGATTTATTTGCGCGCTTCGGGTATCGCGTCC  
GGCAAGTTCGCGCTGACTTATCATCCGTTATTTTATCGCGCGCCACTTCGCGGCGGCGAGGCA

## SEQ ID 6940

LVGTWESLTAINKPRIRIQAQKALSVDYDRHALIQOKMTINLIHLQDYLDPMPLENVLELGGSGMLSALLQKQISANYWLFNDLDCVRSRLAEKLPQSFDFYCGDAENFPFQRFQDLIAS  
ASAVQWPHQPDAPLHCKTGLKTNGLLAVATFGKDNLKEVRQITNIGLYPTLSQWALAKDFELLWCEDFKVILDFDTPLDVLKHLKYTGVTATNQKNWTRKNNLNGFIGDYLSAFGMPIS  
GKVRILTYPHLPFIARSSAAGBQ

## SEQ ID 6941

ATGAGAAAAGCCGCTAAGCCGGTATAAACAATAAACTCATTGAACCTGTTTGTGCGAGCGTAAGTCAAGAACAGCAACAGAGCGCTGACAGCATTGTTTATACGGATTGTTATCGTC  
GCTATGATGTATTGGATGCGAGCGGAATTTAGCCATTTCCGTATCAATCAGCAGACACATTTTCCGGAACGACAAAACCATATTAATGGAATGGGAACTTTTGGAAACCGGCAAAACGTC  
TTTACGCAAGTTTGACGCGCATTTCCCAAAGAGCATTTTGAAGCGGATTTTAAAGAGTGGCAACGCGGTTTAAACAACAGTGAGATAAAAGTTCTTGTGTTCCATT

## SEQ ID 6942

MRKSRLSRYKQNKLIELFVAGVTARTATEPDSIVYTDYRRYDVLDAEGRFSHFRINHSTHFAERQNHINGIGNFWNRKRHLRKFDDGIKHEHFEPLKECERRFNNSEIKVLVVF

## SEQ ID 6943

TTTCTTCTCGCCGCCGAAACCGATAACAGCTTGATGTTTATGCTCTTGGCTTACAGCACCTGCTACTTCTATTAGCCGCTTCGCCGAAAAATACCCAAATGATACTTTTAAATCTCAFTATCC  
TTCTCTAACATAGCCACCCCTTCTGTTACGCCGAAATAAGAAACCGGCTCTTCAACCCCAAGCTGGAGCCGACTCTCGATAAGGGATTCTCTCAATAGCAGCTTCTCTCTAATTTGATCT  
TGCATATATGTTTCCATTCTCTTCAATTTGAGCCAGAGCCCTTTCTACGATCAAAATCAATGTGTATCTAANTACGCCATTATGTTTATCTAACGATTCTTTGGATAAAACCCCATACCGCC  
AAATGCCGAGCTTCTATTTGAAAGCTCCAGCCCTGGGTAATTTGTCTTCACTGTGTGCCAGCCCTCTAATGTGCGCCAGATACAGTCAAAAGGAATCTCTTCAAGATTGTTGTCATCC  
CCTTCTATAGGATTACCGTCTTTTTCGACTGTAGCCAAAATAGCCCTTAACCCAGAGATACGGTGTCTATAAACCCAGTTTAAATAGCCGATATCTGTCTTTATCCGACCGGTA  
ACTCAATCTTTTGTCTCACTCAAAACCTTTGGGAGAACATCTAGTTCCCCCCCCCTTACTACTTCTGATTTTATACATTAAACATATACATCAATCTTGAAGTTGTTCTTACTAAACGG  
CTCTTCGCGCTGTAGAAATAGCATTGCTTTGACAGATTACCCCTTACCGAGCTTACTGATATGTTTTCGCACTCCTGTATATTCATCACCTTTAACCTTTAATACCTTTGGCTTGCAT  
TCTTTTGTGATCATCTTTAATGATGATTCTTTCAGATATTCAATACTTTTTCATCTTTCGATCAACATTTGCATTGTCTTTCACTGTTCCGAAACGCTTGGTTGAACCGACATAGATG  
AATCGGAACCGCCACCGCGCAGCTGTAGCCCCATAGAACAATAACAGCAATAACAAGTTTATTCATTGCTGATTGAGATACCTTTCA

## SEQ ID 6944

FLIAAETNSLMPHLLAYSTCYFISRFAENTQMLFNLIILL\*HSHPFVHAEIRNPVFQPGAGLSIRDSLSNFF\*FDLAILFHSFN\*ARAFSTIKINCYSKYAIMVI\*RFTG\*NPITA  
KCPFTILKAPSLG\*PVFICCHASNVAQIQVRNLFRLSIPFYRTVFSVAKIASNHRIRLLINPSF\*\*RIILFFIRTVKINLLITQTFGENI\*PPPLTTFVFTTINIYIHLKLFTR  
LFAV\*K\*BCLDRFTLZELTCILFSSHCIPTFNL\*YFGLQFPWFYF\*\*\*PLQIFNFFIFRINICIVQLFRNWLNRHR\*IGTATRARC\*PHRSNNSNNKFIHC\*LRYTH

## SEQ ID 6945

GTGGTCAATGGCGCTTTGGCGCGCAGAGGGCATTCGAAGGAATAAGATTAAATCCGCAACGGCAGTGAATGACAGGTTTGCTTGGCA

## SEQ ID 6946

VVNGRLGREGIARNKIKIRNGSEWHFALR

## SEQ ID 6947

ATGCCCGGATGCGTGATTATTTGCCGCAACGATACCGCCGAAACGGTATTGCGAGCGCTGATTGAGTTTGGTATTTTGGCCGACGGGTGAAAAATACAGTTGCTACGGCTCGA  
TGAATCGTCAGAAATACCGCAACCGTCATCCCGCTCAGCGGGAATCTAGCTGTGCGTGCAGAAATTTATCGGG

## SEQ ID 6948

MPGCVIILPQTIPFTVPGRLLDSFGIFARRGGKYSCYGSNRRQKYPNHRSSGNGLSVRKFIG

## SEQ ID 6949

ATGCATAATTTGACGGCAGAGATATGGGACACTTATCGGGCTTATATCCACAGCCTCAAAATGACGAAACGCTTGTTTTCCTTAAATCGGACAAAGAAAAACCGCAAGCTCAAGGC  
TTGCGGTTTTTAT

## SEQ ID 6950

MNLTAARYGTILIGLISTRLKMTTLVFLIGQRKTASSRLAVFY

## SEQ ID 6951

ATGACGGTTCGGGTATTTCTGACGATTATCGAGCCGTAGCAACTGTATTTCCACCCCGTCGGGCAAAAAATACCAAACTCAAAATCAAGCCGTCGGAATACCGTTTTCGGCGGTATCGTT  
TGGCGCAAAATATACGACATCCGGGCAATCAATATCGTCGCGAGTTTGGCATATACATCGG

## SEQ ID 6952

MTVRVFLTIHRAVATVFTSPCKNRTQIKPSEYFRFRYRLRQNNHAGSHSISAVCAYPE

## SEQ ID 6953

ATGAAACAAAAATTTACAATCATCAAGGCGAACATTTAATCTGTATTTTGCAGGTGGGGAATGCCGCCGATGCTGTAATCATTTGATTGTCGGGAAATCAGATTATTGATTT  
GCTATGATTATCAAGATTTAAATTTGGAATTTTCCGCTTATCGGCACATCCGTTTGTGGCGTGGTCAATGGCGTTTGGCGCGCAGAGGGCATTCGAAGGAATAGATTA  
ATCGCAACCGCAGTGAATGGCAGGTTTGGCTTGCATGATAATTTTGGTATCCCTTGGCGCGTTTAAAGGCACATTGGAGAACTTCACAGAAAACTCGTTCAAGGTTTGAACGT  
AGAATCTGTGCGGATAAGCATCTTTGAAGATTACCAACAATTTCCCGCCGTCGTTTGCAGAAATTCATCAAGAACTTACCGCACTTTTTCGATGATCGGGCAAGATAGCGGTACAG

ATCTTTATCCGCTGGACAAACGCCTTGTTCGGATCGGGCGATAAAATTTTATTCCTGCCAATCAGCACCGATATTGGACACCGGTTGCACCGTTCAAGAAACAGACGGCGGGCATTACCT  
GTTTTCAGAGTTTACCCATTGGTGGGCACTATGGAATCAC

**SEQ ID 6954**

SEQ ID 6954  
MRTKTFYNNHQGEHLILYPAGCMPPDAVNHLILPENHDLLICYDQDLNLDLDFDSAYRHRIRVAWSMGVWAAERALQGIRLKSATAVNGTGLPCDWFGIPCAVFKGTLENLNTENTRSKFER  
RIGCDKSAFSEYDVOOPARFPFDEHIOBLTALPAMITGDRDRITDLIRWTNALFGSGDKIFIPANQHYRNTPRCTVOETDGGHYLFSRFTHWSALNNH

**SEQ ID 6955**

SEQ ID 6955  
TTCGCGATACATGTCGCCGTAAACGGCAACCTTTATACGGCTTACCTTTGTATGGCGGATTAACAAAAATCAGGACAAGGGGGCGGGGCGCAGACGGTACAAATGGTACGGAAACCGATCCCGCTGG  
TGCTTTCATCACCTTAGGGAACCGTTCCCTTTGAGCCGGGGCGGGGCAACGCGTACCGGTTTTTGTTAATCCGCTATACAGCAGCGGTGTGGTGAATAATCCCGAA

**SEQ ID 6956**

LRHIAVTATLYGLPLYGGLTKIRTRRRRAADGTNGTEPIRLVLHHLREPPFLSRGGATPYRFLIRYTAGVGGNPE

SEQ ID 6957

SEQ ID 6957

TTTATCCGTTTCTGGGTTTCAGCAGTCTCTGCTCTACCCCTTGCCATTGCTGATGACGGCTCGCGGTGATAAGTCAAACCGGTACCGGCAGGAATCAGGCGACCGCAGTACATTTCTCT  
TTACAGACCTGCGCAGTCTGCTCTGTTTGTGCCATGATGCGAGCTTCGGTCAACACACGGGTGTTTCTTGGAAAGTATGCGGCAGAAATGAAGCTGTCTCGGTGACAGGGAGGCTTTGGTAATAC  
CCAGCAATATGTTTTCGTAACTGCGCGGCTCTTTGGCCTCTCTCCAAGCTTTTTCATTGCGGCCATCACACTCGCGCGTTCGACCTGCTCTCCGGTAATAAACCGGTTTCGCGCGCATC  
CGCAATGTTTCACAGCGGCACAACTTTACGCGATGATGACTTTGATGATGTTTATTCGGAAATCTTCACACCTTCGAGCGGTAAACCTCTTGACCTCTTGGAACAATGTAGTGTGCCAGTGTCT  
TCGATACCTTTGCAGACGAGAAATATCGTGCAGATCGACCGCGCGGTCCACAATGTTTTCGCCCTCGGTTTACCACTPGACGCTCATGTACCGAAATTTGTTCTCTTTGAGGCAAGTCT  
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GACCAACCGGGAATGCCATCGAAACCGAGTGGACGTACCGGGAATACAGATTTCCACGCCGTTTTCGTCACAGAGTTTCACAGTCGGACGCGACAGTTTGGAAGCACTAGAGGAACCGG  
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ACGGGTATGCGGATCCCAAGTTCGCAAGGTTTGACCGGCTTTAATTTGGCCATACCGCTCTTGACACGAGGATGGCACCGTAAGTATGTTTGTGCGCTTCGCGCTTACCGCGGAGTGTACATCG  
TGAATACACGACTTCGCAAGAACGGCCGATGACAACCACTCGCTTTGTTGTTGGCAACATAACGCAATTTGGCTGCTGAAACGCTGACCTTCGTTGGAATTTGGCTTCGACTTCGCTGGCTG  
CTGCGCGACGGGATCGCGCACCAACCGATGTGGAACTGTCAGCTATGTCACGCTACCGGTTTCCAAATAGACTGCTGACCGCAATACGCGCAATACGCGGACTGCCTCGCGCGCATTGACAGTTTGGC  
GCGCGCAAGTTCGCGCGCTAACGTCGCGGCACAGACCGTGGCGGTTTTCACAGTAATCGGAGTACGGACTTTGACTTCATCGACACCGGATTTGGTCAATCATATCCACCAGTTTTCAC  
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CGCATACCGGATGCTTTTAATCTGAGCGCGCAGAACCAACCGGCACGGCTCCGCGCATATAAGAACTTGTAAGTCTTTCGATGACTTTCGTCGCTACCGGTCGATTAACCTTTT  
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GGAATTCGCTCAACATGACGCGCGCAGGTTGTTTCGTAACGGTTAACGACAGGCTCAAACTCACTGCTCTGTTTTCACGCTTCGCGCAGAGCTACGGTGATTTTGTATCCACCGCT  
GACCTGTTTGGTATGTTATGACAGATGCACTTCTTCACATCGGCAACAGGCTGCCCTGCCCTTTGGCATTGATACGCTTCGCGGGTCTGTAGTACGACCAATACGATGTTCTTGGGAA  
GGTACGATAATTCGTTTCGCGCTTGGCAGGACCAATACGTTTGAAGCCAGCATCAGCGTGGCGCTTCAATTTTCGCTTCCAAGCTCAATGGAACGTGTACTGCCATTGGTCAACCGT  
CAAAGTCGCGATTAAATCGGACACCAAGATGGGTGCAATGAAATCGCTTACCTTCGATCAGAATAGGCTCGAACGCTTGAATACCAACCGGTGACGGTTCGCGGCACGGTTCAACAT  
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TTTGACGGAAGCGCGCGCTTTTACCTTTAATCATATCTGCCAAGCATTTTCAGCGGACGTTTGTGGTCTCGGTTACGCTTTCACCGCGCGGCTTATCCACGCGGAATCAACCGCTT  
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AAACCGCGCGCTTCAAGTGAACCAACGAGCAGGCTCAACGCGCATACCGGACAGCATCCATAATCATCACTCCAGCTTCAACCGGAACGATGGAAGGCTTCCAATATCTTCAAGC  
GTTTAGCGATTTTGTGATTTTGGTGTGAGAACCGGTCGATTCAAGCTCTTGGCGCAGGATTTGATTTTCGCTGCTACATCCAAAGTTTCGCAACAAATTCGCGGATACCTTCGCGACCCAT  
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AATACGCGTTTCGATATPACGCAACGTCATGTTCAATATCCATACCAAAGCGGGAAGGACGGGATTTCAAGAACCAATATGGGCAACCGGTCGACCAATTCGATATGGCCATCGCTTCG  
GGCGCATTTTGGACAGGTTAATCTTACGCCACATTTTTCACAGGTTTACGCCCTTTAAATTTCAATCTGATTTTTCGCGACAGCATTCGTAGTCTTTCGCGCGGCAAGATTTTGG  
GCAGAACAAAGCGCTCGCGCTCGGTTTGAAGGTACGGTAGTGTGATGTTTTCAGGTTTTCATCTTCGCAATAGAACCATGACGGGATGTTTTCGCGGAGGCAATACCGATTTTGTATGGCA  
TCAAACTCTCTTCCATACCTTCGGGTTTTCGAACGGATTAATAAGTTTCAACAAATTCAT

**SEQ ID 6958**

SEQ ID 69558

FIRTYLFGSSLLLYPLPLMLTAAVISQGTGRNQATDDDLFTQAQFVLFANDGSFGQHTGGFLERCGRNEAVGGQGGFGNTQQYVYVTCRLFAFFQSPFFIGRHHIAAPDLLSGNKGFAGI  
NRHNTAQLHTLDDDFVFIGNLHTLQAVNLLHLLDNVACQCFDTLQTONIVRIDRAVHNGFASVYHLTVMYQNLFLFGNQSLVCYTVHVSDNQTLFAGLLTBEGNGTGVRQHTGIFRHA  
CQQLGNARQTAGNVAGPGRGLRNTRQYVAFDTFLTFAYGNHRTNGECHRNSRGRTGMDFHAFVQVEPHSRTPQFGSTRGTAFTVNHVYSGQGTYYIIGLFCNGNALFHVLEPHHTCMFGNHR  
TGMRI PSCQGLTFGNHGTVLVYQQDGFVRYVPVAFATADVVNVHDFARTADDNQLAFVVGNTIHLAARTCRTVGFDFLAGCCRTGCKRTDVERTHGOQLGTRFTRNL SRNHADCLAGIDQFA  
ARQVAATVTRAQTAVAGTSNRSRDTDTIDGLVNHIIHQVTSQRTGFNQSLAA\*RIDNRRGNTQNTIAQCFCNHITALYCHLDHAC\*TVAFIDNVNDQVLSYHTGTGQVTVGRVGFQBG  
RQTLTRVTVGRNKVLQYCGTFAEV\*GNRRPNNRSRVRFKHQTHQTCQQLNLSRTRTQTVGRHHINGVE\*LLIDPVAVTVDNLFPGQVVHHRFSNLIAGTTPNIDHFVVAFVAGNQTLTLVLPD  
FPNGIGFSGSQGRFFPNFNFHVLVNGNGTAFCKRSETGVHGVVGEDNR IAAQAAERCVNLGNLGNFFLQRFVDIFKQRAFQDPAAQCTADGCFVTVDNRLKLCFVFFHFAQTAVGDFCTQL  
DLFGMVCIMHFFHIGKQAAALAFGLDVTAGHVQVTQYVDLGRVDNRFVAGRRQYV\*SQHQRACFWHRPQAGWNVCHLVVTVVGVIGKCTGHQWVQLNRPTFDQNELERLNTVQVGRRTVH  
NRMFADDFQDIPYRFLPLFVQFFSEFNGRRQTLTFQFVFNKWEQFQRFHFRQATLVQTVQVAVYGNHGTAGVVTFAQQVLPLEAAAFPTFNHICQRFRTFVSGSHGQFTATAVQDINRIF  
LQHTFFVADDDVRMKPQQAFQTLTVVAVDDAAVQIVQIGSGKTAAVQRNQRTQLRRQYQQLHMHLPQLHGTGHEGQFVQAFSDIFPDGVRTGRFKLLAQDQDFDACYIGSSQFADIRFTH  
PGIEVAVAGTVGVVVIVFVSQTLTLQRSHAGIGHHACPKVVAIFDNDQVLSYHTGTGQVTVGRVGFQBG  
AQQAVLALGPFTVVDGFRFFNFPAIRP\*ADGPRGNVDFDGIKLFHTCGLQRIK\*VQQIH

SEQ ID 6959

SEQ ID 6959  
ATGGCTGCCCGGCAGCGACACGTTTGTGAACCGCTTATTTCGGGATTTCACCAACGCCTGCTGTATAGCGGATTAAACAAAAACCGGTACGGCGTTGCCCGCCCCCGGCTCAAAGGGAACG  
TCCC

SEQ ID 6960

MAAAAATRFEPLIRDFHORLLYSGLTRKTGTALPRPGSKGTVP

SEQ ID 6961

SEQ ID 6961  
TTGTCGGTTAATAAACGTGATGAAGAACTGGTAAAGAGGGAAAATTACGCCGTATTGCTGCAAAAAGACCGGGTAAGTTTTCATCTGATGCCAACCCCAA

SEQ ID 6962

SEQ ID 6962  
LPVNRDEELVKEGKLPPYCCKDRRKFSSDANPK



## SEQ ID 6963

TTGGCAACTGTCCGGTGTGCGCATGGGTTCCTCGCCGTCCTGAGCTACGCAACGGTGTGTGCTTGGCGGGCGGGGTGGCGGCCGGGGGTGTGCTGTATGATCGGAAGTTC  
CGATATACAGGGCGGGCTTCAGCCCGCAAAATCCACCACTCCGCGGAATCCGCGGATCCGCGCGCTCATTCGCGCATAGCGGGAATCCAGACTGTGCGTGGGAACTTATCGG  
A

## SEQ ID 6964

LATVRLCRVVALPLPELRNGCLFWAGAGGGRVCRYDTEVPYIKGLQPAKSTNSAESADSRRRHSRISGNPDLISVRKLIQ

## SEQ ID 6965

GTAGCGTTCACAAATCGATATCCAAAACCCAGTGAGCGAATCTCTTTGACCAATACGTTGAAGGACTCGGGCATACCGGCATCGATTTTGTGTTCGCCCTTTGACGATGTTTTGCTACATTTTG  
GTACGGCCGTTTACAGTCGTGACAGCTTCACAGTCAGCATCTCTTTCAGCGGTGATGCGCGCGGTATGCTTCCAAATGCCAAACCTCCATCTCACCAGAACGTTGGCGCCGCAAACTGAGCTT  
TACCGCCAGAGGTTGTGTGAGTAACAGAGCTGTACGGCGGTAGAACCGCGTGCATTTTTTTCGTCAACCAAGTGTGACGTTTCAGATAGTGCATCACACCGCATGTAACCTTGGCGT  
AAATGCTTTCGCTGAACGGCGGTATACAGCGGTGATTTGAGTTTATCTGTGCTGAAGCCGATTTCTCAACCTCAGGATCTTCGCTTGGGTAAAGCAAGTTCAACATTTTCGCGGATTTCA  
GACTCTTTCGCAACGTCGAATACAGGAGAGGCGAAGATGACCTTTACGAGATPTGAAGCAATTCGATGATTTCTTCATCAGTCAGGCTGTCCAAATCTTCTTCTTACCGTTCGCGT  
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CGGCGCGCATTTTGTACCGGCTTCAGAGCGCGTTCGATGCGGATAAAGACTTTCACCATTTTTTGTACGCGGGTTCAGCTGCTGCGCTTGGGTGAGTTTTTCTTCTTGTATCTCAT  
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CAGATATTCGCTGCTGATTTTCGCTGCTTTCGTCAGCTTCATCGGCGCGCTTGGCTTCTGACCGCAATCATACGCTCGATACGCTCGAATCGGTGCTGCTGCTGCGAAATACGCAATTTGG  
TCGTTCAAAATCCAAACGGTAGCGTTTCAACTCGGAATCGAATGGAATGGCGCGCTTGTGCGGTTGGATGCTTTCGCGGGTAAAGACTTGAACGTCGATAACCGTACCGCTCATACCGG  
TAGGCATACGCAATGAAGTATCTTTTACGTCAGACGCTTTTCGCGGAAGATGCGCGCGAGCAGTTTTTCTTCGCGGTTCAGCTGGGTTCGCTTTTACGGCTTACCTTGCTTACCAAC  
ATCGCGCGCTTCTACTTCCGACCGGATGTAACGATACCGGATTCGTCACAAACGGTTTTGTCATACGCTCGGACAGTTCGGAATATCGCGGGTAAATGCTTTCGCGACCGAGCTTGGTATCG  
CGGCAACGACATTTCAATTCCTCAATGTGAATCGAAGTATAGCGGTTCGTCGCGAGCCACTTTTCGGAATCAGAACTCGAGTCTTCGTAGTTGTAACCGTTCCAGCGCATGAAGCGGATGG  
TCATATTTTGACCCAAAGCAATTCGCGCAAACTCGGTGAGCGCGCTTCGCGCCAACTCGCGCGTTGCAAAACATCGCTGCTTTGACAGCGGACGTTGGTTGATGTTGGTAGATTG  
ATTGGAACGGGTGAATTTAAACAAATGTGAATATCGACACCCACTTCACCGGAGTTCGCTGCTGCTGATGAGACCGGATCACAACCGGTTGGCATCGACATCTCGACACCGCGCT  
CGGCGGCAACGATTCGAGTAGCAGATCAACGGCAACGAGCGTCGATACCGGTACCGACCATCGTTTTTCAGGACGAGACAGGCACTGCTGACGTTGCTATGTCGCAACCCATCA  
ATGCGCGGTTCGCGCTCATCTGTTTCAAGAACGGAATCAGGATGCGGCAACGGATACCACTGACCGGTTCGCAACGTCATATATTTGGAACGGGTTCGCGGTTCGCAATATGTTTCGCG  
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GGTCTGATCCATAACTGACTCAATTTGGCTGAGCGCGAAGATTTCTTGTATGCGCGGAGAAACGGGTTCGCGATTAATCAAGTCTGCGCGCATCAAGTTTTCTGATTCGCGCTGATTTCAA  
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TTGTTGGGCTTCGCGACGTTTTTGTGCTATGTCGCGGATTTAAATTTTCATACGCGCTTACGCGGCAACCGTTCGATGCTTCTTCAGTGAAGAACAGCGGTAAACCAATTTGCTGACCGG  
TCTTCGTTGGCGGTTCGCGCGGACGATCATACGTTAAATCGAACACGCGCGCTTCGCGCGGCGAGCTTCATCGTGGCAAGGATTTGGAATATAAGCACCTGATCCAACTCAT  
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GCTCATTTGCTTTCGCGCAACCGTTCGCGGCAACCGTTCGCGGCAACCGTTCGCGGCAACCGTTCGCGGCAACCGTTCGCGGCAACCGTTCGCGGCAACCGTTCGCGGCAACCGTTCGCGGCAACCGT  
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CGCGCAGAGGGCGAGCATAAGTATTCGCGCAATTTGACATTCAGGATATCGAACAAGGCTTCGCGGAGCGTGAATATACAACTCCAGACGAGCATACCGTTGTGGCTCAACATCGG  
GAAATAGAAATTAATGCGGCTTCGACAGCGTTCGCGTACGTTTGTCAAAGCAATTTTCAGCTGCAAAATTTTCGCAATAAGAAATCAATTTGGGTTCGAGTAAAGGAACCTTCCAA  
ACATTTTCCCGCTTTCGCAAACTCTTACGATACGTTTTTCTCGGTAAACGAATAGTTTCATACACAC

## SEQ ID 6966

VAFQIDIQTQ\*ANLFDQYVEGLGHTGIDFVAFDDVVFHGTAVHVRVRLHSHQLLRVCRAVCPQCNLHLTETLAAKLSFTAQRLLSNQTVRAGRTRVHFVFNQVVFQI VHHITDCNLAV  
KCPA\*TAVIDQLDSFTVVEAQFLNIRIFANVSQVQHFADFLRTVEYRGERCTPTQIGSQDFDFFI SQAVQIFFLTAAVVEFVQELAQLAGFASLPHQHTVDALADTFCTPTQVNFQNL  
DVHGRYAGRVQYDVHRTAVRVHVRVHFRQNRARYHTF ITVAARHFVTGLQAFDGDKDFPHFVYAGLQVLVALGQFLLDLILQIRFFAFLLQANQNLQGLQIFIGQTDLEPVPARQTR  
QIFGRDPAFQQLHRAAVGLDNDHLLDTEVCVVVENTQLVWVQIQTVAPQLGIDNLGAFVALDAFAGKDLNVNDRHTAHTGRHTQ\*SIFFVRRFFAEDGAQOFFFRRLQGFAPRRYLAYQH  
LAGFPYRFDVNDTGFQVTLHLTGQVRNLAGNVFRTPQLGIAGNDIQFLNVRSIAVVRSHFPMQNRVFFVVTVPVRHEGDHLLTQSQFQIGGRAVGHQIAALQNIACFDSRFLVDVGR  
IGTGEFNQIVNIDITHFPGSRFVMDTDHNAVGLDLDHAASAGNDCSSRVNGTDLDTGDRHFRFTQTRHCLFLHVGTQCAVRVIVFQERNQCRNGYHLTGCHVHILDAVGRCHNGFA  
FFTTGNQIANQIAV\*IQIGIRLCNHIAAFDGRQVINFLGYFAVNNAAVRRPQETVIGARVNRQ\*VDQTDVTRFRFRNRTYTSIVGRMHVPHEAGTFAQTARTQCRYTAFMGYFRQGI  
GLIHLQLAGAEFFDGRNGFRINQVVRHQVF\*FRLIQTFPYGTFHTSQTAELVFSQLALRYSTVAQVIDIVHFAMAVTQLDQSRNRGNDIFDAQDITAFVSGTGRILVQQAAPRV  
LLGFQGLFLFCARIKFPIYAYAGQIVAVFTEQAVKQLDLRLFGGRFARTHTTVNRNRLPAGSLIRAQGINISTLIQLIDVKGRRFFYAVNIKFGQQLFCNFIIGRSQYLAFGRINQIG  
SQCPAQAFLFYIQGQACIGNITDIFRSNALTFNGQYLAFFIQDIDLGSFAPQACDQIGLNV\*QIKRFPVVENIQDILLVVAQSLQNNRYRHFAAVDTEIQOIFRIKFIQ\*TTV  
GNDAGGE\*QFAGRVCLTFVMLEEHTGRTVQLGNHNLCAVNHKRTARGHQRNFADHIFVFTFFRRFRFLIQNHQDTRAQRGSISDSALTFRDIQRLAQRVLYKLQTSITVVAHNR  
ENRILKRLQTVIGTFVKSIFQLKFRIRINLGCQ\*KRNPQNIPLCKTLTDTFFLGRIVHTH

## SEQ ID 6967

TACACACTCCGAAAAGTAATTTTCAATAATAGCGCTCGTGAACCAACCGGTACGATCAATCTGATATTTACATTTATTTGCAATGATTTGATAAAAACTATGCAATAAATGTAAACAA

## SEQ ID 6968

YTLRKVIFNNRPSNNTHQSDIYIYLQ\*FDKNYANKCKQ

## SEQ ID 6969

TTGATTCATCAAGGGCGGTATATTACCGGAAAACCGCAAAATGCTGAATATGCTGCTTAATGATTAATTTGGGGTGGCATCAGATGAAAACCTACCGCGGTCTTTTTGACGAATACG  
GCGGTAATTTTCCCTCTTTTACAGTCTTCATCAGGTTTATTAACGGGCAACTTTCCTATTTATACCGAATTTGGAAGAGCTTGTGCGCACACGTTTCCACCGGAAAGCGGTTATTTGTT  
CAACAGCGGCTATCAGCCAACTCGGTATTTTGCCTGCTTTGACGACGACGAAAGTTTGAATTTGGCAGATAAATTCGTTACGCCAGTATGATGACGGCATCCGTTTACGCGGCTGT  
GCGTTTTTCCGTTATCGCTATAATGATATGAACATTTGAAAATCTGCTTGAAAAAACCGTTCGGAATAATTTGACCGCACCTTTTATCGTTACCGAATCTGTTTTCAGTATGACGCGGATG  
TGGCGGATTTGAAACAGCTTGTCCAAATTAATAAACAGTTTCCCAATACTTATCTTATGTGGATGAAGCCACGCAATCGGTGTTTATGGGCAAAACGGATTTGGGATTCGCCAACGGGA  
TAATCTGATTCGCGAGATGATTTATTTGCTCGCACCTTCGCTAAAGCTTAGCCTCGTGGGGCGATGCGCTCTGCAACCAAGTATTTGAAAGAACTGTTGATTAATCAATTCGCGCCA  
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GGGAAGTGGCGCATCGGACGCAAAATATGCCGAGCGAAACCTGTATCGTCCCTATATTTAGCGGGGAATGAAGCCACCTTGCCAAAGCGGAATATCGCAAGGTCAGGGTTATTATTG  
CCTGCCCATCGGACCGCGACAGTACCAAAAAACATCCAGAAATCCGCTGTCTTAACTGCCGATGATGACAACGGATGAAGTTCGGCAGTTTCGGCGCTGCCTG

## SEQ ID 6970

LIHQGRYITRENRKMLNMSNDYLGLASDENLRSLPQQYGNFPSTSSSRLLTGNFYITDLEELVAQRFPRESALLFNSGYHANLGLPALTTKSLILADKRFVHASMIDGIRLSRC  
APFRYRHNDYEHLLKNLEKNVGFDRFTFVTVESVFSMDGVDADLKQLVLKQKPPNTYLYVDEAHAIVGYQNGLGIAERDNLIAEIDLVTGPKALASVAGYAVCNQVLKCLINQMRP  
LIPSTALPPFNWATYTFIFERLPQFSKERSHLEQLSAFLRREVAHRTQIMPSETCIVPYLLGGNEATLAKAEYLQGGYVCLPIGPPTVPKNTSRIRLSLTADMTDEVROQFAACL

## SEQ ID 6971

TGCTCTGAAACCGGGAAGGGCAATTTTGGCGCAGCGCCCGCTCATTCGCCGGAACCTACATTCCTGTCATTCGCCGAAAGTGGGAATCCGGAACGCAAAATCTAAAGAAACCGTTTAT  
CCGATAAGTTTCCGACCGACAGGTCTGGATTCCCGCTTATGCGGGAATGACCGCGCGGGAATCGCGGAGTTTCGGCGAGTTGGTGGATTTCGGCGGCTGAAGCCCGCCCTTGTATATCG  
GAACCTCCGTATCATAGCGACAAACCGCCCGCGCCGACCCGCGCCGCCAAGGCAGACAAACCGTTGCG

## SEQ ID 6972

LSENGKGNFAAAAIVIPANLHSVIPTKVIRNAKSKETVLSDFPHRQVNIPIAYAGMTAAGIGFGVGPGGLKLPALVVRNFRILATNRPAAATRRPRQTIVA

## SEQ ID 6973

TTGAGAATTTGGGAAGCGCATCCGCCGCTCCGCCCTTGTTCGCGCGGACCGCAACCATATAGCCGCCATCCGAACAATCAGTCAGAGAAAATCATGAATCAAAACCGCCATCAACCGCGCG  
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CGTACCGTCCGTGCAACCGCGCGGTGGGACGAAACCGCAGAAATAGCCGATGACGAAAGCCTCGCGGACCTTTTGGGCGGCAACCGCGGTGTTGCTATTGACGCTGCAACCCAAAGACGGCG  
AACCTGGCAGGCGTAGTGCTTTTGAAGGCGGCGAGCATCGCGCAATGTTGGTGAATATATGAAACGTTCCGAACAGCTTGATACGCACATCGCCTGCTGCAAGCGATGAAGCGGC  
GGGCGGGCTGCTGTCAGCGCTTCTGCTGAAGAGGTGTTGGATGAAGAGGCAATGGGAACACGCTCAGTACGCTGGCGCGCAGCTGACGGCGGAGGAGCTGCGAGAATGGACGCGCAACAC  
GTTTTATACCGCTGTTCCAGAAACCGCGCGCGCTGTTGCGAGCGGAAACGTTTGAATCCTCATGTACCTGTTCTCGGGGCAAGGTGACGGATATGCTGTTGATGCTGGCGGGGAAG  
AAGTCGCGCGCTGGTGGCGGAAACAGGACAGCATGAAGTCGATGCGACTTCTGCCACAGCAAAATACGTTGTTGATGAAACCGATGTCAACCGCGCTGTCGGGAGGATGTGCTGCGCGT  
TGCCAAAGGGCTGCCCGACATACCGTCCAA

## SEQ ID 6974

LRIWEAHPSPALFSRRPQPSRHPNNQSEKIMNQTAIRNADARTRFIFDDHVPRLHVRLENVWHIVKQKNYPAAIRCALGELLAAGVLLSGNLKNEGTLLIVQVQGGKMLVBAETS  
RTVBARATWDETAIEADESLDGLLGGNGVFLTLQPKDGPWQGVVLEGGSIQMLVNYMKRSEQLDTHIALSASDEAAGLLVQRLPEEVLDDEANHVSTLARTLTAEELAEIDAGH  
VLYRLPHETPPRVFEPETPESSTCSRGKVSMDLMLGGEEVGVVAEQSGSIEVDCDFCHSKYVFDETDVALFGEDVVGAKGLPRHTVQ

## SEQ ID 6975

TTGATGAATCAAAATCCGGAATCGAACGATATGATTTTGGCGCGGAGTTGTTCAAGCTGTGTCTAAAAACTTTCATTATGATGTAAATATTCCTGAGTTAAGCCTGAAGCAACCCAGC  
ATCAACCAATCAAG

## SEQ ID 6976

LMNQIRNETILILRAELFKLLSKNPHYDVNIPELKPEATQHQTIK

## SEQ ID 6977

TTTGATTTTCGACTTTAGCGCCTGCTGCTTCCAGTTGTTTTTGGATGCTTCGGCTTCAGCTTTAGAAAACACCCCTCTTTAATGGTTTTAGTTCGCGCGTCAACGATGCTTTAGCTTCTTTC  
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GACCTGCAACTGCAACAGCAGCAGCAGAAACACCGAATTTTCTTCAAAAGCTTTAACCAGGTCATTCATTCATTACGGTCAAGAAACCAACTGCTTCCAAAATGCTTCTTTAGTAAT  
AGCCAT

## SEQ ID 6978

PDFDFSAACCFQLFLDVGFSFRNTLFGNFRCAVNDVFSFFQTQTSNCTDNFNHADFLIAGRSQNDIKFGFFFSIGSTGTSRTCNCSNRNTEFFFKSPNQVIQPHYQRTNCFQNVFPSN  
SH

## SEQ ID 6979

TTGCGAAATTGAAGCGATGTAATTTGAAATGAGGCGCGGATATCGTATCGGACAAAAAACATTTGACGCGTTTATCGTTTCCGAAAAACCGCTGTTGAAATGTCGGATTGCGAGAA  
TCCGACCTACGCAAAAAACCGTAGCAAGGACAAAGCAATAGTTGCTGTAACCGGGAAGGCAATTTTCCCGCAGCGCGCGCTCATTCGCCGAACCTACATTCCTGCTATCCGACG  
AAAGTGGGAATCCGGAACGCAAAATCTAAGAAACCGTTTATTCGGATAAGTTTCGCGACCGCAGAGGTCGGAATCCCGCTTATGCGGGAA

## SEQ ID 6980

LNRNKRCKFEMQAGYSYPTKKTTFDAPIVSEKPLLESDSRIRPAKNRSKDKANSCLKTGRAILPQPSPSFRITYIPSPFRKWSGTQNLKPFYPIPSFRITDRSGFPLMBE

## SEQ ID 6981

TTGTTTTTGGATGCTTCGGCTTCAGCTTTAGAAAACACCCCTTTAATGGTTTTAGGTCGCGCGTCAACGATGCTTTAGCTTCTTTTCAGACCCAAACAGTAATTCGACGGACAACTTTA  
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CGAATTTTCTTCAAAAGCTTTAACCAGGTCATTCATTCATTACGGTCAAGAAACCAACTGCTTCCAAAATGCTTCTTTAGTAATAGCCATGCTATTTACTCCAAAATATGTAT

## SEQ ID 6982

LFLDVGFSFRNTLFGNFRCAVNDVFSFFQTQTSNCTDNFNHADFLIAGRSQNDIKFGFFFSIGSTGTSRTCNCSNRNTEFFFKSPNQVIQPHYQRTNCFQNVFPSN

## SEQ ID 6983

TTGTGCGAAATATGCGCTTCGGTACAGTCCGACGGATTGGGTAATGGCAACGGAACAAATATCCGCGAAATTTCCGCTTGGATTATGAAGGCAAGGCTGGCAAGGCTCGCGCGCA  
AAACGATTTTCATTAAGGGGCATTACTTGATTGTTGATGCTGGGTGCTTCAGGCTT

## SEQ ID 6984

LCENMRFGTVRTDWMATETNIAEISALDYEGRGVAKVGGRTIFIKGALLDCLMLGCFRL

## SEQ ID 6985

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CGGTAAGAACAACTTGACACCGCTCCCTGAAAAAAGCATCGGCAATGGGCAAAACACAGGGCAAAACCATCGCGCCGAGAAAGTCGATGCGGTACTCAAGAACCGCACCGGATCG  
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ACTCTGCGGAAGTATCCGAGACAGCAGCGCCGAGTGCTGATGACACGCGCGAGGCAAGCGCATTTAAATACCAATCCGACCGGACGCGAGTCCCTATACCGAACCGGCTGC  
CGATTATCGCGCAAGTAGAATCACTGATCAGGCTGCTTCCGACCGGTTGATGATTATTTTCAATAGATGTGATACGCGAGGGGAATTCGCTTTAGGTAAT

**SEQ ID 6986**

MIKRPFGHTPYFDMNKTI CRTAALLISGFSYANTVVPDVSVAQGHVFINLPQORFLFTDGLTKVYPPVAVGRAMTQNLGEHKIGAKAYNPVWHIPKSIQKERGDGVKTLAAGPTNP  
LGPVFLRLGDPKILGLGHTNAPASVPGIRSHGCVRMKSPDALEPARTLATGSPASVTYQHAGINEDADRNLMWLAARFDYPGKNMLDTASLKKSIGQWAKTQGKTLIAPEKVDVAVLKDRTGS  
AVCLTCGKNRKNMPLKSLAWIQGSSSYQAEVIEQTEETNSAEVSETRTPEVPDVHTPEAQAHNLWTSQDGTPTATYTEPAADSSPQVESPDQAASEPVDVLSIDVITROGNLRGN

**SEQ ID 6987**

AGCAGCTCTCTCGCGGGCTTTTTCCTCTGCCAAAGCAGCCAAACCGCGCGCAAGCCCGATACAGGAGCTTGCATAACGAACAACAGTTTGGACAACAGCTCTCTCGCGGGCTCGGAATAGAA  
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CAGAAGCAGCGCTAAACCAACGGACCAACCATTTGATCGGCCAATTCTACAAATGAAGTACCTTTGCACTGCGCGACGAGCCAGAGTATTTTTCAGAAGCCGCAAAATAACGCCCTTCTTTAAG  
TGCATTCCGCGAGCACTCAGTCATACCTGGAACACTGATACCGCGATATTCAGCGACTACGAGGGTTTGAGCATTAGCAATTGCCGCGCTAAATTTCCTCGACCGCCACTTCTTCGGTTTCA  
ATATTGAGACTCA

**SEQ ID 6988**

SSFFAGFFLCQSSQTARKARYRSLHNEQQFGQOLFAARNRSLSNLSIIHYFAIVRTGFNDNFVIFPRELVQHFSSNSIFRSSVNVQRTNHLIGQFYK\*STLECATSQSIFQNAQINAFPT  
CIRTKLSHTGNFDIALFSDYEGLSISNCRANFLDRHFLGPNLETO

**SEQ ID 6989**

ATGTTTCCCGACCAATTCGCCCCCAATCTGCTGCAAGGCTTGAAACCCGAAACAACCTCTCCGCGTAACCTGGCCGCGCAATTCGCCCTCGTTTGGCAGGCGCAGGCAGCGGCAAAACGC  
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TCTTGGGCGGCGCATTCGCAACAGGCATGTTGGGTGCTACCGGCAATTCGACAAAATTCGCAACGAGGCGTGGTGATTTTCGCGCAACTCATGCTTCGCGAGCTCGGCAAGAA  
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CGCGCGCAAGGGCTTGGAAATTCACGCGCGCTTCTCTCACGCTATGGAAGAGGGGCGTTTCCCCACGGAATGAGCTTGGCGAGCGCGCGCGCTCGAAGAAGAACCGCGCTCATGTAC  
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TGCATCTACCTGTTCGTCGCAACCCGCGCTTCGACAGCTACGGCAACACGCGCAAAACACCGTACACGGGACAAAATCATCGATGACTTCAACACGCGCAAACTACGCGAGCTTCGG  
CATCGGACAACAACTCTTCAACGCAAAATTCGGCACGCGCTGATTCATGCTCGCGCAGACAAGGCGAATCCGCGCGACTGACCATCAACTTCGGCAACAGGGCGTGAAGAGCTGGAT  
ACCAAGTTTTCGAAATTTGAAGCGGAT

**SEQ ID 6990**

HFPDQASAPNLIQGLNPEQLSAVTWPQOSALVLGAGSGCKTRVLTPTRIAWLLQSGQASVHSMIAVTPTNKAAKESQTRIGAMIPINVRAMWLGTTFHGLCHRFRLRLHHRDAGLPPSSFOILDSG  
 DQSLSLKRLLKLSNIAETIAPRSLQGFNIAQKESGLRASVLGADPDTSPMTGCGYAEYDKICQRBGVVDPAEIMLRSYEMELQSNELLRRHYQNFHNLVDFEOTNKLQYAWLKLMAGG  
 NAAVFAVGDDQSQSYTRFPGANVGNMTLMEEPHIDAPVLEQNYRISVGNILAAANAVIENNDERLKGKLRITDABAGDKIRYSSATPDLDEEARFIVDETALKEBEGWDLDEIAVYRSLMAGS  
 RVIEQSLFRSGIPYKITYGGLRPFYERQEIKHALAYLRILAVNPNDNNALRVINPPRGITAGRTVENQITQASNEQOTFLWQAAACNAGAKAAVVPVRLTEALRRHQVQMHLSSEIIVGLKDS  
 GLTFHYTRQKGDNQRLNDLDELVNAALFEKFPDSNFTLPENISDDPAPFILAFSLNAALESQENQAGAGEKAVQLMTVHAAGLEFNAPVLTGMEEGRFPSEMSLAERGLGEBEERRIMY  
 VAITRARKRLYITMAQQRMLHGQTFQGIASRFPVEIIPPEVLHYLSVKKPAFDSYKNTPTQVQDKITDDPKQPOTYAGFRIGQNVHRHAFKPGTGVLTDAADKGESARLITNFGKQGVKELD  
 TSKAKLEAH

SEQ ID 6991

TTGTTTGGCTTTTCCTACACCGCGCCCTGCCGCTTCTGCAACATCCAAGCGCACAATATGCCGTCTGAAGGCTTTAGACGGCATATTTACGA

**SEQ ID 6992**

LFGPSYTAALPLSATSKRTNMPSEGFRRHISR

**SEQ ID 6993**

ATGCGCTATTTTAAATAGAAACGGAAGGATGCCTGACAACTTGATTTCGGTTTGGCAAAGCCCTCGCCGACACAGCAGCAAAACCTTGATAGCGGATATCACATTCGGCGGT  
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CCTATCGGTTGGGGAAAAATTTTCGGTTTGC CGCTGAACATAGGAATAACCGCTTTTCAATTTCGAAACACCGAAATCGTACCGATTGTCAGACACAGCCAAAAACAATGCGGCTG  
AAACCCGGATTGTCAGGCTTCAGACGGCATTTTTGTTTCAGGCGGTTCGCGCTTCTCCCGAACACTTCCCGCCACAATTTC

**SEQ ID 6994**

MYTFNRRNGRMPDNLILISVLAKPSPTHARKTLIGGYHIAAFQTDLDGRIDRMADLPSLTMVKLGKPLRKGGIRIGFDIALSVGENISVCRINIGITAFQFANNENRRTDCSDTAKNKCRL  
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**SEQ ID 6995**

GTATTACCGCTTGATGTATCAACGCGAACCTTAAACCCATAGTGTGGATACAGCAACTTTTTTCAGGTACTGACCTTTAGCAGCAGCAGGTTTGGCTTTAAACGATAGCGTCCAGCAAC  
GCATCAAAAGTTCCTTTTCAAAATCAGCTTCAGCGAATGAAGCAGCACTAATCGTTGCATGAACAATACTGCCTTGTGCGTACGGTACTGCACCTTGACCTGCTTTTGCACTTTTACCGCTT  
CGCGAACATTAGGGGTAAACCGTACTATTTTAGGGTTTGGCATCAGACCCAGGAGACCCAGATGTTACCAAATTTGACCAACGATAGCGATTGCATCAGGAGAGCAATAACACATCAAA  
GTTACAGTTTGCCTCGTAACTTTTTCAGCAGCCAACTTTCGAAACCGACGATCCGCAACCGCCTCTTTAGCAGCTTCTGCATTTACACCTTGAGTAAATACAGCCACACGGGTTGCTTTA  
CCAGTACCTTTAGGCGAAGGATGAACACCGGATATCTGGTCAGATTTACGAGAATCAACGCCAAGTTGAAAGATACGCTTAACAGATTCTGTCAAATTTAGCGGTAGCAGCTTTTAA  
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**SEQ ID 6996**

VIHA\* CINANNT\*THSAGYSNFFQVLTFSSSRFGPNDVSQORIKVLQPLSFSE\*STTRNCMNTLVLGVTLHLTCFCIFYRGNIRGNTRYFVRVWHQTRTPDGTQLINDTHCIRRSNNNIK  
VQLACDFPSSQIFETDDIRTSLSFSSFCIVTLSKYSHTGCLTSTFROND\*TTDLVRFRTRINAOVERYVNRVFKVPSGSSSPFNOGNCVDCVOPVSNRRKKNFOAIFYPSH

**SEQ ID 6997**

TTGGGCGACTATTATCGTGAAATATGCCGTCTAAAGCCTTCAGACGGCATATTTGTGCGCTTGGATGTTGCAGAAAGCGGCAGGGCGGCGGTG

**SEQ ID 6998**

LGDYYREICRLKPSDGIFVRLDVAESGRAAV

## SEQ ID 6999

TACAAACACCTCCACGTCACAGCCCATTTAGCGAGCAGAACTGCTATAGTACGAACGCCGATCCAAAGTCAGCAGCAGTCAAATCAGCGCTTTAGTTTTCAGCAATTTCTTCCAACTGG  
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CTGCAATTCGAGTAATCACAACCGGAATTTGGCAACAGATTCCATACCTTGGGTTGCAGCATTAATGCTTTACAGAAATTCATGATTTCAAACCACTTGACCCAAAGCAGGACCAAC  
TGGGGGGGATGATTGGCTTTGCCCTGCAGGAATTTGCAGTTTAAATATAGCCGATTAATTTCTTTGCCAC

## SEQ ID 7000

YNTLHVQAH\*ASRTCYSTNSRIQVSSQIRLPSFNFQLGTGQFTYLVQRIRTTFLQTGGFPQNRSSRSFHKCE\*FICKCSNHNRRNQTRFHTLGCISKCTFEFHDIQTTLTQSRWN  
WGGWIGFACRNLPNLADNPLCH

## SEQ ID 7001

ATGATGAATTTGGGTTTCAAACCGATACCCCTGCCATTGCGCGCAGTATTGTGCGCCCTGGTTFITGGCACTGCCGTACCCGACGGGGTCAAGCCTCAGGCTTGGACGCTGCTGGCTATGT  
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TTGCCCGCAGTTACGGCTCCAATCCCGCAAAAGGCACAGAAGGACAGATGGTAAATATTTGGCTTTGGTCAATTTCAATTCGAATCCCATTTTCGTGGCTATGTTTATTCGCAACTGC  
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CTGGGATATTGG

## SEQ ID 7002

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LILYLYPPEIKETPNVQFAPKDRLESEMGRMSADEIIMAVIFGILLILLWADVPALITJGNHAFSINATATAFIGLSILLISGLVFWDDVLKEKSANDTIWFGALIMMAAFNLKGLIKWFS  
GVLAESVGGIGVSGTAAGVLLVLAHYMYHMFPASTTAHITAMFGAFLAAAVSLNAPAMPATLMMMAASNTDMLTHYATGTSPIVFGSGYTTMGEMKAGFINSVVNFIPIFVIGISIMWV  
LGTW

## SEQ ID 7003

ATGTCGACCAACCGCTCGACACCGCCCGCCGCTTCCCTGTCTCCGCGCGCAGCTCGACAACGGCAAACTCAAGCCGAAATTTTCCCTGCGCATGTTGGACAAGGCGTTGACGGGATG  
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## SEQ ID 7004

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PNDIKSLVRPVPFRKYLIDYAYEAMRNLRQIRSEVSKKGMADNIKLAGGIREVEFIAQIPQMRGGQHRALQLKGTQETLKKIAEMGIMPSENVETLLAAYRFLRDVEHRLQYWDROPT  
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## SEQ ID 7005

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GGGACCGGTACGCCGTATGCGCGCGCTTGACGAGCAGCGGCATTAATAATCTACGTGGGCTGACGGATCTCGACATCGTCGGTATGGATGTTGTAGAAGTGGCCCCCTCTTACGACC  
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## SEQ ID 7006

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LSLGGDEFTLPLRLAHARYPGKLALHFDARTDYDNGSEYDHGTMFYTAPKEGLIDPSRSVQIGIRTEHSKLLPFTVLSAPKVNEDSVRETVRKIKETVGNMPVYLTFDIDCLDPSFAP  
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## SEQ ID 7007

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## SEQ ID 7008

VARFERETAAPAAVFLSAGIRPNIGARFQTASKVAHI

## SEQ ID 7009

ATGCCGTCTGAACCTTTGCCCGATATTCGGACGGATGCCCTGCCGATAAAAAACAGCGCAAATGCCGCCGTTTCCCGTTCAAACCTCGCCACGCTCTTTTAAACAGCA

## SEQ ID 7010

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## SEQ ID 7011

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## SEQ ID 7012

VNLLNLAEQLNGCFSTKYLNRA\*LIPIIDLLNHPVKIRKRSFIYTNLLTDLKFNFWFRLLYAGLNL\*NNPSLSITNRRGSI SPPSNKTRNTGSAFYKMPRVICHPHLN\*HITRI\*LS  
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## SEQ ID 7013

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## SEQ ID 7014

MEPIIFIREVCNINHSIGYIDVDSGEIIVRPNPSQHNQTVSLQKLTEAVQKQKARLPVLPFCPPQILEHRLRDINRAFTARKECGYKGYCLVYPIKVNQHRVIESLSSGQPHGLEA  
GSKAELMAVLAHAGTRQTLIVCNGYKDREYIRFALMGKLGHVYLVEIKLESIQVMLEBAEKLIGIKPLRGLVRARLASQSGSKWSSGGEKSKPLSASQVLQVLDILKQNRDLCQLLH  
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LNEPIARRAVLLDITCSDGTIDHYIDGDIAGTMTFMDYPEZEPPLGPFMVGAYQELGNMHNLPFGDTADJVVDGQFTVIDYDEGNTVADMLEYVYQDKELMKRYREQIEHSL  
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## SEQ ID 7015

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TAACATCTTTTTTTCAGCGGTATGCTCTGTCAT

## SEQ ID 7016

TFPSQVYIKK\*PRNCCI CRIDKYRKHSNKHYNKYSHSDGIPTLRPNHLFEPGPRI\*EICKKTL/TGIRCFPIILNQLIHFNILFPRMPCH

## SEQ ID 7017

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## SEQ ID 7018

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## SEQ ID 7019

ATGCCGATTGCTGGATATATCCCGAGATGGCAAGGGACGAATCGACACCGGCACAGGTGCGGACGATTTCGGTTTTCCCGATATGCACAAAAC

## SEQ ID 7020

MPILLDISRDGKGRIDTGTGADDFGFPDMHKT

## SEQ ID 7021

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## SEQ ID 7022

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## SEQ ID 7023

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CGTGTGCTAGTGGCGGTTTCGTTCTGATTTACGTGCGAGGTGTTAATGTAATACCGCGTCTTTTCTTCGGGTGCGTTGTCGATTTGGTCTGAAGCTTTTCAGCGCGCGCGAA  
TTTTTAGC

## SEQ ID 7024

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AGQVADPHFNQFQQLGIVDHVAFVHEHDDVRYAYLTGQDVFAGLRHRAVGSRTYQDCTVHLGAGNHVFNVGVTRTTYVVCVAGFGFVYVRGVNGNTACFFPGCVVDLVVSPCSAAE  
FFS

## SEQ ID 7025

ATGCCGCTGAAGCGCTTCAGACGCCATTTCGCTGTCTCATCAGTATGAGCGAGGCTTTCTTATTAATAAATGACATTTCACGCTGATTTGTTA

## SEQ ID 7026

MPSEAFRRHFACSSSGMRQAFLIKMTFHADLL

## SEQ ID 7027

ATGAACCTTGATTTAAACCGCTCAAAAGTCCGCCCTTCTTGGAAGGATATCTGTGGGGGTATGAGATAAATACTTGGGTGGGCTGATGTGGCAGCTTATGCCGAAAAATGACGCTTT  
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## SEQ ID 7028

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## SEQ ID 7029

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## SEQ ID 7030

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VARLTFVQQAETHFNAGTGGLFPPQTDNPLVNVDDTSLYTAGDYTAAGNGEHVDRQEQWVHGTLSRDAVQCGSQFEDFFVSGIAPQPGCTLYDRAVAVAGEVAGQVADP  
HFNQFQQLGIVDHVAFVHEHDDVRYAYLTGQDVFAGLRHRAVGSRTYQDCTVHLGAGNHVFNVGVTRTTYVVCVAGFGFVYVRGVNGNTACFFPGCVVDLVVSPCSAAEFFS\*NSSQ  
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## SEQ ID 7031

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## SEQ ID 7032

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## SEQ ID 7033

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## SEQ ID 7034

MPSERTFCRSDGIFIDWYPTVEIAISRHLDF

## SEQ ID 7035

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CCGACGCACTGCGTCAGAGGTTGGGGTGAATTCGTAATTTCTCGCTTGGGAAATGSCATCATTTGGGCAATTCGGGTTCCGATACGTCGAGTGAATGCACTCGTCGTAATAAAA  
GCGACAT

## SEQ ID 7036

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## SEQ ID 7037

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SEQ ID 70471

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CGTCCAAAGTGATACCGGATTGATATACAAAGGCCCGCGGTTGTCAAAGAATTGTTGAAGGCATTGGCGCGA

SECT ID 1042  
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MGAFNNESGIDAMIRNIEKSKYQVGLGINIGKNAVTPIQNAADDVYLCEKAYAHASYITVNISSPNTKNLRALQGGGELGALLEALKNKQAQALAAHNGKTYPLAVKIPADLDEAQIEDIARV  
VKSVPMDGIIATNTIDKSSLSGSHPLAGEOGGLSGFPVREKSNELKKLAEHIDGALPIGVGGINEGGDAAEKIRLGTAVQVYSGLIYKGPALVKECKLALAR

SEQ ID 7043

ATGTCACAACTCGAACAACAAGTTAAGAAAATATTGCTGAACAACTGGGCGTAAACGAAGCCGACGCTGAAAAACGAATCTTCCTTCCAAGACGACTTGGGCGCGGATTCTTTGGATACCG  
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MSNTEGQVKKIIEAOLGVNEADVKNESFPDDILGADSLDTVELVMALEEAFGCEIPDEDAEKITTVQLAIDYINAHNG

SEQ ID 7049  
ATGCGTACCAACTATTGGCGCCTGATCAGCGAGCAATACTTTATGCCAAACCGTTACCGTCAAAGGCTGGGTACACCGCGGCGCGACCACGGCGGTGTGATTTTTATGCACCTGCOCGAAC  
CGCAAGGCAATCGTCCAACTGTGATCGATCCCGACACGCCCGAAGCGTTTGGCGCTGCCGATTCCGCCCGTAACGAATACGPTTTGGGCATTGCCGGCCGCGTACGCAACCGTCCGAAGCA  
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SEQ ID 7047

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CAATAATTCTCTAACTGTGTGTCGATGTT

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SEQ ID 7049

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TGTCGCGCGCGAAGTGCCTGCTTTCGACATCGGACAAATACATCAGCGCGAAGAAGCGCGCGGATGGACGTGTTCATTCACATACGCGCATCGCCGCGCATTCGACGGCGATTCGCCGATTTCG  
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GLIDVENLIDKDRIGVNISSGIGGLPSTIEATGKAVIEGGARKINFPFIPGSLINLISHVITILKGYRGPSPYGHVSACTTGAHAIGDSARLIKYGDAIDHVAGGAEGAISTLGVGGPAAHKAL

STRNDPATASTRPDKGRDGFVIGEGAGILVLEELHAKKRGAKIYAEIVGFMSSDAYHITAPNEEGPALAVTRALKDAGINPEVDVYNARSTSTPLGDANETKALKRAFGEHACKTVI  
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SEQ ID 7051

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SEQ ID 7052

FSHLENP\*FKCTLPRLPLPISRQPIRFVRLPACLDINICAVIQACAQYIEKTFPTLPRKRRIKEDDIEFLF\*VCQIGNAVRTDGLHLPTQFAAVFLKGLHRLTVVVCNHDFFCITRCLH  
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SEQ ID 7053

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SEQ ID 7054

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DSSRFKTPVLVFPQSGIWTIAFVSGQVSNVAKALPDQDGLSVYVPTPNPTGGYIMVKSDVRELMVDEALKYVLSLGHVIEDDLPVKTLAGFMPPEKAELEPQQ

SEQ ID 7055

TTGCCGCTTCCGCGCGAGGTTCCGTCATCTTCTGATTCCGACAAAGTCCGTACAAACCGCACATTTATACCGGTTTGGCGGATTCAAACGAATTTTATCCGCGCCGCCAAACCGC  
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SEQ ID 7056

LPPSAAGSVILLDSKVRTNRTLYAFARIQTNFLSRPAKPPAASDGTAT

SEQ ID 7057

TTGGTATGTTTGCCTGCCGCAATATCAAAAGCTGAAAGTTCAAACGGTATTATACAAGACCTGTGCAAGAAATATGCCGCTGAAACCTTTTTCAGACGCGCATATCTGTTAAACGGTT  
TCGGTCAGCTTCCGCGCAACTCGATTCTTGTCTTTTGTTCACATTTCTTTGCAATTTTCAATTTCCATTTTAAACAAATCCAGCTTTACCGATGCATCC

SEQ ID 7058

LVCLPAALIKSLKVQTVLYKTCRRICRLKTFRRHICLNGFGQLAEQLDFVFCNSLQCFNSIPKSSFTDAS

SEQ ID 7059

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SEQ ID 7060

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SEQ ID 7061

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AA

SEQ ID 7062

MTPFRKAVWLLFAVSVCAFGSLAAQYVLGMEPCVLICISRLCVLATALCAAVLACKPKGRVGLSGAVFISIPAVTGISVAAQQLWLQSLPFGAAPSCGAPWTPRLKGWPLFDWFEV  
VRGFGNCAEPDYLLGVALPWSAAYPFAVVLTVWNAWAK

SEQ ID 7063

TTGAAAAAGAAATCCATATCGGTGTTTCCGCGCAGGAGGATCGTGCCCGCGTGGATGTTATGCTGTATCAGTCGAAAAATATCTTGTGATTGTATATAAAAAACGGCTGTTTGGCAA  
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SEQ ID 7064

LKESISVPRRRRAAVRCYAVSVENILLIVYKTAWQKAC

SEQ ID 7065

TTGATATGCGGTTTGAACCGTATTTCAGATGCGGTTCCAGTCTGTTGAACATCAACCGGATACCGATACCGTCTGCTTGTGTTGTAGTCGATCAGGCTCTCGCCGTAAACCGTGGAAATCGG  
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CTTTGACTCTGCTGCTGCTGCTGCGGAGACGGAAGCTGTGCGCGCAAAATCTGTCGTAACAGCGCAACCGGTAACATTTGCTGTAAGCGCGGCTTTCAGCGCGGCTCTCTCC  
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SEQ ID 7066

LICRLKRYSDAVFVVEHQPDFTDVLVVVVQALAVTVESAYHAFELNKRKVGPNRAVARFVVAQYGIHLPVVQAVLQLHVAIPHIVGNIGIVVFIAALIERTHPHARNHRQFAFF  
HACHGINPVPRPTGALSGLVLDKTRTEHTQPAERQIRLHRLQENFRFRVIRIAERRFPALVNLPIGSLGVAEPQIRAGFKPIGNFAFERNLQFPRTFLLEPFLYSRTARRRTR  
GIVGRIVIPKRRKHVRIVFAYAQPAQIVFVQVHQAQRRIIDIGPARTVGRKRIPAPFNNDRLLALIAAADFRQIEYGRILPLPCRRRLKRNKVFVTRQTRNIVRQSGALRGLS  
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SEQ ID 7067

ATGACGCAACCGCATGAAAAACCCAACTCTGGCGGTCATTGCCGCGCGCGCATTCATCTCTGCTGATTACCATCGGATGAGGATGAGCTCGGCTGTTCTGCAACCGCTGCTCA  
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SEQ ID 7068

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**SEQ ID 7069**

GCTGTGGGAGCAACTCGAATTTCTTGTCTTTGTTCCAACTATTTCTTTCAGTGTTCACATTCCAATTTTAAACAAATCCAGCTTTACCGATGCATCTGAGCGGTAAGATTGCAAAATTC  
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**SEQ ID 7070**

ACGATRFLLCFQHFPAVFQHFH\*QIQLYRCILSGIDCKFPAVGIIHIVNLQHHP SATRFERIPTNPDSRLRGNGGF\*GYGVSAMAVRVFPRTCPAPVNGERVEKNAV\*RFRRH

**SEQ ID 7071**

GTGGGGCGTATTTGCAACCAATTGTCGGGGCGCGCTGCGGACCGGTTTCGGGCGGTTTCAGGGTATTAAAGCGGCGGTGCCCTCTGCTCGTCTGCGCCTGCGTGAATTCGCTCCAAACATCCOAGCT  
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TCAAAACGCTGCTTCAAAACCGACGCTACATCTCTGCAACCTGAGCTTTTCGCTGCGGCTTCACATGCGCTTTCCTGTAACCCACCTTACCCACGGAAGTTCGCCCTGTGCGGACTGCG  
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SEQ ID 7072

VGRIATIVRRACRPFRFVQGIKRCPPARLELPDCLQHPDLLGADDCRRAAARIRHFRFVPHFYGTGRRSPSPHTQTRLGIRTGQRRRFGRTPVPTAGSRTQGLVVLPEVGTGTFYVFG  
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SEQ ID 7073

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CAGTCGTGGTTCTTTTTCCATTGAAPGAACCTGATGTCTGACGTGTCCTGTAGGCGACGCGCACGCCGATATAGGGTTTGAATTTATTCGTTGGCTCTGAAATCGPAAACGGTGACAAAGCC  
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SEQ ID 7074

EAVAHAQ\*GFVGFAGVFPQASPIVVAVAGVQQAGRDVYAHARHRAEAQAAAAAVVIGRPGGHF\*WNRSPFTTVAWVSGNSRGFFH\*MNLSMDVSVGDADHADIGFEFTVGSBTVMG\*QA  
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## SEQ ID 7075

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SEQ ID 7076

LKTMPTMGAEINTRNRMRYILLTGLLPASAFGETALQCAALTNDVTRLACYDRIFAAQLPSSAGQEGQSKAVLNLTTETVRSSLDKGEAVITVVEKGGDALPADSAGETADIYTPPLSLMYD  
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LRMLGAGFVHQSNQSRPESRSWNRIYAMAGMEWGLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYRLNDRQNVYSVLRYNPKTYGAIEAAYTFPIKGLKGVVRGPHCYGES  
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SEQ ID 7077

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SEQ ID 7078

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NPKLHPAAPELFRLLRPLRLSRNPPTHGSRPVRTARHRRILDHRHRTGKHRRRLVLRMLMHTLQKTKHPVRTLRLTRREGADLHLLTQNRPLLHFRRTTRIEMAHRRPDRRRYQTLR  
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SEQ ID 7079

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SEQ ID 7080

MVLIVIFSPKTDLNFYIFAAALGFTWLATVAPTAAVTGKLEFTRYLATLFGLVMLTHOIGGFGLGSYIGGIVITOFGDYGMHAYADAVLAGTAALLVLPVREPTAA

## SEQ ID 7081

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ACTGGCGGGCAGCTTTGCGTGTGTGCGCTGTTCGCCATATTGGAATCTCC

## SEQ ID 7082

LAVLQKSSQCTYFCRAAFVARSFVFMKHFVGDVDDFDGLLVNRLOGSF IACFDCFYFFHCGABCQTQASVVGALFDGLAGTFACLCVCHIGIS

## SEQ ID 7083

AAGAATGTATTTATTTTTTAAATCCCGCCAGCCGGGATAAATCTGCTTTACCAATGTTTTTAAATGGAATTCGAACTTTTACCCCACTGTTGTCAAACCGCGTCCGCACTCCTTC  
AAATACAGCCCGAAATGCTCTTTTGGGAATGCCGTCAAACCTTGGCAA

## SEQ ID 7084

KNVFIF\*NPGQPG\*ILLYQLF\*NGNSNFYPTVVRTPSALLQIQPEMLFGNAVKLAQ

## SEQ ID 7085

GTGATGATTTTACACCCGAAGGGAAAACGGGCTTATTGAATGCGCGTTAATCGCGCGGTATTTCGCGTTTGATAAGCGTGATTTCGTCGCCGTGACGTCCGCAACCGGGCGGGTGT  
TTGGAAATGCGGCTCTGAAGGTTTCAGACGGCATTCGTGTCATGCGCGGTTCGGGTTTCGCGGACGGCAGGACAGCAGGGCTGCCGTGCGCGCGAGTACGGCATCGGCTACCATATCC  
AGCCGTAGTACACGAATTTGTGAATCAGATGCCGCGATGTACGAGCGAGGAATCCGCGGATTGTGTGGTGAGCATCACCAGTCCGAACAGGTTGCGAGGTAGCGGTGCGGAGAG  
TTTGGCGGTAAACGCGCGGTGCGGCGAGCGGTGCGGAGCCATGTGAATCCGAGTCCGCGCGCAAAATGTAAAGTTGAGGTGCGTTTGGG

## SEQ ID 7086

VMI LHPKGRAYLNGGLIAAVICGLIRLICVPCSPATGGVF GKCRKLVSDGILSCGSGFADGQDKQGRAGRYGIGVPHPAVVTLECNHDAADVRAESADLVGBHHQSEQGGEVARAE  
FAGNGGGRGDGGEPCRESECGENVKVEVGF

## SEQ ID 7087

ATGCGCGCGCTTGCACAAAGGTTTGCCTCCGCGCCGCCCTATCCGGCATTTTCATCAATGACAGCCGATTTCCAATCTATATTCAAGGTGTCGCCCTTATGAAATCGTTTTATCACAA  
CAGTCCGATCCAGCATTTACGGTTTTCGCGCCCCCGTCAATAAAAAATAATCGGCAAAACCATCAGGTGATGCTTTGTATCGGAGTTTTCCGATAATGAGTTGACATTATCAGGA  
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CCTTATTTCGCAAAACCGGTGATTTTCGGCACTTTTCCGCCAAAATTGGCAGCGGTGCCAGATCGTCGGATGCTGGAAGGTTTGGGATTTCGCAATTTACCCCGCAGCGGAAGCATAC  
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CATCAAAATAAAACATTTCATATTTCGGCGGAATCGGTTCGATTTCGCGCAATATTCCTTTATTCGAGGCGGATATCCCGATGAAAAAGAACCCGTAAATTTCTCTTTATCGGCAGA  
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ATCTTGGCCGAAAAATGATTATTATTCGAAAAACAGGGTCCGCTCCGCGTATGCGCAATGCAAGTTATGCGATTGCCAAAGATAAATTCGATGCCGAAAAAGTCGATTGAAATTTTC  
TCGATATTTTGAAGGCG

## SEQ ID 7088

MRRARQRFARRAPYPAPFQCRPHFQSYIQVRLMKIVFTTTVASSIYGFRAPIVKKLIGKNHQVYAFVSEFSDNELDIIREMGVTPVYRNSRSGVNPFSDIKSTFLIFKALKKISPDLVF  
PYPAKPVIFGTFAAKLAGVPRIVGMLEGLFAPTPQBPGLPKTKIILKILALYRIALPMLSLIVLNPDDKDELLEHQYGIKIKNIHILGGIGLRLQYPYSEADI PDEKEPVKFLIFGR  
PLKERGIDDFIRAAEQVKYKYPDTVFTALGAIDKSRGGGDLERFIARDIIRFPGVNINVSEVIKAHIFVLPFSYRBEVPRSTQEMAVGRAVITTDVPGCRETVADKVNGLIEPWNFR  
ILAERMIYFIENRAAVRIMANASYAIADKFDKEDVLDKFLDILKA

## SEQ ID 7089

AATACAGCCCGAAATGCTCTTTGGGAATGCCGTCAAACCTTCGCGAATGACGTTTGGCCGATTCCAAAAGTTCCTCAATTCGCTTGATATGTTTTGCGCTTCGCAAAATGTGTCGCGCA  
TTGATACGGAAACGGCCAAATCCGCTTACAATCTGATACATCGTAACACGCAATCCGTATAAACAATGCTGCGCGGTTTCAACCGCTCCCGGATAATAGGCAATAAATAGCGGTTTCG  
AGTGTCCGACAGTAACCGTACAAACCTTGCCTTGCCTTCAAAAGCCCGAATACGCGCGCTTTGCCGCGGCACTGCGGCGCGCTGCTGCTTTACGGAATAAATTTACCCCGCCCTGCG  
TTCCGCGTCATACATTTCCAAATGCCGACTGTTTTCAGCGATAAGTAATCGTAAACGATATGCTGATGCTCCATAATTTCCGAGATTTCGTCCTCAATGCGGTGAAAGGAAGTTTCCCG  
ATGATGTGCCAAACACTATTTCGCCATAGAAAAATACAGGCTGCCGTGTTTTGATTAACTGCTGCCAA

## SEQ ID 7090

NFARNALNECRQTCANDVCPKPVNCVDMVLPFGMKCAALDTEKASYNLHNRVQSV\*THLPGRTPRPIIGNKIAVRVSDSNRTNLAVLQKPEYGGFAGSTAAASAPTEITPTRPC  
FAVHFQMRVLTDK\*S\* TICRMP\*FRFRPNACKGSPDDVPNTISP\*KITGCRVLINCCQ

## SEQ ID 7091

ATGGCAACAGCGCACAGCAGCAACAGTGCCTCCGTCAGTCAAAACACCGCCACACGCTAGCCTGCGTACCGCATTCGCGACCGCAGTGAAAAAGTATTGAAAGCAGTCGAAG  
CAGGCGATAAGCTGCGGCACAACCGGTTTACCAAGATCCGTCAAAGTCATCGACCCGATCGCCGACAAAGCGGTGTTTCAATAAACAAGCGGCTCGCCACAAAGCGCGCTGCTGCG  
AAAAGTAAAGCACTGGCT

## SEQ ID 7092

MANSQAQRKRRQSVKQRAHNASLRTAFRTAVKKVLKAVEAGDKAAQAVYQESVKVIDRIADKGVFHKNAARHKSRLSAKVKALA

## SEQ ID 7093

TTGCGGTGACGGCGTTGATTTGTTCTTTCCAGCCGATTTCTTTTTCGCGGCGAGCTTTTTCACGCCCCGGCGTTTGGTAGTTTGTATGCCAGTACCGGCAATGGCAGTTTCGGCAT  
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TCGGCGTGGCGTACAGGAAGTCCGGCGATCGCTTCATGGCTTCTTGGCGCTTTTGGATTGTTGTTTGTATTGTTTGGCGGCACTCGGCAGATATCTTTCGCGGATTGTTTTCAA  
TGTAATGGCGATTTCGGT

## SEQ ID 7094

LRCRRFDLFFPAFFLRADFFHAPFGSFDQYRPMARAFFGKGRVPSGVVAVGIGAATVKQFVAVAGFALDEVAFALRALDAGIFGFQRLDVFAGVVGATDEFTAGAAVVFHQPASAA  
FGAFATVEFDLFGFRPGDAGSFPFGFVDVAGVTALGTTGTRNETAHFELDLQFVPAARFAGFVKFLRSEFGAFDALFFHFLDERFPEFVHGNPAAPAVGDFVKLVFEPGGEVVIDVL



GEVFGQEFIDDVACVGGHEAFLLKGNVFAVFERNNAGVGRGAADAVFEGFNQCGFVARRRGGEVLFAVEFVDRQFVFAHFQGFVAVPALFVAAPFVNAERACGLHLSGYSEHAF  
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## SEQ ID 7095

GTGTTTATGGGCGCGGGGTTTTCTTTTTTTCACCTCTTTTCATCAGGAATCTGCCCGTATGAAAAATCCGTATTAGCCGTTTTGGCCGCGCTGTCTCTGGCAGCCTGCGCGGCGAGCG  
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CAAGCTGAAATCTCGCGCATCGCTTGTGGGACACCCCGAGCAATGTTCCCGATTTTGTCTGAATCTTTGGGCAAGACCCCAAGGTTGCAATCTCGAAGATTTGAAGGCGCGCG  
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## SEQ ID 7096

VFMGRGVFFSNLPHQESARMKKSIVLAVLAALSACGSEKNVQFQAGSAPANAEEAATDTLNIYNWSNYVDESTVEDFKANNLKITDLYENNETLEAKHLTKSGYDLVVPGLAF  
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EVLKSIREFDKRSPSIIDELARGDIDLALAGNGDLNLAKARSEVNKVVGLVLTPEKGMFIESWLPADAKNVANAHKYNITLDPKIAKNGLAVTAPASKPARERMPAELVNTES  
IPFNEQDKDGFVMPQMSADAKLLSVSLWQKIKVGTN

## SEQ ID 7097

TTGACCGGGATTCGACGATTAAGAGGTTTTTCGCCATTGTCTGCTCTGATGCTGTTTTGACCGCGTGTTCAGACGGCATCGGCGGGCGCGCGCGCT

## SEQ ID 7098

LDGDSYIKRFFAICRSLDGGFDAGVSDGIGRAGAV

## SEQ ID 7099

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AAACGCGCTCGACAGATTGACGGCAACCGCAGCAAAACCGCGCGGAATAAAAACGCGCTGCGCCCAACCGACAGCGGCACATCTGAGCGCGACTCGCGCTCAFTGCTTCTGCTCAAC  
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## SEQ ID 7100

LRRQAEENWNPRIITLIGIKLKQTLQDLQRLQSLRLVQMPNIELEREVENWPNLIERKETDEFSDAEFSHYTAPARQIGGDEGEDMLSNIAAGEEDFKQYLHAQACEHPLSDQEAAC  
VHILIDFLDEQGYLTDSIEDLIDHTPLEWMLDEAMLKQALTALKKFDPAAGAAADVTESLIQIERSGECAKPAALHIVRNALDSIDGNRSQTPARIKNACPKPTAAHSPKPSASILRST  
PPPPFVLPFRPSPSILTRHSPCTHLSAV

## SEQ ID 7101

ATGCCGTCGCAACGATGTTTCGAGCGGCAATTTATATTTGGATTGAAATAGAAATATTTATACCGTCGCCCGCGCGGATTTTCAGATTGCGGACATTTATAGCGGATTAACAAAAACCG  
GTACGCGGTTGCCCGCTTAGCTCAAGAGAACGATCTCT

## SEQ ID 7102

MPSERCSDGILYWEIEIPSPPRPGFIADIYSGIMTKGTALPRLSSKRTLL

## SEQ ID 7103

CTCTTCCGCTGCGAGCGGTTGCAATTTGTTCTTTCAGCGCCATCTTTTTTGGCGGCGAGCTTTTTCACGCGCGCGGCTTTGGTAGTTTGTATGCCAGTACCGGCCAATGCGAGTTGCGG  
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## SEQ ID 7104

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LGEVFGQEFIDDVACVGGHEAFLLKGNVFAVFERNNAGVGRGAADAVFEGFNQCGFVARRRGGEVLFAVEFVDRQFVFAHFQGFVAVPALFVAAPFVNAERACGLHLSGYSEHAF  
ADGNIDGGLVEFGRRHLTGNTLPHLLIEFELVCTQEGFADFRAVHGSRADRFMGLGVFGFVLFGGTRQIFPADFVFNHADFG+RFVSQIHAVGTGHTGNQDGTLEFYVTTFKLLG  
GTHGAVGGEAQTHGILLHGGCGKRRGGVAAALFLFDGNDGLFAFEFFQHIIGLSGFRVQVLEFPRVAVGFEFGGELAAAFMAVEMHRPILRFRADFPVAFALANQPGGCTLHTARAQTA  
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AAFGDEADVSVGREDFKIAAQ



**SEQ ID 7106**

**SEQ ID 7107**

**SEQ ID 7108**

**SEQ ID 7109**

**SEQ ID 7110**

SEQ ID 7111

SEQ ID 7112

**SEQ ID 7113**

**SEQ ID 7114**

SEQ ID 7115

SEQ ID 7116

SEQ ID 7117

SEQ ID 7118

SEQ ID 7119

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VHTAFGDDFAHEVGBFFTOPIOLROOGAARAGGAVALVVGNGRAVAVVQMGYAFGSGHRSCTSPVOVGMGKRLTVRFKGGRIRNRPLDNCNKLESTFYFPFARTDAIITRODFR

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GCGCTGCGGAAATTTTCGGCGAGGTTTGGTGTGTTAATGTCATCGGATACATGGAAGCGCTCTTATCGGCTTGTGTTTGAATCTTGAATCAA

MSLYALLLVAGLMSDAFAVALAKGAAVRPEPRKIAATLVFGTVEAFMPLAGNVGGFYAKPFISENDHWVAFVLLGGLGLKMMRGLSGEAEVRESIQESLMTVLTAFGTSDISMTV  
VGLAFNEVNIAPAAAVIGMAATVMVTIIGLTAGKAGVGLFGRRAEFAGGLVLLAIGTWLLSHLGLIQ

AGTTCCGGATACGCTGGTATCTGCCGCCGGGCATTGCGGCAACGCTGCCGTCCAATTCCAATTCCAACAGTGGCGCATACAAATCTGCGGCAGGCATAGCCAACTGTCCGGCAAGCACGTCG  
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GGCCCGTGTGCGGCGTATCCCTATTATAGAAATATGACGAAGCACCCGTATTTTGGCAATAGCCCGGGCATTCGTTCCAGGATGTGCTCCAAATCTCCGTGAGTTTTCGCTCCGCTCTTAAAT  
CAGTTTGTGGCAGCTTTGCTGTGGGGGTGCTATCTGAACCGGTCGACGCCATCACTTCCGCGCCCATTTCTGCCCGCAGGCGCGCGGTATCATCGCAAGAACGGATTTCCAGGCGGCCCTCT  
ACCCACACGGGTAACTCTGCAGACGCGGGTGCTAATCAGCGGCTTGGCGCGGGAAGGTTGCCGGCATTCAGCGCGCGTCCGATGCGGGGAACATCGCTGAACATCAGCCCTTTTTCGGCGAATTTCAAT  
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ACCCGACACGGTATGAATGCTTTTCCACCCAAACGCCCTGCCGAATCTTTGGCAATTCGCATCGCTTGGCGCTGGCATGGCGGTGCCGACGATGGCGGCGGAAGGCTTGTGCAGCAG  
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GTCCTGCAAACTGGCATCAGCAGCAGGAATTTTCCGCGCGATATAGGCGGTAAACGCCAATTTGACCGACCGGAAACGCTGCTGCTCTGTGATCAATAATCCAT

SSDVLVSAAGHCGNAAVQFQFOQCGIQCGRHSLGSKHVGNRVETHFIQYADGCAACRPFRHRFCGRRRGVCRLLNGAAAVGRI LIYRI\* RSTRILQ\* PRAFVDVQVTFQFRSVFI  
QFVAAPAVGVVYRTGYRHHFAPHFCRQAGGNQRTGFGGLDQHNRLRQRGNQAVARKVAGIRPRADGELADNPFFGDFIGKVFVGRRLNAVYARPPHGDGAAPCLQCALMGCGVDARSH  
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AAETAHCOOETFRADIGRKROLQPRETFVLCHKIH

**SEQ ID 7135**

EQ ID 7135  
ATGCCCTCTGAAAGGCTTCAGACGGCGTTTATTTTACACAATCCCAACCGTTTCCCATCTCTCCCGATACACCGTAATCCCGAAACCGTCATTCGCGCGCAGGCGTGCATCCGGGTCTGT  
CGGGTTTCGGTTTCTCCGATAGATTCTCGCTCCGTTGGGGTTTC

**SEQ ID 7136**

MPSERLQTAPFLNPHRFPSFPIHRNPETRESRAGVHPGLSGGFGSDRFSLRWGF

**SEQ ID 7137**

SEQ ID 7137  
ATGATGTCGGAAAATAAAATGCCGCTGAAGCTTTACCGGTTTCAGACGGCATTTCGTTAAACTTGATTCTCTATCGGTATTATTGTGTAAAGCTATTGAAAAATAAAATAT

**SEQ ID 7138**

MMSENKMPSEALPVSDGILLNLILYRYYCVKLLKIKY

SEQ ID 7139

SEQ ID 7139

TTCCTCGGTTTTTCCCCTCCGCCGCGCAAAACGCCGATGCCGAGCTGTTTGAGTTTCGGGTAAAGGTGCGTGCCTTCCAAAACGACCTCTGCGCCACTTTGCTCATATTCTGACCTTCT  
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SEQ ID 7140

SEQ ID 7140  
 FFGFFPPARNADAELEFAVKVRAFQTDLLRHFAHILTFGLGDVVLEITPLHLPL\*FAQRQVKVEPARHMPRSVGRHAAAPCRRSRADTDFLEPVLQQQRCHDVLQLLEIIPRVVTVQGYGK  
 RIVTECGRRDLEAFPRHIAAGNPLYQEGNVMLHTQGRNTDDRFRKKPGQFFPT\*NAV\*TCRVAARSNHPTAAAFCLADDKGNAGLDIAAVLGDVADIQNAALLRLQLQFHRHIDQIPDPCRTD  
 PRRTVMEIARHGFGKRRRTLRLARQYGRGALCRRFDFAVHLLNRGTVAQFVEHRSRFDLRRTVFORVFDRRQQLLQGNRRFQKIDRADFGRFYGGTDAGMPAHFHHRHLELPEVFRPLILQKGD  
 TVAIGHNPNIQQHCCRARIQAQLARLPGIFRDRDLAFVLQDFRQVADADFFVYN\*NIAATH

**SEQ ID 7141**

SEQ ID 7141

ATGCACACGCAACATTTGTCCGATTCAATATTTTATGCGCTGTCTTTAATGACTGCGCTGCGCGCTTATGCAGAAAAATGTGCAAGCCGGACAAGCACAGGAAAAACAGTTGGATACCATAC  
AGGTAAGAAAGCCAAAACAGAAAACCCCGCGGATAAGCAAGTAACCGGTTTGGGCAAAATTTGGTCAAAACCCGGACACCCCTCAGCAAGGAACAGGTACTCGACATCCGCGACCTGACGG  
TTACAGCCCGCGGATCGCGCTGCTGCAACGAGGGGCGCGCGCAAGCTCGGGTACTCGATACGCGGTATGGACAAAAACCGCGTGCCTTACGGTGGACGGCTTGGCGCAAAATACAGTCC  
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AAGGCAGCGCGCATTTGGCGGGCTCGGTCGCAATTCAAACCAAAACCGCGGACGATGTTATCGGGGAAGGCAGGCAGTGGGGCAATTCAGAGTAAACCCGCTATTCCGCGCAAAACCGGG  
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CTACATCGGCGGCATACTCGAACGCGACGCAAACTTTCGACACGCGGATATGACGGTTCGCGCATTCCTGACCAAGCGGGTTTTGATGAAAAATAAAAAATACGGATCGATTAAGAGGC  
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GCTACGGTTTGAATATGTCTATACCAATCGCGATAAAGACACTTGGCGGATTTGTCGCCGCTTCTACGACCGCGGCGGATCTTACGACCGCGGCGCATCGTTTGGCAGATCATCTTTACGAGCGCACTGTTT  
CGCGCAGCGTTTCGGAATAATTTGCGCGCGGATGCGCAGCGCGCTTCTACTACCAATTCGACCGCGTGATTTACGGGAAAGCCACAGGCTCTTTCAGGCGCGCAATCAAAAAATCC  
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TCCGTTTATTAACGTTTAAAAAACACTTCAACCTTCGTCGCGGCGGTACAACTCTCAACACCGCTATGTTACTTGGGAAAAATGTGCGGCAACTGCGCGCGCGCAGTCAACCAAC  
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SEQ ID 7142

SEQ ID 7142

MQQQHLPFRFTLCLSLMTALPAYAENVQAGQAQEQQLDITQVKAKKQKTRRDNEVTGLGLVKLTADTLSKEQVLDIRDLTRYPGLIIVVEQGRASSGYSIRGMDKNFVALTVDLGIAQIQS  
YTAQAALGQTRTAGSSGAINIEYENVKAVEISKGSNSVBSQSGALAGSVAQPTKTADDVIEGGRQWGIQSTAYSGKNRGLTQSIALAGRIGGAELLTRGRHAGRTIAHEAAGRQVQS  
FNRLVFPDDSTAYAIPIVEECKNEGYEKAKKQVDGKDERQTVSTRDYTGPNRFLADPLSYESRSLFRPGPFPENKRHYIGGILERTQQFTFTRIMTVPAFLTKAVFDENKKYGSIRG  
YGYKAGGRKYSGLITNGENGAEEVGAEGYGTGVFDETHTKSRYLEYVYTNADKDTWADYARLSYDRGIGLGNHFPQQTHCSADGSDKYCRPSADKPSSYYKSORVITYGESHRLQAAPFKS  
FDTAKIRHNLWSNLGYDRFGPSDLRHQDYTYQHANRAYSLKTFPPQNGGKLNPNNGSEKNPTWYSIGGGNVVTVGQICLPGNNTYDCTPRSINGKSYAAVRDNRVLGRGADWAGLAGLYDYS  
THSDDGSVSTGTHRTLSWNTGIVLKPADWLDLYRTSTGFRLPSPFAEMYGWRSGGKIKAVKIDPEKSFNEAKGIVFGDGPNGNLEPFPNNAKRLDITVRGVEAQIQKDGKEQVKGDPAYLNAQ  
SARITGINILGKIDNGVWDLKPEGWYSTFAYNRVVRDKIKRADRTDIQSHLFDALQSRHYTVVGSYDVGQPEKGWNGMLTYSKAKRITELLGSRALLNGNSRDTKATARTPRPWYIDV  
SGVYTVKKKHITRAGVYVNLNHRVYTVWNRVDTAAGAVNHKNVGVYNYRYAAPGRNYTFSLMKF

SEQ ID 7143

SEQ ID 7143  
TTGCGGAAAAATCAATATTTTATTTTCAATAGCTTTACACAATAATACCGATAGAGAATCAAGTTTAAACAAAATGCCGTCYGAACCGGTAAAGCTTCAGACGGCATTTTATTTTCCGACAT  
CATTGAATCAAACCCAAATGCCGA

SEQ ID 7144

1RKINILFSLAHNNFDRESSLTKCRLKPVKLOTAFYFPTSLNOTQMR

SEQ ID 7145

SEQ ID 7145

CGCATAAGTTTCACCGTTTTGGCAAGATGATCTTGACACACGCCCAACCGCATCTGATTGCTCAGGCTGATCGGGCCGCCGTGTTCTCCAATGATTTTTCTACTACAGGCAGACCC  
AGTCCCGTTCGCCCGGCTTATCCGTCACATACGGCTCGAAAGCATTTGTGCAGCATTTCTTGCCGAATCCCTTGCCGTTGTGCGCAAAACCGTCAGGACAATCCGTCGTCCTGCCCGGTTT  
CCGATTTTACCCGACTTCGGGCATATCGCGTCTCTCCGCCGCTCGCGCGCATTTTTGAAAAATATTGTGCAGCACTCGCCGATGGCGTGCTATCCGCCGCATATCAGCGGTCGCG

GCGAAGTTCGCGCTCAAAACCGGCACGGGCGCGCTTGTGTACAGGGCCAAAACATCGCGGATTAAAGCGTTCAAATCTCTGATTTTCCAGTTTGAGCGAAAGGGGCGCGCGCTAAATTCGGGAAT  
GCCTCGACCAATTTCTTTTAAACGCGCCCACTGTTTGTATGATGGTGTGCGGTGCAAGCGGTGAGGATTTGCGCGTCCTGATGCTCCAGCTTCCGCGCCCAATTTCCACGCCAGCGGTTCGCGGG  
AAAGCTGGATGGGCGGTGAGCGGATTTGCGGAATTTGCTGTGCCACGGCTTCCGCACATTCACCCCAACGCGGCTTCTTTTTCGCGCGGTATCAGCACGGGTGATGTCTGCTCAATCAACATCACCA  
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CGTCCGCTGTATAAATCTGCGGAAATCGCGAACAGGAACAAGCCGGGAGTACGCGGACCAAGCTGAACTCCCGAAAGGCGTTTTCGCAATTCGCGAACCGAACAGCGCGGTTCGCGCTG  
TCTTTTCAACAGCAATATGACATAGCAATGTCGCAAAACGGCGGACAGCACAGCAGCAGCATTCGCTGTGAACGAGCATATCCACGAAATTAATCCGCAACGAACTGTGTCTGCGCGCGCG  
CCGTCATTCGTACAGCAGGACGACGGCGCATATGGCTGCGATCGGTAGGAAGCGGCGCATATTTTGTTCGCGATGATGTTTAGAGGTTTCCAA

**SEQ ID 7146**

RISFYRFWQDDSDTRPTRILIAQADAAAVSNDFFHYRQTQSRSRRLIRHRLSEIVQHFLAESLAVVANRQDNPVLPFRFPTDFGHIQFFRRFGGIFENIVQHLPHGGRIRRHQRFA  
 GKFLKPARAGVPGQNIAD\*GVQILIFQFERRGARVIAECLDHPF\*RRHLFDQDVGTRQDLRLVLIQVLEPAQFPQPGKGLDGRERTADVFCQPIRHFPTFRGFFLRAVQHGDDVMHHH  
 AVAVVFGQYRRLAQDDPGIVRRGIFHIDRFPVTRCRRDQGGKHFQKQGLLNRNNAVPTVPAAPQGGERHPQNLFRRLVEGFTQATFFVKHHHTGSQPIQHALEVVTTGGFLAPAVAFVCFPGDG  
 KLLGHMVEQLQDSELVVAQYGARLAEITLRLRLCALGRKQVFDETAGKIQCHYQRKKNRQGRNQNGYQKGLQVPTFTVQVQIFRFLPNQXILGICNRLAEERQVIAPVVRCE  
 QPSRLRQVAAAYAPQTPIRNTGLINLPHMFFQVKKRKLVELVRIDAFDPACGIVQYKGLGTAAGVVQVQTHAIRAARGGGADEVLYGNGVSDAGVLCRQIQCGLAITKAAPEGVGVVAEPRI  
 RAVDKILRGNABOEQAGQYGDQREHPGKAFGNLRETEHAVPVFQQQYDITQCGNGGQHQHCAERYYPEIIRQRTGAAGRRRQSVQDDGAYGCDR\*EAAHYLFPMHFRGQF

SEQ ID 7147

TTGAAAGACATCGTGTATTCCTTATGGGAGGTTAAAATCATTTGTTCAAACCGGCAGGCAAACCTGTTCTGCCGATTAATTCTTCAGTGTACCTATGCACCTTTAGCCATCTTTGGCGAAA  
ATCAATAATTATTTTCAATAGCTTTACACAA

**SEQ ID 7148**

LKDIVYSLNEVKLIIVQTGRQTC SADYFFSVPIAPLAIFAENQYFIFNSFTQ

**SEQ ID 7149**

ATGTCCTTTCAAACCTCCGTTACCTCGCATCAGTATTGGCATTGTCTTCACTGTGGCGGCATCGCGCGGTGAGGAAAATCTGCGGGCAGCGATGCTTCTCTGCTTCCGAGACCGGAAGCGGCTGCCAAGTACAGGCGCTCGGAAGCCGCTCCCTTCGCGTTTCATCGCGCTTCGCCGAAGACCAAGACATCTTTGAAACGCGCGCAAGGTGTATTCCAACTTTGCGGCATGTGCGAAGAAATGCAAAAAATCCGTCGTTTACCGAAGAACAGGTCAACTCGGCACCACTCTGGTATGCAACCAAGCCCTTTTCAAAAGGCAATACCGTAAGCTGCAACTTTTGGCCACAACCTTGTCTTCGCGCGGTGTGGACAATGTGCGACAGTCAAAAGGACCAAAAGGACATTTGCGCGACCACTTCGCTATGTAATCTGCGCTGTGCGGCAAGCTCTTTGGAGACAGCTGTGCGCGCAATGTTGAAGAATCAGTCGTGGCGGCTTTGTGTGAATCCGGTGAAATGGCGAATGATTTCGCAAGAGGCGGCTGCAGCCAAAAATCGCCAAAGTTCGCCGAATATCAAGAAATGTTTAAAAAAGCTTTTCTGAAGACGCGCGGTTTTCGTTTAAAAACATCACTACCGCATTGGGTGCGTTTGAGCGTACCTGTGACGCGGACCAAAATGGGACGAATACCTCAAAGGCAACGTCAACGCCCTTGAGCGAAACAGAACGAAAAGCGTGCAGCGCTTATGGACAACCGCTGTATTGCTCGCCAACCGGTGTAACCTTTGAGGCGACAGCTTCACAGAAATTCGCTGTGTGTCGAAGGGCGGTATTGGAAATTCATTGAAGATCCGAAACCGCAACAGGCGCTGTAGCTGACGTAAACAAAAAACGGAAGCAATTTTCTCCGTGTTCCGGGTTCGTAACGTGGCTAAAACCTTATCCGTATTTCCACAAACGCGACGCTGTGGAGCTGTAAGAAGCCGTTACCATCATGGTGAAGGCGCAATTTGGGTAAGAAGATCTCGGAAGAAGATGTGGATAACATCTGCTGTATTCTCGTAATGCATTTTCGGCAATGTTCGGAATCAGCGCGACAGATGCGCGGAACCTGCCCTTGACCGACCCGATGGAATCTAAGCCGGACAACAAA

**SEQ ID 7150**

MSFKRLYLASVLIALSSLLAACGGQKSAAGDASPASETEAASVQVASEAVPSASSASPEDDLLKRAQGVFQPLPTVEEMQKIRPFTEEQVKLGHQLYEPRLSGKNTVSCNSCHNLASAG  
VDNMPTSQGHKGQPGGRNSPTALNAALLGSPFDGRAADVEEQAGGPLVNPNVEMANDSQEAAAAAKIAKVPEYQEMFKAPFEDGAVSFKNITTAGAFETLLTPTKWDEYLGKGNVNAISE  
QERKGVRAFMDNGCIACHNGVNLGGTTFOKPLVQGPYKWFIEDPKRDKGRADVTKKTEDEFFFRVPGLRNVARTYYPYHNGSVWELDKAVTIMGKAQLGKDIPEQVDNIVVFLNALSGH  
VSESARTMPELPLTAPMESKPDNK

SEQ ID 7151

TTTGTTCCTCCGATGATGTTTATAGAGGTTTCCAACTCCGAATCCAAATGCCAGTTTGTGAGAAGTCAATGCGTTGATTTGGAAAGGCTTGGGCAGTTTGAAGTGGACAGCGTCAGCGGATTTCC  
GCCTTGGTTTCCCTCGCTTCCGCACCGGACAACGCGCCTTTGTTCAGACTTTCCAGTTTGGCAACGCGCGCGGTTCGCGCGCAATGCCAGCATCCAAAGTGTCTGTAATCGGTGGAAAAATGCGC  
CGACGGTAAACGCGGTAGCGGTTGGTCAGCGGATGGAACTTAGCTTGTAGTCAATATGTTCGCTATCCGCAATCAGTGTGCCCACTTTAAACCTGAAGAAGACCGCGCTGTGTGGGGCGGAAAG  
CTGCGCAGCTTAAAGTTAAAGTTGACCGTACGCCCGCGGCGCAAGCTCTGTGGAGCTGTGTGGGCGACGCTGCTTTGGAAGCGGCTGCTGAATGGAAAGCGCGCGCGCTGTGTATCTCGCT  
TTCGCGCGAGTTCGCGGCAATGCCCTCGCGCGCGCTCGCGGAAAAAGGAGGATATCGGCAACAGCACAAGCCATTTGTTTAATGCTTTTGAAATAGCGCGTAAATAAAGCCAT

**SEQ ID 7152**

FVPDDV\*RFPTRIQMPVLRSQCVDLERLGQF\*SGORQADPRLGPPCFRTGQRAFVQDFPVVGNRAGRAQCTIQSVVIGGKCADGNAVAVGQRMET\*FVVNVIVIANQLPQPKPIRSDCRGGK  
LPA\*GKVERYAPQRLLELWGOLGLEAAADGKPPAVGVYPRFGAGRGNALRRVRQNGEYROQHKPLPNAF\*ARNKSH

**SEQ ID 7153**

ATGAGCAGACCCGTAACCGCCGATTCGGCAGCGTPTTTTTCACAGTCAAATGCCCGTCTCGCCTACCGGAAGGCAAAATGGCAGCCGACCGAATGGCAATCTTCCCAAGACCTTACCGTTC  
CACC CGCGCGCATGCCCTGCATTACGGCAGCGAATGCTTTGAAGGTTTGAAGGCTTCCGTCAGGCAGACGGTAAATCGTGTCTTCCGTCGACCGCCAAATATCGCGCGTATCGCGCA  
AAGTGGCGGACATTTTGCACTCGCGCGCCCGGAACCCAAAGCTTATCTCGATGCTTTGGTGGAACTGTGTCAAACGTGCGCGCGACGAAATTCGCCGATGCGGCTGCCCGCGCTGTACCTGCGC  
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TCTGTGTGGAACCGAACACATCCGCTGCGCCCGCATATGGGCCCGCTCAAATGCGCGGCAACTACGCTTCGCGCATGCACTGGTGTCTGAAGCGAAAGCGGAATACGGCGCAAAATCA  
AGTCTCTGTTCTGCCGAACGGCGAGCTTCAGGAACCCGCGCATCCACTTTATCTCTGATTAAACGGCGATGAAATCATTTACCAAAACGTTGACAGACGAAATCTTGCACGGCGTTACCCGC  
GATTCGCTGCTGACTGTTCGCCAAATTTGGGCTATACCGTCAGCGAACGTAATTTACCGGTTGACGAACCTGAAAGCTGCTGTGGAAACGGTGGCGGACGCAATTTTGACCGGTACGGCG  
CGGTCACTCTCGCCGCTGACTTCTTCGTCATTCGGCGGCAAGAAATCGAAGTGA AAAACCAAGAACCGCGCTATGCCATCTCGAAGCGGATTACCGACATCCAGTACCGTTTGGCGGAGA  
CAGTACCTGGCTGGCTTCTCGAAGTGTGC

SEQ ID 7154

MSRPVPAVGSFVHSGMPVLAYREGKQPFTEWQSSQDLTLAPGAHALHYGSECFEGLKAFRQADGKIVLFRPTANIAMRQSDAILHLPRPETQAYLDALVELVKRAADEIPDAPAALYLR  
PFLIGTDVPWIGKAGSPSETALLYLTLASPDVGDFYKVGSPVKLLVETEHIRCAHPMGRVKCGGNYASAMHLLKAKAEYGANQVLFPCPNGDVQETGASNFILINGDEKITTKPLTDFELHGVTR  
DSVLTVAQDLYTVTSERNFTVDELKAAVENGAEAILTGTAAVISPTSPVIGGKEIEVKNOERGYYAIRKAITDIOYGLAEDKYGWLVEVC



**SEQ ID 7155**

TTGATTTTTTTTATCGCGTGTGTCTTTTGATTGCGTAAATTTCGCGAAATTCAAATTCAAATCTCGGATGTATTTTTTCGGGCATGTGTCGGACAAATCGCGGTTTTGTCTTTGTCAAG  
TTTTGTGCATATTCGGGAAAACCGAAATCGTCCGACCTGTGCCGGTGTGCGATTCGTCCCTTGCCATCTCGGGATATATCCAGCAAAATCGGCATATCGGTATTTT

**SEQ ID 7156**

LIFLSAVAFDSLNLPKFKFKSSGCIFSGIVRTNRRFVLCQVLCISGKPKSSAPVPVSIRPLPSRDISSKIGISVF

**SEQ ID 7157**

ATGAACAATCCATTGGTGAATCAGGCTGCTATGGGTGTGCCCTGTGTTTTTGTGTGAGCGCTTGCTGGCGGAGGCGGCAGTTCGTGATCTTGATCTCTGCGATACCGAAGCCCCCGTCCCG  
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TGAGTAAGACTCTCTGGAAGGTGATTGGGAACAAACGGGTAAATGTAATATCAAAAACCCCTTCCAACAAAAAAATATTATGATGCCCTTATCTGGAATGGGAGGCCACCATTCGAAGAT  
TCCAGTCAACAAGGTGAGGATATATCTAAGGTTATCGGACTATCCAGTTTAAATACGTATCGGTGGGTTTCTTTTTTATAAACAAGTATGGGAATACAAATAAAAAGAGGATTCATCTAGTGA  
AATAATCTGAAGCGAAGAACCGGTCTCGAGCGGTTATTTTATTAAGAAGCAGAGTCCCTCGAGGAATCTTCTGTGTTCAGGAGTGTGTGAGTACAAGGTATTCGGATTTTAACTGA  
TGTGCAAGCAAATCAGAAATTTACAGATTTAGGGAGTGCTTTTACGAAGTCCGGCAGCAGATATAGTGCTTTTTTCCGGGGAGTTGGATTATATAGTCAGGAAGAGGAGGATAAAAAAGAC  
GGGCACGTAGGTTTGGGATTAACACCGGAATAACGTTAATTTTGAGAAAAAACCCCTGAGCGGAAAAATTAATTA AAAACAACATGGTAATCAATAATGGCGATGAACCCACCACCCAAAT  
ACTACAGCCTTGAGGCTCAAGTAACAGGCACCGCTTCAACGGCAAGCGCATGGTAACCGCAAAACCCGAAAAACAGCAAAAGTAAACAAACATCCCTTTGTTTCCGACTGTCTCTCTGAG  
CGCGCGCTTTTTCGCGCCGAGGGTGAGGAATGGGTTTCCGCTTTGTAGCAACAGCAACAAGTTGCCCTTGTGCGGAGCGCGAAAAACCAAGACGAAACCGCAAGCAGTGGCGGCCT  
TCGGGCGGTGCAAGCTTTCCGCATCAACCGTGGCGACGGCAGCTTCCTGCGAAGACGTAATCTGACCAACGTTTGGATGCGGTTGGAATGTGACACAGCAGCAAGGAAATCAAAAGATC  
TCGACAACCTTACGCAACGCGCCCAATCTGGTTGTGTGACGGCATAATGTTCCGCTCTGTCACGGAAGCGGGAAACGTCAGGCAAGATTAAGACAAAAACGTCGGAACAGATTTACCTA  
CAACAACACCTACATGCCGGAAGTGATAAAAAAGACACCAAAAGCCCAACCGGCGCGGGCGGCATGCAAAACCGCTTTCGATGCGCGGGCGTTAAACGGCGGGCAGGCAGGAACAAAAAC  
TATAAAGTCGAAGCTGCTGTTTCCAACCTCAATTATCTGAAATACGGGTTGCTGACACGCGAAAAACAGCAATTCCTGTGATGCAGACAGTCAGAAACAGTAGGCCAAGCGCGCGCCGGAACG  
CACAGGGTGCACAAAGTATGTTCTTCAAGCGGAGCGCACCGATGAAAAAGAAATTTCCAAAAGAACAAAAAGTCGTTTATCTAGGCACTTGGTACGGGCATATTGCCGCACAGGCACAG  
CTGGACCGGCAACGCCCTCCGATCAGCAAAAGTGTAATCGGGCAAAAGTTTGACGTGAATTTCAAGACAAAAAAATTAACCGGCACGTTAACCGCTGCAAAACAGGCAGGAGGCAACCTTTACC  
ATTGATGCCATGATTGATGACAAACGCTTTAAAGGTACCGCGAAAAACCGGTAATGACGGATTTGCGCGCGATCAAAAACAGTAGCACCGGTACATATAAAGTGCACATCGCAATGCCGAAG  
TCAGGGCGGGTTTTCACGGCGCTAACCGCCGAAGGTATGGCGAGTGGTTTGCCTATTCGGCGCAATGGACAAACGAAAAATGCGCAAGAAAAATGCGCAAGCTTCATCCGCAATGGAAATTC  
AGCACTCAGCGCGACCGTGGTATTTCGTTGCCAAACGCCAACAGCTTGTGAAA

**SEQ ID 7158**

MNNPLVNQAAMVLPVPLLSACLGCGGSGFDLSDVTEAPRAPAPKYQIDVAPSKPPEARKDQGGYGFAMFRFKRRNWYPPSPNKEINEIRLSEGDWEQNGNLIKPNFSKQKNIIDALSGNGEAPLQD  
SSQQGBGISKVDTYHDFKPYVSGFFKYQIGNTIKDSDSSSKIKIDPARGSGQFYIFKYGTPDRSKPLKQSGVEYKGTWGLDQVANOKEFTDLGSAFTLSCGSDRYASFGSELDYTVRKEDEKKU  
GHVGLGGLTETVYNFKKELKSLKIKNMVNNKNGDEPTQYYSLEAQVTGNRPNGKAMVTKDPENSKSRQHFVYVYSSDSSLSGGFFPGQCGELGSAFTLSDNKAUVASGVGATYKTEBTASSGG  
SGGASVASNGNAGTQSSGNSNLITVTLDAVELTPDGKEIKOLDNFNSNAALVVDGIMILLPSSSGVNGQADKKGNGGTDYITTYTTPSPESDKQTKAQGTAGGGMQASDAAGVNGGQAGTKT  
YKVEACSNLNLVLYKGLLTRENSNSVMQTVRNSSSQAARATAGGQSMFLQGGRTDEKEIKPEQKVYVLTGYWGHIAANGTTSWTGNASDQSGNRAKQDFVNFKDKKITGTLTAANGREQATFT  
IDAMIIDNGFGKGTAKTNGDGFAPDQNSGFTKYVHIAANAEOVQGFYPNABELGGWPAYPNGNQTKNAEQASNGNSNVASTVVPQAKRQQLVK

**SEQ ID 7159**

TTGTGTCGTCATTCCCGCGCAGGCGGGAAATCCAGACTGTGTCGGCACAGAACTTATCGGGTAAAAACGGTTTCTTCAATTTTATGTGCCGATTCCCGCTGCGCGGGGATAACGATTCAGGTA  
TTTCTACATCGAATCCGCTTTTTATATCAACC

**SEQ ID 7160**

LSSPRRRESRLVGTETVRVKRFLQFYVPDSRLRGDNDSGISTSNPLFIST

**SEQ ID 7161**

ATGCTTTTGAAATAAGCGCGTAATAAAAAGCCATCTTGGTGTTTGTTCGGTAAAGACACCCGCGATTTCGATCGGTTCCGGCATCGGCATGCGCGGTGAGGAATTTTGCAGTTGCCCGTCGTTTCTCTCGACGAACCGGAACAGGTGCGCAAGCAGCATCTCTGCCCGCCCTGTTCCTCAACGCTTGCCAAAGTGCCTCCACGACGGGCTCTCTGCTGCGCGGGCGGTTTGTAGCGCGCTCGGTCGCTGCGCGCACGCCATTTTCACGTGCGGATTTGCGCCGCGCACGCCGGAAGCGTTCACGTCGAAAGGCTTTTACCATCATACCGACGCCGCAAAATCCCGCGCATCGGCACATCGCCCGGATGCGCTTGTAAGAGCGGCAACCGGGCATATTTGCTTCCACGCTTCAGACGGCTTCGATCAGTATGCTCCAAAGCGGTTCACCGCGAGTCCGCGCATCTCCAAATATGCGCCGCTCTGCGCGCGCGCGCGCATCGCTGCTCCAAATCCGTTCCGTCGCGCTTTCGCGGTTAAGAGATACGCCGCTGCTCGCGCGCGAAGTCTGTATACCGACAGCTCTCTTCGCGCAAAACCGGGCAGACGGTTTACCGGCACGGCTTCTTCCAACGTAAACGCATATTCGTCCAAACGCTTAGCCGCGATACCTTCCGCCACCAAGTTTTCCAAATAGCTTTCGGCATTTGCCGTGCCGCGGTTGACGCGCAACGTTCATCGCGGATGAGGATTCAGCGCGCGCGCGCATGTTGTGCCAGTGTTCGGATAATGGTTTTCAAAGTAAGCCACCCACACAGCGCGAGTTGTGTTCGCCACATCTGCTCTTTTTCGAGGAAGCGCCCAATTTTTCAGCTTCGCGCAAAAGCGCGCAAAACCGCGTTCGCAACGAAACGGTACTGCCCGCGCCGATTTTGGCTATGCTTTTCAACAGCTTCGTTGACCA CGGCGTGGGGCGCGTTTCGCGGTGAATGCAGTTGCTGTACACCGCGCCCAAAAGCAGGCTTTCGAGCTGCGGATTTGATGATGGGCTTTTCAGCATCTGCGCGAGCATATGTTTCAAACCTGCCCAAATAAGCTGCGCATGCGGTAGGCGATATCTGCAACGCGCGCTTCTTCGCGCGCTCAGTTCGCGGATGCGCGCGCGGATGTCGCCCAACAGCTCTGAAGTTGCGCCCTTCGCGCAACCGCGCAATGCTGCGCGGCAAGTTTTCGGCAAGTGTGCATCTCAT

SEQ ID 7162

MLNKRVIKAILVFR\*KHPRFDRPGICMAVEEFLQLPVVFFDEHGTGGKQHSAAFLQRLPKCVQGGFLLAGGFEKVRGSAQPFHVGLAPRHAGSGARHVGDKDCVERLSIIPRQTPRIGT  
RRRCRLKAQGTGDIVLHTLTQACIDVQGGNAAVRQFQNMPLRAARRGARVQNPFAVFRVKEIRLLRAEVLRYHSGFSGKTQGVYRHGGFFQNRNIFVQRLSRDFFRHQFFQLAFGLAVPAVD  
AQRHRRMGLQRGGDVVVFVRIMVFQVSHPPQVVRHIVFVAGSRQFFTFQAQKAQNRVKGRTVLPAPDFGYAFNSFVDHGVGRVARVMQLVQRQKQAFELRIVDGLFQHLREHMFYTA  
QITLAAVGDILORAVFLRROLRMRADVROHVLKVAQFNGNRNNAVGGKFLKCHTH

**SEQ ID 7163**

TTGGGAAAGATTGCCGCAACTTGGAAAGTGCCTCTCCCGACCCCTCCGCCGCGCAGGGGAGGAGCGGATTGCAGCAGGTTTGGCGGTTGCAGGCGGTTTTAAAGCAGCGCGGAATGA  
CGGTAATTGTGGTTTATTATC

SEQ ID 7164

LGKIAATWKVPSPOPSAAGRERLAAGLAVAGGFKSSAGMTVFWFTY

**SEQ ID 7165**

CAGCTTCGCCCCCTGCTTCAATAGACCGTCCGCCGCGCAACGCGCAATATTTCATACGCTTCCGCCGGCAGGCTGCAATTTCGGTAACTCTTCAGCGCGCTTTCGCCGAGGCAACGACCAA  
 CCGTCGCCGCAACAGGACAACACTTCGCTGCCGTACCTTGTTCGCCACCACTTCGGCAGCGCGGATTTTCATCGGCTTGCCCTGATATTGACCCACGCGGAGGCAAGGGGTGAAG  
 CGCGGATTTTCGGTTCGATAAATGTCGCCGCTTTCGCTCCAAATCGATAGCGCGCTTCTCTTTGCTTAGTTTTCGGGCGTAAGTTACGCCCTTCTTCGGGCTGTTTGAACCGCGTTCAGACGGCC  
 TTTCCTTTCGAAGCTGTTCGAAATCGGCAACAACCGCCGCCGCAACGATTTCCATCAGCGCGTCTGTGGACTTCGTTTCGGCGTATCGGTAGGTTCGATGGCGTAGCGGTGTTCGCTGACCACA  
 TCGCCGGTGTCCAAACCGATGTCCATCTGCATAATGCCACACGCGGTTTCGGCATCGCCGGCTCAATTGCGCGCTGAATCGGCGCCGCGCCGCGCAACGGGGCAGCAGCGAAGCGTGG  
 TATTGAGGCAGCGGTGTTTCGCCGCTATCCACACTTCTCGCGGACCACTCAAGCGCTACGCGGGCAGCCACCAATTACGTCCGCGCTCGACCTCTTTGAGCATTTTCAGGGCTTCGCGGCTGTTGT  
 CGGCAGTTTTCGGGCTGCGGCAACGCGCGGCTTCGACAGCGCGGCTTTGACAGCGCGGCTGAGTTTCATACCGCGCGCTTTCGGACGCTCGGCTGGGTCGGGCAACGACGCGG  
 ATCTCAAAAAACGCGCGCAACGCGCTTTTAAAGCGCGCGCGCAAAATCGGCGTGCGCCGAAGATGACTTTCATACGCGGTTCCTGTGCGTGTGCGTAAAGTTGTTCGGACAA



## SEQ ID 7166

QLRPFNRPSSRRKRNIHTPAAGRLQFNLQRAFAAGNDQTVRRTCQHFACRTLLRRHFGTDFPHRLALIFDPGRGRHGVGADFAFDPNVRAFAPIIDTRFFFA\*FLGVSYAFFGLFDRVQTA  
FALKLLQIGNNRRTDFHQRVDFVGGIGRLDGVAVFADHIAGVQTDVHLHNAHAGFGIAGLNRLNRRRAAPTQQRSVDIEAAVPRRIQHFLRQNAVRGNHNYVRLDLFELHQLGFGVV  
AQFFGLCHAQTFQRGLFDRRGGLHTAPFRTVGLQHQDRDFTGGGNGF\*GGGKIGRAGKDDFHSVFLRVRKVVQG

## SEQ ID 7167

TTGCCGCAACTCGGAGAATGCCCTCTCCCGGCCCTCCCCACGGGGAGGGAGCGGATTTCGGCAGATTTCGGGTTCAGCGCGTTTGAAAGCAACTTGGATTACCGTTGATTTCAG  
GTCGTATGAAAAATAAAAAACAGCCTGCACAAGCTGAT

## SEQ ID 7168

LPQLGECPLPGPPFRGRERIAADFAVAGGLKSNLDLPLISGRMNKKQPAQAD

## SEQ ID 7169

ATGCCGTCTGAAGCAACAACGCAAGAAACCCATCTTATGATTGACAAACGACTGCTCCACTTGGGCGAAGAACCCCGTTTAAATCAAATCAAACCGAAGACATCAAACCCCGCTCC  
AAAACCGCATCGCGGAAGCGCGCGGCAAAATCGCCCGCTCAAAGCGCAACCCACACCGGCTGGGCGAACACCGTTCGAGCGTTCGACCGCATACCGAAGCGGTTCGGCAGGATTTCGGG  
CGTGTGTCCATCTCAACTCGCTGTCGACACGCCGCAACTGCGCGCGCTTATAACGAATGATGCTGTAATCAACCGTCTTCACCGCAATTCGGAACAAGACATCGAATGTACAAC  
CGCTTCAAACCATCAAATAATCCCGCGAATTCGACAGCTTCCCGCGCAAAAAACCAAGCTTCGATCAGACCTGCGCGATTTCGATTGAGCGCGCGGAAGTTCGCCCGCAAGCGC  
AGGCAAGAACTGGCAAACTGCAAAACGAAGCGCGCAACTTTCGCCCAAAATCTCCCAAAACGTCCTAGACCGGACCGGACCGGTCGCGATTTCGAGATTTCGCGCTTACCTTCAATACCGCGCAACCGC  
CATTCGCCGAAGACCGCTTCGCATGTTTCGCCCGCGCGCAAGCGAAGCGCAAAACGAGCTTACAAAACGTCCTAGACCGGACCGGACCGGTCGCGATTTCGCGCTTACCTTCAATACCGCGCAACCGC  
GAATCGCGCGAACAATCTACCGCGCTTACCTTACCGTTCGCGCAAGCGCAAACTTTCAAACGAGCGCAAAATTCGACAAACCGCAACATCGACCGCAGCTGAAACCGCATGAAACCGGCA  
AACTGCTCGGCTTAAAAATTCAGCGCAATTCGCTGCGCAACCAAAATGCGCGACACGCGCGCAAGCTTTCAAACGAGCGCAAAATTCGACAAACCGCAACATCGACCGCAGCTGAAACCGCATGAAACCGGCA  
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GAAGTCAAATAATCTTCCCGTTCGCGCAAGTTCGCGAGGCTTCGCGCAAAATCAAACCACTTACGGCATCGGATTTCGCCGAAAAACCGTTCGCTTCGCAAAAGCGCTTCGCGTTCGCAAAAGCGCTTCGCGT  
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CGGACCGCTGCAACTGCCACCGCTTACCTGCTGCAACTTCGCCCGCGCGCTTCGCGCGCAAAAGCGGCTTTCGCGCAAGCGGTCGCGGAGCTTTCGCGCAAAATCAAACCACTTACGGCATCGGATTTCGCCGAAAAACCGTTCGCTTCGCAAAAGCGCTTCGCGT  
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CCACAGGCAACCGCTTCGCGCAAGAAATCTTCGCGCTTCGCGCGCTTCGCGAGCGCGCGGCAATCTTCGCGCAAAAGCGGTCGCGGAGCTTTCGCGCAAAATCAAACCACTTACGGCATCGGATTTCGCCGAAAAACCGTTCGCTTCGCAAAAGCGCTTCGCGT  
CTTCGCAACCGCGCT

## SEQ ID 7170

MPSEAHAKETHLMIDNALLHIGEPFRNQIKTEDIKFAVQTAIAEARGQIAAVKAQTHGTWANTVERLTGITRERVGRIGVSHLSNVDDTPELRAVYNELMPETTVFTEIGQDIELYN  
RFTKIRNSPEFATLSPAQKTKLDHDLRDFVLSGAELEPERQAEALAKLTQEGAQLSAKFSQNVLDATDAFGIYFDAAPLAGIPEDALAMFAAAQSEKTYGKIGLQIPHYLAVIQYAGNR  
ELREQYRYAVTRASELSNDGKFDNTANIDRTLENAKLTAKLLGPKNYAELSLATKMDTPEQVNLFLHDLARRAKPYAEKDLAEVKAFAREHLGLADPQFWDLSYAGEKLRKAYAFSET  
EVKKYFPVGVKVLGAFQIKILYIGFAERTVPMHWDVRYPELQNGKTIIGVYNDLYAREGRKGAWMNDYKGRRRFADGTLQLPTAYLVCFAPFVVGKEARLSHDEILLFHFETGHS  
LHLLTQVDELGVSGINGVEWDAVELPSQPMENFVWEYNVLAQMSAHEETGEPLKPELFDKMLAAKNFORGHFLVRQMEFALFDMYISSEDECRLEKNWQVLDVSRKEVAVIQPEYNRB  
ANSFGHIFAGGYSAGYYSYAWAEVLSTDAYAFESDDVAATGKRFWQELLAVGSGRSASRSPFAFRGREPSIDALLHSGFDMAI

## SEQ ID 7171

TTGCCGCAACTCGGAGAATGCCCTCTCCCGGCCCTCCCCACGGGGAGGGAGCGGATTTCGGCAGATTTCGGGTTCAGCGCGTTTGAAAGCAACTTGGATTACCGTTGATTTCAG  
GTCGTATGAAAAATAAAAAACAGCCTGCACAAGCGTATTAGTTTCGATAAACCCTTAACCCCAACAGCCACCCCGTCTCTCTCCCTCGCGGAGAGAGTTAGAGAGAGGGCAGCAAGCCGT  
MTTAGTTTCGATAAACCTTAACCCCAACAGCCACCCCGTCTCTCTCCCTCGCGGAGAGAGTTAGAGAGAGGGCAACAGCCGCAAGGTTTGATTTCAG

## SEQ ID 7172

LPQLGECPLPGPPFRGRERIAADFAVAGGLKSNLDLPLISGRMNKKQPAQAVLVCINLNPNSHPVLSPCGRELERGGQAVLVCINLNPNSHPVLSPCGRELERGGQAAARFVF

## SEQ ID 7173

AATCGTATGTTTTCGACGTTTTCAGTTTGGCTTAAATCCGCCCCCTGTTGAGTTGGGAAAGCGGTCGACAAACAGATGCCATCAGGTGATCTAATCGTGTGACGCAAAATCGCC  
AGCAGCCCGTCCGCTCCAGCGTGAATTTTCGCCCTTTTCGTTCAAAGCGCTCGACCTTCAGCGCTTCGCGCGCGGTAAACCGCGTCTAATGCGCGTACGAGCAGGCGAGCCCTCTTCGT  
AAGTGGTTTCGCGCTTTTCGTTCAAAGCGTTCGAGCGGTTGATGAACACGCGCGGTCGCTGCGGCTTCGCTGCAATCCATCAAGCAACCGGTCGCGACATCGACTGCGTCCGCGCGAG  
CCGATGCGCGCGGATTCGTACATCGTTTCAAACATATCGGCAACAGCTTCGCGATGCGCTCGTCAACTTGTTCGACAGGCTTTCGACCGGTTCGCGCGGATTCGCGGATTCGCAAG  
ATATTAGTAAAGCCATAATTTCTCTTCTTCGCGGATACGCGCTGTTTTCAT

## SEQ ID 7174

NRMFLTFPQGLNPLLELKGAFDKHDAHQVI\*LVLHANRQOPVRLQREFFAFVQSLDLDAFGAGNVVNRARYGQALFVSGFAVFNDDGVDEHARFAAVFGQIHHDHAFVHIDLRERQ  
PDAARFVHRFKHQLPDALVNLFDRLCHRVQLVGLIQDIQ\*SHNLFPSADTPPVFH

## SEQ ID 7175

ATCGAGTTTCGATGATGATTCGTCATTCGCCGCGAGCGGGAATCCGAACCTTCGGAACAGAACTTATCGGATAAACCGTTTCTTGAGATT

## SEQ ID 7176

HQSVWMDSSFPRRRESEFVGTETRIKRFLEI

## SEQ ID 7177

ATGTTAAATGCGGAACATTTGTTATCACAGGCACATCCCGAGGGCTGCCCGCGCTTTTTCACCAACCAATCAAGCAAGCAAAACCGAAATTTATCAGATAAGGGGAACGGTTATGCAAC  
GTCGTATTATAACCTGCTCTATATTACAG

## SEQ ID 7178

MLKCGTFVITHIRPGCRRFPQPNARQTEIYQIRGTVMQRRIITLYIQ

## SEQ ID 7179

TTGCCGCGGTFACGGCGCGGAATTTGCCGCAAGTGGCAAAAGCGTTCCTTTCGCCACTAAATCTACACCTTATCTTTTCGACAGGCGCGCGGAAATGGAATATGGAATATGTTGA  
ACACTTGGCCGATGCGCTCCGATACCGCGCGAGCGCGGCAATTCGTCGCGCGGCTTCGCGCTTCGCTGGCGCGCGCTTCGTTGTAATTCACCTTCAGACGGCATCCGATTTC  
CGGCACTGAAGCAAGCGCGGCTTTTGGTTCGACGCGCAATATAACGCTGCTTTTGGTCTGTTTCGCTGCGATTTCGTCGCGCAAAATCAAACCGTTCGCTTCGATGTTT  
CGCGTGGCGCGCGGCTTCGTCGCGGACAAAGAACTGATTATGTCGTCGTCGCGGAGTATTTAAGTCTGCCACCCAGCAATACGCTTCGCGGAGCAACCGCTTCCTTCCCAACAGCGCTTCGTTGAGCCA  
CGCGGCGGCTTCGATCAATCTGTTGAACAGCTGATGATGAGGTCGCTTCGCAACCGCTTCGCGGAGCAACCGCTTCCTTCCCAACAGCGCTTCGTTGAGCCA  
CCCCGTCGCGCGGACATAATTTTGGGCGACTATGTCATCATACGCTTCGGAATCCCGCTTCCTTCCATTCGATTGGAATTCGATGAGGCGTATGCGCTTCGAAAGCGGTACTTCGAGCCCTTC  
TGC CGCGCTTACATCCCGCATTCAGCGGATTTCGGAACAGTTCGAGCGGAAAACTGTTTATCAACCGCGCGCGGCGCGGCTTACCGCGTACCGTACGACGCAAGGCAATAC

GCATCATCGTCCGCTTCGCTCCCCCGTTTCAAAGCGGCTGGAAATCCAACAGGCGGTTTATGGACGAATTTTTCGCGGTACAAATACCGCTGTTAAATCATCCCGCGGGCTCCGAAACACT

**SEQ ID 7180**

LRPVRARNLPKAKWKRFPAFKIYTLFSDRGEMETWNMLNTWPDVAPIRAEAEESVAAVAALLLARALLINTHFRRHDFGTESKRKRFVASRNITLLVLVFLAFTWSAQIQTALSMF  
AVAAAVVATKELNCLSGSILRSATQYVSVDYIEINGLRGRVVDINLLMTLMQVGNPLVGLAGTIVTSFPNSLLLSHPVRRDNLGDVYIHTVETVPVPHLSDAEVCRLLKAVLEPL  
CAPYIPIAQRYLENVQAEKLFITPAARPRVTVPYDDKAYRIIVRFASPVSKRLKIEQAVMDEFLLVQYRLLNHPAGSEFL

**SEQ ID 7181**

GTGGCAAAAAACGCTTTTGGCCACTTTGCGGCGAAATTCGCGGCCCGTACCGGCCGCAAAATGCGCGCAGCCCTTTACAGCGGCATCCGGATCGCGATAACGCTGAATCAGGCGCGGAAA  
TCGGCTATATAATACAAATATATATGCGCCGTCGCCGCCGCTTTTCCACAAGGTGCGGCAGTGTTTTGGCGGCATCGCAAAATCTTTTCAAAATTCGCGCAAAAAATATGACTGAACAAAAACA  
CGAAGAATACGGCGCCGACGACGATCCAGGTCTCGAAGGCTTGGAAAGCGGTACGCAAAACGCCCCCGGCATGTACATCGCGCAGCAGCAGGACGGCAGCGCGCTGCACCATATGTTGTTTGA  
GATTGGACAACGCAATCGACGAAGCATTCGCGGCATTCGCAAAAAATCAGGTAAACGATACACGCGGACCATTTCCGTCAGCGTCCGCGCAAAAGCGGTATGCCACCGGCATCC  
ACCCAAATGAGAGGCGCTTCGCCGCCGCAAGTCATPACGACCGTCTTGCACGGCGCGAAATTTGACAAACAACAGCTACAAAATCTCGCGCGCCTGACAGCGGCTGGGGTATCTCGTCTGT  
CAACGCGCTGTCCGACTGGGTAAAGCTGACCATCTACCGCGACGGCAAGAACACTTTCGTCCGCTTCGTACGCGGCGAAACCGAAGAGCGCTGAAAATTTGTGCGCGAATTCGACAAAAAA  
GGCAGGACCGTGCCTTCTCGCGCGCAGGAAACCTTTCGCAATATCGAATAACAGCTTCGACATCTCTCGCAACAGTATTTCGGAACCTTTCGTTCTTAAACAACGGCTGGACATCGAAT  
TGACCGACGAGCGCGACGCAAGCAGCAAGAGCTTCGCCCTTTTCGCGCGGGCTGGCGGGCTTCGTGCAATATCATGAACCGCAAAAAAACGCCCTTGACGAAAAAATCTTCTATPAGCGTTCGG  
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ACCTTGCCGACTGCCCAATCTCTCAATCCCAAGCAAACTAACGTTGCGCAAAAAATCGGCCCGCTTGCAACGAAAGTCAACATGCGACTTACCGACTTCTCGTAGGATGATTCGCGA  
CGAAGCCAAATCATCACCGCAAAATCTGTCGATGCGCGCCGCGCACGCGAAGCCGCCGCAAGGCCCGCAAAATCACCCGCGCAAGGCGTGAAGGAGCGCTTGGGACTGCCCGGCAAA  
CTCGCGACTGCCAAGAAAAAGACCTTGCCTGTCTGAATCTTACTCGTTCGAGGGCGACTTCGCGAGGGGTTCCGCCATGCAGGGCCGCGACGCAAAATCCAAAGCGAATTTTGGCGCTCA  
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CAGACGGCGCACCATCGAAGGCGCAGAACTTGGCGACACCGGCCAAACAATTTCTGTTGGCGAAAACCGTCATCGAAACAGGAAAGCCGCTTCGTGGACGAATCTGCTGCTGCTCCATGCT  
GCACGCGTCGCCCATTTGATTTGACGTCGCTGAAAAACCGCGATAAAGCCGTTGCCGAACTTTCGGTTTGGCTTGACGAAAAAGAACGCCCTTCGAACGCATCGAAGGTATGAAGGAC  
CGGTTATCAAAATCAGCGCGAAGCTGACGCGCAACGTCATGCTGAGCTACATPCAAACCAAGTTCCTCAACAGCAAGGCTTACCAAAACCTTACCCAAACCGCGCGCGCTCAAGGCT  
TGGTTCGGCGAGGGCGCAAGCTCTCAAAAGGCGGAGAACGAGTACGACGCGGACAGCTTTGAAACCCGTTTGGAACCTTTGATGATGAGCGTTGCCAAAAAGGTATGTCATCAACGATACAA  
AGTTTGTGGCGAGATGAACCCGCGACATTTGTGGAAACACAGTGGATTCGCCGCTGCGCGCGCTTGTTGAAGATGCGCATCGAAGATGCCATTCGCCGCCGACGAGGTGTTTCGTTACCGTG  
ATGGGCGACGAGGTCGAACCGCGCGCGCCTTTATCGAAAAACATGCGCGTGATTGCGCAAAATATCGACGCA

**SEQ ID 7182**

VAKKRCHFGAGKFRARTGRKCAARPRFRHFDADNAESGGEIGYNQTLAPSRPLFPQAGDCFGGIKSPQNPKNMTEQKHHEYGADSIQVLEGLEAVRKRPGMYIGDTPQDGSGLHHMVFE  
VLDNAIDEALAGHCDKITYTLIHADSVSVADNGRGMPTGHPKEGRSAAEVIMTLVLHAGGKFPDMSYKLSGGLHGVGVSVVNLSDMTVITLYRDGKEHVFVRVGRGSTEPELKIIVGDSIK  
GTTMVFLAGTETGNGIEYSFDILAKIRKELSPFVINGMDIELTDERDGKSHESQGVAGVFPVNMRRKTKPLHEKIFYAFGKEGKMGMSVECAMQWINDSYQESVQCPNTNTPQRDGGTHLPAK  
QVVRTRINSYIEANVAKKARTEAGTDDMRGLFVCLVSLKDPDKFSSQTKDLVSGEIGFVNVNEINQALDTLEENFNKALITGKIVDAARAREAKKRIETRRKGWMDGLGLPGK  
LADCQEKDPALSELYLVEGDSAGGSAMQGRDKFQAILPLKGLKILNVEKARFEKMLASQEVATLITAGAGIGKEEFNPEKLYRHRIITMTDADVDGAHIRTLLTFFFYRQMPELVERGYI  
YIAPPLYKAKYQKQERYLKDBLEKQDWLLGLALEKAKIYVSDGRTEGAELADTAQKFLAKTVIYBQSSRFPDBLVLRLAMLHASPDLTSSENADKVAEKLSEGLDDBKEAALERIIGHSEH  
RFKIKRKLHGNMVMSYIEPKFLNSKAYQTLTQTAALKGLVGEAGKLYKGENEYDASFETALDINSVAQKMGMSIQRYKGLGEMNPBQLWETTHDPAVRRLIKVRIEDAIAAEVFPVL  
MGDEVEPHRAFENNIALQINIDA

**SEQ ID 7183**

AAATGCGGAACATTGGTTATCACACGGGCACTCCGAGGGGCTGCCGCGCTTTTTCACCCAAATCAAGCAAGACAAACCGAAATTTATCAGATAAGGGGAACGGTTATGCAACGTCGTA  
TTATAACCCCTGCTCTATATTCAGTAAAGCCATAAATTTCTCTTCTCTCGGGGATACGCGGCTGTTTTTCAT

**SEQ ID 7184**

KCGTFVITRHI PRGCRREFQPNQAROTEIYQIRGTVMORRIITLLYIO\*SHNFLFPSADTPPVFH

**SEQ ID 7185**

TTGCTCCCGATAAAATGCCGCAATCTCAAATCCCGTCATTCCCGCGCAGGCGGGAATCCGGACCTTCAATGCTAAGGCAATTTATCGGGAA

**SEQ ID 7186**

LLPINAAISNPVIPAQAGIRTFNAKAIYRE

**SEQ ID 7187**

ATGACGGGATTGTGAGATTGCGGCATTATTCGGAGCAACAGAAGCCGCTCTGCCGTCATTCCCGCGAAAGTGGGAATCCGGTTTTTTTGAATTTCAGTCATTCCCGATAAAATGCCCTTAGCA  
TTGAAGGTCGGGATTCGGGCTTCGGGGGAATGACGGGAATT

**SEQ ID 7188**

MTGFEIAAFIGSNRSRSVIPAKVGIRFFEFQSPINCLSIEGPDSRLRGNDGI

**SEQ ID 7189**

TTGGGAAACCACGATGGATCCCGCCGTCGCGCGCTGTTGAAAGTGCGCATCGAAGATGCCATTGCCCGCGACGAAGTGTTGGTTACCTTGATGGCGCAGCAGGTCGAACCGCGCGCCGCC  
TTTATCGCAAAACAATGCGCTGATFTGCGRAAAATATCGACGCAATAGTGCCTGTTTAAAAAAGGAGACGGGCAGCTTGCCTGCTCTCTTTTGGTTTGTCAACAGCGGAAGCCATGCCGCTCTGA  
AACCGCTTTTCGGAGAAACCAACCATGATCAGCATTTTGGATATTTTCAAATCTGGTATCGGCCCTTCCAGTTTCGCATACCGTGCGCCGCCGATGAAGGCCCGCCGCCCTTTTCGCGCAGGCTTG  
GACGCGCAAAACCGCCGCGCATGCGCATGCATCATTTACGGCTCGCTTGCCTGACCGGATACGGACGCGACCATTTGACGCGCTGATCGGTTTGGAGAAGCAGCATCTCCGACGACATCG  
CGCTTGCGCCGATTCCTCGAACGCTTCGGACGCATCCGACGACAGCATCTCTCCGCTCAACGGGCAAGAAATCCGCTTCACTCCCGACGCGCATCGAACATACCGGCCAATCAAGTGCT  
GCCCAAACACCCCAAGCGCTGCGATTACCGCTATGCTTTCAGACGGCACGCTATTTGAAGGAACAGGTTTATTTATTCGCTGCGCGCGCGCTTTGTGCTTACCGAAGAAGACTTCGAGTGG  
CAGTCGGAACCGGAAAAGCGCTTCTTTATCTTACATACAGTTTTCGCGCGGCTGCTTCCCGCATGTCGCTGAACCGGGCTGCACATCTTCGGAAGTCTGTTTTCGCAAAAGCGACCGCGCTTG  
CCGGATCGCGCGAAGCGGAATCTCGCCCGGGTTCGCGGTTTTCGCGAGATTGGAAGATGTCATCAACCGGGCTTAAACGTCAGCGCGGCGGCAAGTCCCGCGCGGATGGAACGTCGCGCG  
CGCGCGCCGCGCATCTTCGCGCAAACTCAAAGTCTCGCGGAAACGAATTCGCAACACCGCGCTTCGGCGATGGTGTCAGCCATGGCGGTCAACGAGAAGAACCGCGCGCGGACGCT  
GTCGTTACCGCCCGACCAACCGCGCGGCGAGGCATCATTTCCGCCGTATTTCGCTATTATTTCCGCAAGTTTCAACCCCGACGCCACAGGAACGCTGTGCAAAATCTCTCTCACCGCAGGCG  
CAATCGGCATCTCTCAAAACCAACGCTTCCATTTCGCGCGCGGATGTCGCTTTCAGGGCGGAAGTCGCGGTAGCGTGTTCAATGCGCGCGGGTGATACGCCGAAGTCATCGCGGCAC  
GCCCAAACAAGTGAAGAACCGCGCGCAATGGCAATGGAACACCATTTTGGGCTTAACTTCGACCCCGCTGCGCGGGTTGGTGCAATCCCTGCATCTGAAGACCAACGGCATTCGCGCGCGAA  
AAAGCCCTCAAACTCGGCACGCTCGCGCTCTTGGAAAGACGGCACGGCAAAAAAGGCTCTCGCTGACGAGTCTCGGCAACCATGCTGCAAAACCGCGCGGACATGAAGCGACCTACAAG  
AAACCTTCGCTTCGCGCATTCGCGGCCACGCTCGCGGAAAAGACCGCTCCCGGTATCTCGTGCAGCTGCTGAGTGC

## SEQ ID 7190

LGNEHDSRRAPVESAHRRCHCRRRSVRYPDGRRGRTPAPRLYRKQCADCAKYRRI SAVLKKEGTSLPRLLLVQCTEAMPSETAFRSKTMISIFDIPKIGIGPSSSHTVGPKAHAAAFAAGL  
DAQTARIAIDITYGSLATGYGHGTFDALMLGLESLPHDIPLAGI PERLGRIRITQHILRLNGQETIRFIPDRDLNIRGNVLPKHPNGLRFTAYASDGTVLKBYVYVSUGGGFVVTEDFEH  
QSETEKAVPYPYNSCAGLLARCLNRLDISSEVLANEALAGCGEAEIRRRVAGVAIMEECIKRGLNAGGELPGGLNVRRRAPQLAAKLKVLRETEIVNTRLWPMVYANAVNEENAAGGR  
VVTAPTNGAAGIIPAVLHYFRKFNPHATQERVENFLLTAGAIGILYKTNASTISGADVCGQGEVGVACSMAGAYAEVIGGTPKQVENAEMAMEHHLGLTCDPWGGLVQIPCIERNGIAAE  
KALKGLTALLDGDGDKVSLDEVIRTMLOTRDMKATYKETSAGLAATLRKKAVPVSVRVVE

## SEQ ID 7191

ATGTTAAATGCGGAACATTGTTTATACGCGGCACATCCCGAGGGGCTGCGCCGCTTTTTCACCAACCAATCAAGCAAGCAAAACCGAAATTTATCAGATAAGGGGAACGGTTATGCAAC  
GTGCTATTATAACCTGCTCTGCGCGGCGAGTATGCGATTCTCAACACAACTTTGCGCGCAATCTGAGAGTGCGCCCGGATGCGCCGCAACCTACACGGTCAAAACAGGGCGACACCT  
GTGGGGTATTTCGGGCAAACTCTGTACAGCCCTGGCAATGGTCCGCTGTGGGGCGCAACCGGGATCAAAATCCACAAATCCCGACCTGATTTATCCGGCCAGGTATTGGTGTTCGCG  
TACGTTGCGCGCGAACCCTCGCTCGGCTTGGAACAGACAGCGGCATCCCCGTCTGCTCAAAATCAGTCCGGATAAGGAAGTGTCCGGATACGGTATCCCGCATCGATGTCAACTCTTACC  
CGCTCTTTATGACGACCCGCAATCGTTCCCGCAAGAAACCGTGGCGCGCGCGCTCTCTCGGGCCGGAAGGCAGGCTGCTGTACACAAAGGCGCCAGGGTTTACACCAAGG  
CCTGAAAGAACCAGGCGCTTATCTGACCTACCGAATCAATAAAACATCACCAGTCCGGATACGGGTAATTCCTCGGACAGAAAGTGCATTACGCGCATCGTCCGCTCCCTCGACTAT  
ACCGACTCCGCGCTCGAACAACGCTCGAAGCAGGCTGAAGAACCGCTGAAGACACGAATACACACCGCACCCATCTTTGATTACCCCGGTGCGACCCGCTCGATACAGCGCTGG  
TGGTCGAAACCGCGCATTTCCGAAATACAGCAGGCGGACTACCTGATGAAATGCGGAAGACACCGACCGCTTCAATATGGTGGCGCAGCAACCGTCCCGCCCGGTTACAGGCAAAATCGT  
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CAGGTCAACCTCTCCAAATTTGACCGAAGAACCTAAAGCAGGGATACCGCTCGAGCTGATTTCGACACCTGCGGAGAAAGTGGGCTTGGCAATGGTTTACCACACTGCGCGGAACTGG  
CTTACGCCATTAATTTTGAAGAACATCTCCGATATTTCGGAAGGCGACACCGCGCAATCCGGGACGGGATTGGGACAATATGCCGATCAGGGCGCGCCCGCTCGATTCCGACCTTT  
CCAA

## SEQ ID 7192

MLKCGTFVITRHIPRCRRFPQPNQARQTEIYQIRGTVMQRRITLLCAAGHAPSTQTLAANLEVRPDAPQRYTVKQDGLWGISGKYLSPWQWCLWGANRDIQHNPLIYFGQVLVLR  
YVGEPRPLGLEQTDGIPVVKISPDKEVSGYGIPIADVNFYRVFMQHPQIVSRKETAAAPRLLSGPEGRLLYTKGARVYTKGLKEPGRVLYTRINKNITDPDTGKPLQBEVAFSGIVRSIDY  
TDSALEQRSKQABERLKDNEYTRTHPLITPVTRSIQPLVVEITAISEIQGDVLMKMPEDTDRFNMVPHPSRFPVQAKIVSVFEGVGVGGQFKTITIDKGGDDGLDKGAVLSLYKRRKTM  
QVNLNNLTREPISRDTVELISTPAEEVGLAMVYHTAPKLAYAILENISDISGDTAANPGRDLNMPDQGRARVDSDFQ

## SEQ ID 7193

TTGGCTCCATGTATCAATCGTGAATCTATATCTTCTGCTCCTCGCGAAATAGTCTATGCCGATATACAATTTTGATACACAACTTGGAAATATGGGTATCGTCCGCGGAGCGATAG  
AATGCGGACAGTTATATATATACGCTTTTATAGGGAGCGGCGAGA

## SEQ ID 7194

LASHYSIVIEYIFVLAEIVYARYTILHLKGNMGIVAGAEICGQLYIYGFFRAGR

## SEQ ID 7195

ATGCCCGAAAAATACATCCGAGGATTGAAATTTGAATTTGCGCAATTTAGCGAATCAAAAGCAACAGCCGATAAAAAATCAAAAGTTTATTTCAATGTTTCAACACACAGGACGACA  
CA

## SEQ ID 7196

MPKIHPEDLNINLNGKFSKATADKKIKSLPQCFNTQDDT

## SEQ ID 7197

ATGAGTATGCCGAAATGCCAAATGGTACGCGGATGACGGACAGATCGTATCTGTACCGAAAGGTCAAAGTGATGTCCGAAATATGGCCGAGCTGTATCAGACGGCACAAGACCGGT  
TTGAAGACGCGCTGCTGATGGTTCGCGCGAAGCTCAGTTGCGCGCTTACCTGCTCGGCTGATTGAAGTTTGGAAATCCCTACCGCAAGTC

## SEQ ID 7198

MSMPKPKWYDGDQIVSCTERVKVMSNNMAELYTAQDAFEDALLMCGGERQLRAYLLALIEGLENPYRKV

## SEQ ID 7199

TTGATGCAAAACCTGATTAGTTCGGACAAAATGCTTTTATCCGATGGAATCGTTTCCGCGGCAACGGAATACAGCGGCTGTCTCCCTTGCAGACAGATATAGCGAATTAACAAAA  
CCGATACGCGCTTCCCGCGCGCGCTCAAGGGAACGATTCCC

## SEQ ID 7200

LMQNPDLVGQNAFYPMESVSARTETIAAVSLADRYSELTKTGTALEPRPGSKGTIP

## SEQ ID 7201

ATGCAAAATGACTTTTCCGCGGGTTTATCCGCGCATATATTACAAAAGCCAAATTTTAAACATATATCTTGATATATACAGCGGTAAACATATATCGGAACATCTTTAAATTTTC  
CGAAATTT

## SEQ ID 7202

HQIDFCGRFYRPIYKSIQIFKHSIYTRRKHILETSLNFPKF

## SEQ ID 7203

TTGCGGGTTTACCGTTCAACGCCAACGTCAACAGCCCGCGTAACAGCCCAAGCTATCCATCTCTGCTGTTCGGGCGTTCGTCCAAGAAACACCGCCATCAGGAATGCAAAAC  
GGCGTGTTCAGCATCCGGCAAGAAATTTTATAGTGGAT

## SEQ ID 7204

LRVYRFMANVNTPAVTSFKPIHSCVFGRSSKRTTAIRNANRCLQHPARIFVD

## SEQ ID 7205

ATGAGCAACTGGAACCCGATATCCCTATAACGATTACACCCCTGCCGCCAAAACAGGATATTGAAAGCAAAACCATCTGAAACGTTGTATAGCGCGCGTGCATCCCTTGCCTGTT  
TAAAGCAGGCGGAGAAATGATACCGAATCAAGCATGCTGATTAAACACCTTCTGTTATGGAAGCCCGTCAAGTTTCGGAATTTGAAACATCTGTAACCAACCAAGCAAGCTGTGTTCA  
ATCCCTGCAAAATGGATACGGAACCGCAAGACCTGCCAGAAAGAGCCCTGCAATACCGCACCGCCCTGTTTGCAGGCTATGAATCTACCTGGCGAGCGCCCTTTATGCACACAAACCGCC  
ATCATGTGCTGCAACCGCATCAAGCACCCCTACGAAACCGCCATCCGCAAAACAGGCGGCACAGCCCTAAAAGGAGGTAACAGCGGAAATGTGTCTATACCCGCGCGAAGGAGAAGAAA  
CCATACCGGCAAGCTGGCAATTTGGGAGCGGTTTATTCACGAAAGCGGCGATTAGACCCGCTGTGTCATCATGCGCGCGGCACATTACCAATTTGAAGCATCCACCGGTTTACGGACGG  
CAACGGCGGCGGACCGCATATTGAACAGCGCTGCTATTGATTGAAAGAGGCTTTTGGATTGCTTATTTGTATTTGAGCGCTACATCATGCAAAAACAGGCGGACTATTACCGCTG  
CTTTTAGGCGTAACCGAAGCGGAGGATTGGGAAAGCTGGATAATCTACATCTTAGAGCGGCTAGCCGACACCGCGGATTGGAGCGGTATCGAAATATAGATCGGATACCGTCTGTTTCGAGC  
AGACACGTCACACATACGACACACGCAAGGAATCTACACGACGCAACTGGTAATCTTCTGTTTGAAGCGCATATACACGCAATGCCAACTAGAAAGCGGCGAGGATAGCCAAACG  
GCAGACGGCTCTAAGTACCTGAAAGAGCTTTACGATAGGTGTCTGCAAGAAATCCCATCGGAGGACAAATATTTCATTATCCCGCGCTAATGGAATCTATTGCGGGGAGAGGCG  
AACAGCTTTACTTCATTC

## SEQ ID 7206

MSNMKPDIPYNDLPLPKQDIESKTIILKRCIAARASLARLKQAAELIPNQAMLINTLPVMEARASSEIENIVTTTOKLQSLQMDTERQDPATKEALQYRTALFAGYESLASRPLCTQTA  
INVCAIKHPYETARTKGTGALKGNGSGNVVTPPEGEETIRKLANWERPIHESGDLPLVIMAAAHYQFEATHPFTDNGRTGRILNLSLLIEKGLLDLPILYLSRYIENRADYTRL

LLGVTERQDWESWIIYILDGVADTADWTYSKIDAIRCLFEQTRQHINHTAQGIYTHLWNLLFEQPYTRIANLEAGIAKROTASKYLKELSGIGVLQETAIGRDKLFTHPRLMELLAGEB  
NSPTSP

SEQ ID 7207

ATGGCTAAAATAAAATGTTTAAATAAACAAAATGTTGAAACTTAATTTCGATAGAGCCTCTGCATATCGTATTGAGGCGTTAATGGAATTTGAGAAAGCTATTTTTTAAA

SEQ ID 7208

MAKTKCLJNKMLKLNFDRASAYRIBALMEFEKAIFK

**SEQ ID 7209**

GGCTTTTCCGGTGTTTTCAGAGATTTCCTCTCAACGCCCTGATTAGCGCGGCCAAATCCAACGCCGTTTCCGAACGGCAGGCATCGCCGAAGATGTTTTTATATATCCGCCGTCAGTTTCAGT  
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CCAACTCGCGCGCAATCGTCCGCGCGCTCTCGTCGTCGGGCAGCACCTCCGCTTTGAACCTGACCTGTTCGCCCATGCTTTTGCCTGGTTTTTGACCAAGCAGGCGGAGCAITTCGGGCTT  
GTGTTCCAAGTGTGTCAAAGAACGGTGCAGGACGGGGTGATGCTTTCGTTCTGTATCATTTTTTCGGGTAGAACTTTTCTGCCCTTAGCCCTTTGAACGCACCCGACACGAACGCCCCACGCC  
AGCCACACCCAGCGCGACGCGCGGACCTCGACAGAGAAGATCGGACGAGCTCTTCAGTATAGGCTTCTGATTGAACAGAGATTTGCGCGGTCAAAAACCCGGCAAAGAAATCAAAACATATAA  
GTATCGGTGCGAAACAGCTTTCAGACAGAAGCGGTGTCATCATG

SEQ ID 7210

GFGSVGFESISLNA\*LSAPKNSAVSERQASPKMFFIFRRQFYQYPERAPFQSRRLQENIGEHAPIGFARGDRVPRQCEHIHFQCLGNNARVVFVVGQHFRLQEPDLFRHAFVAVVFDQOQGEHLRLVFOVILORSDDGVVAVFVIVHFFAVELFCLSL\*TERHERPHOPHDGGCGGOKRROLFISIGFLIEPDLRGQTKGKENONIKYRCETTLDRSVHH

SEQ ID 7211

ATGCCCGCCTGAAAGGCTTCAGACGGCAATTTTTACACAATCCCAACCGTTCCCATCATCCCCGACAATACCGTAATCTTGAAATCCGTCATCCCGCGCAGGCGGGAATCCGGACCGTTCCGTTGGCTGTTTGGCTGTGTTTAAACGATGTGT

SEQ ID 7212

MPPERLOTAFPTOPPPFPIIPDNTVILKSVIPAOAGIRTVRFRFFFGCVLTM

SEQ ID 7213

GTGGTTCCTCCGGATATTGTAGGCTTTGATTAGGAGATCGGAGCTTCAATATATATTTTCTCAGTTACAACAACGAAGTCTTGATGTCGTCTGGGCGAGTAAGGCGAGATTTTGTAGTGTTTCGGCA  
AATATAATTGTGTTCAACCGGAATACCGGCATTTTAAGCGGATAAGACAGAAAAACCGTAATCATAAGGCAAAATCGACATTCGAATATCTGCATATTTTAGAAAAGACCTTTTATAGTGG  
ATTAACAAAAAACCGGTACGGCGTTGCTCGCCTTAGCTCAAGAGAAACGATCTCTC

SEQ ID 7214

VVPVFEALIRDADFOYIFLSYNNEVIMSGOVREIFECFGKYNLVOTEYRHFKAADKTENRNHKA NSTFFEYLEILLEKTFYSGLTKTGTALPRLSSKPTIL

**SEQ ID 7215**

ATGCGCTGTGAAGCCCTTTCAGGCGGCATTTCGGCATTTCGGACATTTAAAAATCCCGTCATTCCCGCGCAGGAGGGAATCCGAATACATCCGCACAGAAACCTGCATCCCGTCATTCCCGC  
GAANGCGGGAATCTAGAACG

SEQ ID 7216

NPSEAFQAAFAAFGLKIPSPRRRESEYIRTECIPSPRKRESRT

SEQ ID 7217

TTGATCTCAGTTCGCGCCTAAAACACATCTGTACAGCGCAAAACGGATGGGAATGGCAAAATCCGGAAACAAACATTTTTCAAAGCGTACAAACAAAAATACCAACCGGAGGTTGGTATTTC

**SEQ ID 7218**

LIKSALKHIVORKTGWENONPETNIPQSVOTKNTNRRLVPLNFWRGGRGSNPRPPA

**SEQ ID 7219**

GGCTTCCGCCACCGAATCCCGGTGTGATGGTTTTTCGCAGTAGTGGCAITTCAGCCGGGTCTGCCGGTGTGTGTTCTTAACTAAAAACCGGCTTTTGACCGGCTCGCGGTGCCGGCGCAA  
TTGGGATTTCGGGCAGCGGAACACTTCGGCGATTTCGTGCGGCAGGGTCAAATGCCGCTCTCTGTACGACCTTGAAAATTGTCGATGGTGTGACCAACCGCTTCGGGGCGCAACAGGGCGAGGC  
GTTCGGCGGCTTTATGCTCAAGCACACGCCCTTGATTTTGATGATGCTCTTGCTGCCCTGGGTTTTGCTGGGCAGGTGAAGCCCAACGCGTACCGGTTGCCGTAGTGCAA

SEQ ID 7220

GFRHRI PVVGGFAVVAFOFRLPVVFLNIKPAFDRLLAVAGAIGIRAAEHFGDFVGQGGOMPLLYDLRLIVDGDVDRFGGEQGEAVGGFTVQAHAFDFDDVFAALGFAGQVEAHGYRVAVVQ

SEQ ID 7221

CACTCTCTTCGTTCAACACCGAGCGACAATATCGCCATACGCGCATAAACGCCGTGTGGTGCCTGCTCGAAATAATAGCGGTGCGGCGCGGCATCGACATCGGGGTGGATTTCGTCCGTGCGC  
GGCAGGGGGTGCAGCACCGCAGGTTTCGGTTTGGCGCGGGCGAGCATAGACGCTTCGAGGTTGAATTTGCCTTGGATTTTGGCAAAATTCCTGTTCGTGCGAAAGGTTCGCGCTGGAACGGGG  
TCATATACAGGATGTCCGCCCAATTCGCGCGGCTCTTCAAACTGCGAGGGGGCGGTATTCGCGAGTCGGCTTCTTCAACTCTTTCGGTAATGTAGTCGGGCATCGCGAGGCTGGGGCGGGA  
GACGAAGCGAAATTCGACAGCCCCAGCGTTTCAACGCCCTGACACAGCGAATGACAGGTGCGCCCGCTATTTCGAAGTCGCCGCCATGGCGATTTTAAAGCTTGCCAAACGCCCTTCGCTTCA  
TAAATCGTTACAGGTCCAACAAGGTTTGGCTGGGGTGTGGTTTCGTGCGCTGCGCGGCTGTGATGACGGGGACGCGCGCAAACTCCGCGCCACGCGCGCGCGCGCTTCCTTGGGATGC  
GTTGGACAATCGCGTCGGTGTAGCCGGAATGATACGGGGGTATCGGCAAGCGTTTGCCTTTTTCGCACTGGTATTTCGCGCGTCCGAAAAGCCGATGACCTTACCGCGCCAAACGGC  
CACCGCGCTTTCAAACGACAGCGCTGCTGCGCGTGAACGCGCTGAAAGACGAAACCGATGAGTTTGCCTTCCAAACAAATCCCGCGCGGATGCGCTTCAGCTTCAATGCGCTTCGAAGC  
AGTTATTCAACTCTGCGCGGACAATCGCCAAATGGAGATGAGGTGCTGTCTGTAAGCGGATTAGGCAT

SEQ ID 7222

HFFVQHQHQYRHRTRINAVGRLLLEIIGVRRGIDIGVDFVVRARQGVQHAQVRFAGAGEHRRFVEVEFALDQKFLFVETTFALDAGHIQDVRPFFRLFTQAEAGSAVSGVGFQLPGNVVGHREAGER  
 DEGKFAAPAFQRLTQRMHGAPVQFVARHCGDFKLVTPLRFINRYQVQOGLAGLVRAVAGVDDGDARKLRRHARRAVFGMALDNRVGVAGNDTGIGKRFAPFTGTIRAVRKADDLTAQTL  
 HRFKRPAPRARGLEKANTDEFAFOOIAARMRLOLOCRLOVFPOLFAOIRNGDDVLSVKRIH

SEQ ID 7223

GTGGCGGATCGGAGGGGAGGCGGTGCGGCAACCGTGCGCCGCGGGCGGCATTGCCGTACATTATAACAGCCAAATACGCATCCTCGCTTTCAGACGGCATGGCTGTCAAGAAAAAGCGCGCGTGTACAATATCGCGATTGTATGTTTAGGACGGATTGAAAAAGGATGGAATAATTCGGCAGGCACGGGCCCATTCGGCGTTTTTGACTCGGGAATCGCGCGTTTGACCAATGTGCGCGCGCTGATGGAACGGCTGCCGATGGAGAACATCAATTATTTTCGGCGACACGGCGCGCGTGCTTACGGGACGAAATCTAAGCGGCACCATCGAAAAATTTCTCGATGCGAGATTGTCGATTTTTTTTATTGGGACACGATGTCAAAGGCGATGGTTATCGCGTGCAAACGAGATTGCGCGGTTGCGGGCGGAAAAATCCGTCAAAGACGGGCAATATGCCCGTTTTGAGACGTGATTTCGCCCGCGGCCCAAGCGCGCGCTGGCAACGACCGCGCAACAATAAAATCGGCATCATGCCACCAATACGACAGTCAACAGCAATGCTTATGCGCGCGCCATCCACAGGGACAACCCGACACGCTCGTCCGCAACGAGGCCCGCCGCTGCTCGTCCCTTTGGTGGAGGAAGGTTGGTTGGAACACGAAGTATCCCGCTGACCGTATGCGAATACCTCAAACCAATTGCTTGCAGACGGCATCGATCGATCGTGTGTTGGGTGCACGCACTTTCCCTTGTCTAAGCCCTTAATCGCAGGAGGGCGCAACAATGCTGCGGCTGTGATTTCGCGGATTACGACGGCGGAAAGAACCGCACGCGCTCTTCGACAGCAAGGATTTGCTCGATACCGGCAACAACAATCCCGACTACCGTTTTCAGCTCAGCGATATTTCCTTTGAAATTCAGAACCCATTCGGCGAGCGTTTTCTGGCAGGACGATGGAGCAGATTGAAATGGTGATCTTTGGGT



SEQ ID 7224

VADRRGRSRANRPPGGGIAVHYNSQIRILLSGMAVKKRRRVNMRIVCLGRIGKRMENIGRQRPIGVFDSSIGGLTNVRALMERLPMENIITYGDTARVPYGTYSKATIENTFSMQIVDFL  
LGHDKAMVIACNTLAAVAGRKRIRKTKGNMPVLDSISAGAKAALATTNRNKGILATNTTVNSAYARAIHRDNPTDLVTRTQAAPLLVPLVEEGWLEHEVTRLTVCEYLKPLLADGIDTLV  
IGTTHPLIKPLIGREAHNVALVDSATTAETPARVLAORGLLDGNNPDYRFVSDIPLKFTTIGERFLGRTEQIEHVSIG

## SEQ ID 7225

ATGGTCGATAAACCGTGCCCTTTTCGATGGCTTCGACACTGAGTPTTTTTCGCGCTCCCATATCGGTTCCCTCACACTTCTTCGTTTCAACACCAGCAGCAATATCGCCATACCGGCATAAACGCCG  
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CTTCGAGGTTGAATTTGCCCTTGGATTTTTCGCAAAATTCCTGTCGTCGCAAAACGTTCCGCGCTGGACGCGGGTTCATATACAGGATGTCGCCCATTTCCCGCCGCTCTTCCAAACTGCCGAGGCG  
CGGGTATCGGCAGTCGGCTTCTTCCAACCTTCTCGGTAATGTAGTTCGGGCATCGCGAGGCTGGCGCGCGAGACGAAAGTTCGCGACGCCCAAGCTTTCAACCGCTGCACGCGGAATGC  
ACGGTCGCGCCGATTTTCAAGTCGCCCGCCCATGGCGGCTTTAAGCTTTCGTCACAAACGCCCTTCATATAAATCTGCTACCAAGTGTACCAACAGGTTTTCGCTGGGGTTTGGTTTCGTCGCCGT  
CGCGCGCGCTGTATGACGGGAGCGCGGAAACCTGCGCGCCAGCGCGCGCCGCTCTTTGGGATGGCGTTTGACAAATCGCGTTCGGTTGAGCGGAAATGATACGGCGGTTATCGGCAAG  
CGTTTCGCCCTTTTTCGCACTGGTATTTCGCGCCGTCGCAAAAGCCGATGACCTTACCGCCAAACGCTGCACCGCCGCTTCAACACGACAGCCTTCGTGCGGTGGACGGCTCGAAAAAGCAC  
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TGTAAAGCGGATTAGGCATTTTGGCCCCCTCCCGTAAAAAACCCGCGTCAGCGGGTATCCGGTTATACGTCCACGCCGCCGATATGTTTCGGGAACAGCTTCGCAAAAGCGCGACACG  
CGCGTATTATCGCATGTTTGCCTCCACAAAGTTTATCCGCAGCAATCTGTATTTTTCAGACGGCATTTCAACACGCCCGCATAAAGCATAAAGGTATATCGCGCCAGACATTTCTTTT  
CAGGAACGCCCGCATTTAACTGCTCAACCCCTACGAAGTCGCTACACGCCCAACAGAGTTCGCGCAAGTATTTCCCGCCGCGACGTGGCGGAACGCTGTGCGGCATCTGTCCTCGT  
CTCAACAGAGCAACCGCTCTCTATTCGAAATGGGTGCGCCCATGCTGTTGGACAACATCCGCTCGGTCGCGCGTGA

**SEQ ID 7226**

MVDNRAPFDGDFTEFLRFHIGSSSHFFVQHQRQYRHRTRINAVGRLLLEIGVRRGDIGVDVFRARQGVQHAQVRFGAGEHRRFEVEFALDPGKFLPVETFALDAGHIQDVRPFRRLPQTAE  
AVSAVGFPQFLGFWVGHREAGRRDEGKFAAPAFQRLTORMHGAPVFQVARHGDFKLVTPLRFINRYQVQOGLAGLVVRAVAGVDDGARKLRHARRAVFGMALDNRVGVAGNDTGGIGK  
RPAFFGTGIRAVRKADDLTAQTLHRRPKRQPRARGLEKARTDEFAFQOIAARMRLQQLCRKQVQFLFARQIRNGDDVLSVKIRIHFCPPSVKNPRQAGIRLYVHAARMFAEQLRKSGLT  
ARIIAHLPPQSFTARILLYFDGSIKHSIRSYNRARHFSGSRHVNQLPLRSRHPRENEFRQDPPRRLGGTPVRHPLVHQRPPLLFEMGAPHAGGQHPLRRRR

SEQ ID 7227

TTGCCGACCGCGTGCCTCCGATCCGCCACATAAAGTTGTAAGCCCCATGTCGTGATTTTCCCOCGTTTCCCGATTCCCTGCCGACGAAGCCGCCACACTCGATTGGGGCGCGCGT  
GGTCTTCCCGTTTAAACGCACCGCTGGTCATTACCTCGAAGGGGATTTGGGTGCGGGCAAAACCAACGCTGACCGCGCGCATCTCTGCGCGGATTGGGTCACCAAGGGCGCAGTCAAAAGCCC  
GACCTACGCCATCGCTCAAACTTTATCCGCTGGAAACGCTTGCCTCGACCACTTTCGACCTCTACCGCTTCTCGTTCCCCGAAGAATGGGAAGACGCGGGCTTGACGAGCTGTTTGGCCGA  
AACAGCGTCTGCCCTGATCGAATGGCCGCAACAGGGAGGCGAAATTACCCGCGCTGCCGACATCGCAACATGTACACACGCGCGCGCGCGCAAAATGCCCTGACCGCCCAATACCG  
AACCGACGACCGCAAGCGCTCCGCTCA

SEQ ID 7228

NSVCLIEWPOOGGEFTPPADITATILTHGGGGRKCLTAHTERGRESLPL

SEQ ID 7229

[illegible]

SEQ ID 7230

VAVIVR#CGSGRILSELYAAPVSDGARCVPVIRRRMPPTQAFPCIFLGRSMNEFSLAIPVVLLVSVITVILCRKNPISMLGYLLVGLFAGPGHLSLIPKSHATDYLGIGIVFLMPS  
IGLEFSLPKLRMRRLVFLGGLQGVGVTLSVMGILMTGVPPNMAFAVSGALAMSSTAIVSRILSEKTELQPHGQAMGVLLMQDIAVVPMLILIPALAGGDDGNITWAALGLAFARELL  
FTGLLFFVSGKMSRWFPMFAKRSSELPMINVLVTIGVAYLTELEGLSHALGAVFAGMLSETETRYRQVBDITRPFRRDILGFFFTITVGMKLDIQALIGWRQVLLMLLMLVVKALVV  
FAIAFKMKHSVGDLSKLTALYLAQGGEFGFVMLAAGLDMSPELQDQATAAVLLSMITAPFLGSGDALVGRLLVSSWDMKSLDLHSMVMSKSDHVLIVGFRGGQTVGRVLAQED  
PYFALDDIARVQVARSAGEFSGDGAARREVEAAGLGRMNVVTLNNMHQVHLDNVLSHMPNMPVYARATNDIVYKFTPLDGMAGEAAVSDMKTGFLVLAGYAMLNGASRYHRVYQTM  
ANTRHSRYAAELGLFVSGDDEAGFGENKDETRHAFPLAAEAYAVGKTVCGLTLPMAAYGLLTPVRRRTGRLENPDASFTLGGDVLVVGAGKKRKNYLF

SEQ ID 7231

ATGTTAATCTGCAACCCCTACGAAGTCGTATCCACGGCACAAAGAGTTCCGGCAAGATTTTCGCCCCCGGGACTGGGGCGGAACGCCCTGTGGGCATCTGTCTCTGTTACCAAGAAGACA  
ACCGCCTCTCTTATTCGAAATGGGTGCGGCCCATGCTGTGTGGACAACATCCGCTGTGGTGCCTGATATAAAACCTGGAAACCGACAATCCGCAGATGTTCGCTTCTCTGATGGCATTTTGC  
CGCCGACACGACCTTGGCGCTCATGACTGCAAGGCCCTGCTCGAAGAACGCGAACAGGGCGGACAAAAACGACCTTGCTAACGAACCGCTCTGCTCGACAGGCAATCGAAGAAAACAC  
GCCGCGGAGAAAAACAGGAAACAGACCGCCTTGGGGCGCATCTACGTTTACGCGAAATCGGCGCGAGCAGACCGCCACCGCCTTTGCGAGCTTTTGAGCGTTTTCCTCGTTCGACCG  
ACATCGGCCGCTTTACCGAACAGATACACAAAATACACATCGCCCTTACCGTTCGCGCTGCTGGGTATTTTTGAAGAACTGCAACACCAACGCGCTGCGCGCTTCGGGCTTCGCGGACCGTGC  
CACCTCTCGCGCGCGCGCCACATCCATACGACGACCTGTACCTGCGCGCAAGCCGACCAAGGCTACGCTCGCGCTTTTGAAGAAGTCCGCAAAATCGGCGCGGAAACAGGG  
GTTTACCAAAATCCACTTTAAGCTCCACGTCAACACGACCGTACCGACGCGCACCGCCTGTATTTCAAAAACGGTTTGAATCTCGCGCTTACCCTTCGTTCCGACCCCAAA



**SEQ ID 7232**

MLICNPYEVVINGHTSSGKIFRPGDWAEERICGLSSPTKDNRLSYKSWVRPMLVDNIRCAVADKKLETDNPQMFRLMDFADNDLRVIDCKALLEERBQGGQNDPANERVLLAQALEKH  
AAEKTQEQPASGASYVLRIGADDATATAFALSVLRSLLFDIGRFTEQINKIQRPQGYRLGLGPEECKHNAVAVCGFRACTLAGGRHIHIDDIVTLQPQSRKGYASRLLEEVKIGAEFG  
VTKIHLNVHVNEDRTDAHRLYPKNGFETICAYHFRCDPK

**SEQ ID 7233**

ATGCCCTGCTGACCGGCCCATACCGAAGCAGGAGCGCGAAAGGCTGCCGCTATGACCAAACTGACACGAAGACAAATCATCCGCCGACCGCCGGCACACTGTTTCGCCCTGAGCCCATATCGCAT  
CCGCCGTGTCACAAACGGTACGCGCCCGCCGAGTTTATCCGCCGACGCGATATGCGCGTTCGCACACCTTACACCCGCTGAGCGTGGAAAGCACACGCCCGGCTCAAATACCGACACTTCGCGCT  
CGACACCCCGGGCAGGTTGGTGTGATATACAAACGCAAAACATCAATACCGTATTGCACGGGCTTTCACAAAAGTTATGGCGGACGACCCCTTTATCCGACGATACACGCCGGGTACG  
AAGACCGCGACCAACGCTCCGCTGTGATCGACTGCAGACGCCACCCGACCAAGTCTTCGCGCTTCCGCCCTCGCGCGCTTTAAGGACCCGCTCGTGTGCGACTCTATTCGCGACG  
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CGGGCGCAGACCCGTCATCATGCTCGATCCGGACACCGCGGTGAAGACCCCGGCGCGTCAGCCCGGGCGGTTTCAGGAAAAACACGTCGCTCTCCATCGCCCGGAAACCAAAAA  
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CGGCGTACCGACACGCGGACACCGCAACGCTGATACCCGCTGCTCGACATGACGCAACCAAGCCGACATGCGCGACAGCGCAAACTCGGCAAACTGCTGCTTGAAGAAATTGGGACGGCTC  
AACCATTCTGCACAAAGCGAGGTGGACGAAGCAAAATTTGCCGTATTTGCCGACCCGCTATCGCTGTATCCCTGTGCAAAACCGCTTCTCTGTCCAATCTCGCGAAGAGAACTGCTGTG  
CGACGCAATCTTCCGTCCGACGATGCGCCCAATCGCAATTGCTCGGCTGCTCAACGCTACATCAATACATCCGATTTGAGCGGGGT

**SEQ ID 7234**

MPADRPYRTRTRKPAAMTKLTRRQIIRRTAGTLFALSPFIASAVAKTVRAPOQTAARIWPSHTYTRITLLESTAAIKYQHFDALNDPGRLLVDDIQANNTINVLHGLSQKVMDPPFIRSTRAGQ  
NPTPTVRLVIDLKQPTHQVFALPPVGGFKDLVDLPHGMDADPPMALLNGSLNKTLRGSPADPAQNTTPRPGRGKNGRRPVDLDPHGEGEDPGAVSPGGQKEKHVVLISARETKK  
QLEALGYNVFMTRNEDVFIPLGVRVAKGRARRADVFSIHADAFTSPSARCTGVYMLNTKGATSSAAKFLBQTPONNADAVGGVPTSGNRNVDLALLNTQATLDRSRKLGKLVLEELGRL  
NHLHKGRVDEANFAVLRAPDMPSLIVETAFLSNPAEKKLGSESPFRQCAQSLASGVORYINTSVLKR

**SEQ ID 7235**

ATGACCGCCACCGCCGCGGATTTAGACCGACCTCTCCCCCAAAACCAATGCCCGGAATGCGGGTATGAAGGTCGCTGCCCTACGCCCGCGCGATGCTGCGGGGGGAGGCGCACAACTCT  
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CTGCACCGCTGCATCCGCGCTGCCCTGCCGATGCCATTATGGGCGGGGCAAACTATATGCACCCGTCATACACGAGCAATGCACCGGCTGCGGACTCTCGCTGCCGCCCTGCCCGCTG  
GACTGCATCCATATGCAGCCCGTTGCCGACACCGTCTGCCGCGCGCGCGCGCTTTCAGCCTGTCCGACGACACCGCTTTTCCGCGCGCGCGACCGCGCTGCGCGTACCTCAAAGCA  
ACGAACGCAAAACCGCGAAGCGCAAGCGCAAGCCATGCTGCCGACCGCGAAGCGCGCGTTCGCGAACCGCGCTTCGCAAAACCGCCGACACCGGAAACACCGCGCTTCAACCCCGC  
CGACTCTATCGCCAAAGCGATGGCAAAACCAACCAAGATGCTCGCTGCCGCGCGCGCGCGCAACCGCAAGGCTATTCAGCGCAAAACAGATAGCGCAAGCCCGCGACCGCGCAATTG  
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SEQ ID 7236

MTATAADLRLLPOTQCRECGYEGCLPYAKAMLGEAHNLCPAGGATVVRDLAALIGKPLVAPAKTQAKALARIDETACIGCTACTIRACPADIMGAGKLMHTVITDTECTCGCLCVAPCFV  
DCIEMQFVADTVLPRARRFLSDDSRFAAAEHARARYLKRNKQREADERKAMLAEREAAVRNARPOTPDTPKPAFNPADLAKAMAKAQTOQDRLAAADNRQGYQAKQIAERERAEI  
RRAORDMKYGDSEKAAALEYLKQYKAKQEAQNTAS

SEQ ID 7237

TTGGTATCTCAATTATCCATACCTTTTCATCATAAAAACCGGGTTTGGGGCGGAAGTAGGTTTATGCCTGCCCTTCATCCGACAACATATATTTTGAACACACCGCCTTTTCAATCAACCCCGC  
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GCGGCAGAGCTGGTCGCGCTTTTGGTGTTCAGCATATAAAACCCCGGTTCCGCGCGCGGAGGGGCTGTGAAAGCGTCGCGCTGGATGGAGACGAATACGTCCGCCCGCGCTGCGCGCCCTT  
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GGATGATTTGTCTCTGTGTCAGTTTGGTCATAGACGGCAGCGTCTTCGCGTCTGTTTCGATATGGGCGGTGACGAGCAATTTTTCTGCCCGCCCGCGCTGTCAATGTTCGCGGTGATGTGCG  
CGAGCGGGGTAAATTCGCTCCCTGTTTTCGGCGCATTCGATCAGGCAAGCACTGCTTTTGGCGCAACAGCTCTCAGGCCCCCGCTGTTCCCATTTCTGGGGAACAGAGAAGTGT

SEQ ID 7238

LVSPQIHTFHKNNAVGGSRFMPAFIRQLYFETPPQSTFLPYQYCIDVALDTRGNGLGALPTESFAAQQLFGRIGQEGGFQDRRHIGCAQYGEIGFVHPAFVQMVEPAQFFKHQFAEFA  
AVAQCGGLRHVBQGGIDVAAGRYAADRVGIIILGLFQYFEGGRAGRAPGVQHIINPRASARGGAGESVGVGDSEYVRPPCAPFGDTHAQWDEHVFVARHKDVVTQGFQFFFGAGDEDDVFF  
LQATARADGAGVFTAVSRIEHDGSAPIVAPPSSGSGVLGGVGFRRAAQCFVQAAVEQRHHRIVGIIHPVRIEVDDEAVLKAADGKRKRBDLCVGGFLQVDDDEADGGRRLVTRAYAADKGVVRR  
NFLGKPVQYGLIDCVLYIDDQPARVVEREVLFERGGAPQRQAGVGVRRPYPCGKGLRGYFNGNGCDDGAQGBQAGGAGAADLSSCQFGHSGRLSRPSRVMAVSRHFLPPPCPNVAVMS  
AAGVGLSPCCGHSIRQTLFAANSSSSPASHSSHEKFR

SEQ ID 7239

ATGATATATGGGTGTTATTAATTTTTCCTAATCGTTCCAAATTTTGGGATTTATTTCGGCTACGATAAAATTATTTTATTATTATAAATTTAAACTTCCAAAATACATGGCGTATTACTCC  
CATCATATACCTATTTTATTCATATTTATTCATGCAATAAAATGCGATATGATTTTATTTTTTATGTTTCATGCGTTTATTTCCGCGTATACATATTATGATAAAAAATCTTTA

SEQ ID 7240

MTMGVLIFFLLIVPILGFICATINFYIINKFKLPKYMAYLLPSLSILFIFTHAIKLEHMLFFYVSCVYSAYTTYDKKSL

SEQ ID 7241

AFGCCATCCTGAAGGCGATTACCGACATCCAGTACGGTTTGGCGGAAGACAAATACGGCTGGCTGGTCGAAGTGTGCTGATGCTTTAAATAAAAAATGCCGCTCTGAACCCCGTTTGGCGT  
TTCGGACGGCATTTCGCGTTTCGGACCGTTTCGCGCGCACCTGCAGCAAGTCGGTACAAAGGCAATCGGTTAAACAAGCGTCCGCACTTTCCCATCCCGCTGCCGCAAGTCGGGCATTTC  
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CCCAAGAGTTTCGCGAAATCGCGGATGCGGAGGCGCGCAGCGCTTTTGATCGGGCGCGGAAATGCCCTGCGAGCGGATGCCCTCTTTACCAGACAGGCGCGGTAAGCGGATGCCCTG  
CCTCAAGGCTGGCTTTTGCCATACCCATACGTTGTAATTCGGAATCGCGCTACCGCGCCAAAGTAGCTAAGGGCGACGATGGCGGAGTTCCTGCCGCGCATCATCGGACGGCGCGCTT  
TGCCAAATCGCGGACAGGCTGTATGCGGAAATTTCTGTGTCGGTGTGAACGCTTCGCGGTGATGCTGTGAGGAAGTCGCGCTCAAGGCTTCTTTGCGCGCAAGCCGATGGAATGCAAC  
AAACGCTCCCAAGCATCCCAATGTTGCGC

## SEQ ID 7242

MPSEVRLPTSSVVRKTNVITAGNSKADALNKKMPSETRLAFTAFPSRDRFRRTCSKSVQRQSVKTSVRISHPACRKSGLISLEIRFKRQTAARNRYSARTAHGFENGGLSLGAQGINAVTA  
VNI.SDFAGNAGRQVQGGSGSIDPFDGNVAAQVRVGGDVQSQEFARIGDAGGGERFDRAGNVAADALPTQTGGGKADACLKAGFCHTHVIVIRNAYRAQVAKGDDGGVPAABHRTGGF  
CQCGQAVCGNFVCGVERFAADAVEEVAQGFPRREADGMHQTVQALPMFA

## SEQ ID 7243

GTGCGCGCTTCGGCTTTTCAGACGGCATAATTGACGTTATGATTAAACAGTTAACAAGATTATCACACCGCGTCAAAAGACAGACACACAACA

## SEQ ID 7244

VRGFGFSDGIFDVHIKQLTRFITTPSKDRHTT

## SEQ ID 7245

TTGAATGTGTGCCAAGTCTACAAAGGAGAAGTAGAGGAGAAAAATCAAGCTGCATCAAGCAACTCAACGGCGGTAATTATCCGCCGTTCTTATCTGCTGTCAATTATTTTGGAAATTT  
ACCCGACCGATTCAAATTTTGCAAAAACCTTGCCCGATGGCTATCCGGTAAACAAATTCCTCAAAAACCGGTCAATCCGATTATTCAAAAATCATATGCTTTTCATCGGTTCCTTTTCG  
GTTGAAACCTGCCCTTTAGGCGCG

## SEQ ID 7246

LWVCQVYKGEVEERKQAASSNSTAVIIRRFSLAVNYFLKIYPTDSNFARNLPDGYFVINSKPNSTRIFKKSTAFIVFPFLKPCPLGR

## SEQ ID 7247

ATGTTTGTGACCCCGCTTCTTACCAAAACATCCATGTACGGAGTTGGAAGACACGGCGAGATTCCGGCATAGTAAAAACAAGATTGGATTTCCTTGGCGCGCGCTTCGATGCCACG  
TTACTGAA

## SEQ ID 7248

MFVDPRLFKHPCTELESTARFRHSKTRFGFFLRGFDCHVTE

## SEQ ID 7249

TTGTCGGATGAAGCGAGCATAAACCTACTTCCGCCCAACCGCGTTTTATGATGAAGGTATGGATAAATGAGATACCAACGGGATTTTTAAATATCCGCCCATTTTACAGCGG  
GCGAACAAGATACCTGACCGAATTTGCCGATCGGCTTCTTATCTGTTTTAAACGGACTCCGTCGCTAATTTGAAGAAATCGGTATCGATTTCGTGACAGTCTTCCCAATTTGAAGG  
AAACACTTATATCAATACGATACGACAGGCATTCCTTAACTCGGCAAAACCGCAGCGGGAAAGTTTATATTCGGATGCCGTAATGTTAATCAACCTGAGGGAAGTTACCGGCACCTGCTG  
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TAATAATTTGGCGTATCTCCGATATTTTAAGGACTGCAATAAACGTAAGTCTGCCAGAACTGTATGACCTTTGCGCTGATGCGCTCCGCTTTTTCCTTGGCTATTTCTCCCGGACAGTTAT  
CCCGCTATGCGCGAGGCTGCTGATGACCTTATACGAAACCGCGGATACGCTTTATTCAGAAATATTTTATTTCCGCATACGAAAAATACCGTAATAAGTACGCTCCCGACGCTGATGTG  
ATATTTCCGAAATTTCTCCATT

## SEQ ID 7250

LSDEGRHKPTAPNRVFMKGMKLYQRDLNIRPIFTAGBEYL/TELSRLPLSVLTVDSNRNIEIGIDFVYSPAKLEGNTYNYQDVALKLQTAGGKLYSDAVMLINLRESYRHL  
SGLDSPKPFMDLPLKTHSLISENLEKSGGVRRDSVTISGTDYTPLSNPQSLDTLKWLLQEAPEIENPFDRAVYLHNNLAYLRYFKDCNKRRTARNCTLSLMRSFFPCVPSDSY  
PAYABAVVAYIETGDYGLPKKFFISAYENTVKNYGPQDVIDIFRNFPI

## SEQ ID 7251

ATGCCGCTGAAGCGCTTCAGACGGCATTTTATCAAGCTCTCCGTCGCGCTACCGCTGCCGTCGCTATCTTACGCCCAACCTTCGCGCGTCCGCTTTTCAA

## SEQ ID 7252

NPSEASDGLSSSPASVPPSVSYRPPFRPCRPQ

## SEQ ID 7253

TTGCTTGGCTATGTTGTGTGACCCCGCTTCTTACCAAAACATCCATGTACGGAGTTGGAAGACACGGCGAGATTCCGGCATAGTAAAAACAAGATTGGATTTCCTTTCGCGCGCGGCTT  
CGATTGCCACGTTACTGAATAATTTTATGGCAGACATTTCTGAAGCGGAAATCTTAGACAAAAATGGATAAAACCAATCGGTACTTCTTTGATGATATGCAACGCATAATGCCCGA  
ACTGGTTTGAACACACAGGTATGCTTTTGCATTTGAACAGTTGGTACAACATAAAATTCCTGTAATTTGTGATTATAAATACCGTAATAAACCAACCTTTTCGGTATTGAACGCTATT  
AACGGAGAAATCTGTTTGTCTGGCTGATCCATCGCTGGGGCAGCTCTAACAGCAAAATCAACAATTTCTGAGCGCATGGAAGACAGCTGATGGCGAATGGAAGGAAAAATTTAGGACATCG  
TGCCAAAAATACTGATTTTGTAGAAATCAGATGTTTTTATAAAAAATCCCGTTCTGTAACACAGTTTACGCTAGAACAAATCCAAATCGCGCAAAACGA

## SEQ ID 7254

LLGLCLILTPASYQNIHVRSWKARRDSGIVKQDLDFSCGAASIATLNNFYGRHYSEAEILDKMDKTQMRSTFDDMRIMPGLFPAQGYALPFEQLVLQKIPVTVYLKYRKNHFSVLNGI  
NGETVILLADPSLGHVSTSKSQPLSAWKTRDGEHEGKILAIVPKNTDFVRNQMFNKNPVRQTRFTVBEQIQMRQR

## SEQ ID 7255

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TCCTTGGTAGATTGAGCTTCCAAGCGCGCGGACACCACTGCAAGAAATCAACGCACTGATGAAAGCGCTCTCGGAAGCAGGCGGCTCAAGGCGGTTTGGGCTACAACACCTGCG  
CATTTGGTTTCCATGAGCTTCAACCAACACCGAAGCGAGCACTTCGACGCAACCGTGACCAAGTCTGCGACGCAACATGGTCAAGTGTTCGCGTGTATGACAAACGAATGGGCGCT  
CAGCTGCAAAATGCTGACACCGCAGCGCTATGTTTCCGACTTGAAGTGCAGCGCTCAAA

## SEQ ID 7256

MGIKVAINGYGRIGRQVLRAIYDYQIQDLQIVAVNASGSLETNAHLTKPDTVHGRFEADVSHDGNLIVNGDKIPFSTRNPAELPWKELGVDLVMECTGAPTSEKAKIHLESGAKKVL  
ISAPGGDDVADTVVYGVNDVSLTADMTVVSNACTTNCISPVAKVLSVSVIGKAMTTHAL/TNDQTVTVDRHKDLRRARSQGVENMIPKTGAAKAVGLVLPGLKGRDLGLAIRVPTVNV  
SLVLDLFOAARLTVEEINALMKAVSEAGALKVGLGYNTLPVSMDFNHTTEASHFDATLTKVVDGNMVKVFAWDNEWGFSCQMLNATARRMFLGLEVRPLK

## SEQ ID 7257

ATGAATACCTTTATATACACTTTTTCGCCACCTGCCCGCGCGCTTGGAAACCGTTTATCTCAAGAACTCGGAAGCCTCGGCTGTACCGATGTCCAGCGTTTTCAGCGCGCGGCTTCTCGCC  
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CATCAACTGGTTCAACTGGTTTACCTTGCAGCAGAGCTTCAAGTCAAAATCGAGGCAAAACGCGCAACCGTCAAAAGCCTCCAAATTTGCGCGCTGACCGTCAAGATGCGGCTGCGGAC  
GCTTTCCGCGCATTTACGACGCACTCCGAGCGTGGACAAACCGCGCGCGCATCTGCGGCTTTTGGACGAAACGCAATGTGCAATCTTCATCGACACTTCGCGCGGAGCGCC  
TGTTCAAACGCGCGCTACCGCTGGATACCGCGGAAGCGCGCTGCGCGGAAACCTTTCGCGCGCGGCTGCTGCTCTCGCGAGGCTACGACGCGCAGCGCGCTTCAAGACCGGTTTTCGCG  
CAGCGCGCAGATTGCTATCGAAGCGCTTGGATTGCCCGCGCGCGCGCGGATGATGCGCGCTTTCGTTTGAAGAACTGCAAAATTCGATAAAACGCTGTGGCGGATTTGCGC  
CGCGCGCGGAGCGCAACCGCGCGCTGCGCGCGCGGATTCAGGCGAGGCAACCGCGCGCGCATGCTTCAGACGCGATTTGACAAACGCAATGCGCGGAGCGGACATCGTTT  
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## SEQ ID 7273

TTGCAGGTAAATATCAAAACCATTAATTTAAATCATATTTTACAGAATATTCGCGCGCTTCACCAATGGACATCAAAACGGTTCAAAATTTCTGTAATTTTGCAACAAAATACCGCAA  
AACACCCGATTGAGACCGAAAGGACTTTCATA

## SEQ ID 7274

LQVKYQTLNHLHIFTEYSAAFTKWTNRFQISVLQONTAKHPIETERTFI

## SEQ ID 7275

GTGATCGACGATCGGTAGCCGTTTCTCGCGGATTTGTCTTCAGGGCTTCGATTTCCGGATTGTGGAATTCGTTACCTCGCCGCACTTCACGCAGACGATATGGTCTGGTGGTGG  
CCCTTGTCCAACTCATAAACCGCTTGCCTTTCAAAATGGTGGCGTTGCAGAAATGCCCGCTCTCGAACTCGCTCAGCAGCGGGTAAATCGTCCGCACACCGATTTCACACGCCCTCTT  
CCAGCAGAAATGGGTACACATCTTCGCACTCAAAATGCTCTTCGCGTCTCTCGAACAAATCCAAAATCTTCAAACGCGGGCGGTAACTTCAGACCGCTGTCTTTCAGTTGCGCAAT  
GTGCTGAATTTTCCATATAATTAATATCCCTGTAATAATAGACGCTATATACGCAATTTACGCTGCTTGCCCACTATCACACCATAGCAGTTGCAATAGCAAAACCGCAACGG  
CGACCGGCACTCGGACACAGACAGGGTAAATACCGCTTAAGCGTA

## SEQ ID 7276

VIDDAVAVFLGDFVLQGFDFGIVEFRYLAALHADDHVVVALVQLINRLARFKMVALQVARLLELRQHAVNRHRTDFHALFQNAVHIFRTQHLFVLLLEQIQNLQTRAGNLQTAVFQLRN  
VAEPFHNITQPKIIDAIRNFSLAHYHTIAVRNKTATADGQSDTDRVKYRLSV

## SEQ ID 7277

ATGATCCAAGATACCGCCCCCTTATCCGCGTTCGCGGCATCTGCTCGATTTCAGACGGCAATTTACCTGCTCGGCTCGCGCCCGAAGGCAAGCCCTATGCGGATATTGGGAATTTG  
CCGGCGGCAAGGTCAGAGCGGGGCAACCGACTTCCAAGCCCTGCAACCGGAGTTTGGAGAAGAACTCGGCATCCGCATCTCGCGCCGACGCTTGGCTGACCAAAATCCATTCTCTACGA  
ACACCGCCGCGTCTGCTGAAATTTCTTATGGGTAAACCCGATCAATGGGAGGCGGACCGCAATCGCGCAAGGGCAGGAATGCTCTTGGCAGAAAGCGGGTATTTCAGCTTCCGCC  
ATGCTGCTGCCAACGCTGCGCTTTTGGCTTCCGTGCTGCTCCGCGCGCTTTGTACCGCAGCTGAAACAGGTTTGTACGCGAAGAACAGTATGGGCGGCTACCGCGTCTTCCCTTTGG  
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GGAAAGGGCGCGGATGTGCTGTGTCGCGCTGCGATGATGTTTACGACACAGAGGCGGCAAGAGCTTCCGCGGAGGCGTATCCGTCCCGCTCTGACTTCAGCAAAAGGACAGAGC  
GTTGCACTTATGAAAACATATGGCTCGGATTTGGGGCGCACGCGTGTGAAGGATGAAACAATAGGAAGAATCATGAA

## SEQ ID 7278

MIQDTRPLIRVAGILLSDGNYLLGSRPEKPYAGYWEFAGGKVEAGETDFQALQREFGEELGIRILAAATPWLTKIHSYEHARVCLKFLNVNPDQWEGGPQSRREGQENSWKAGDPTVAP  
MLPANGALLRSLVPRRLYGLTKTGLYGENSMGAYRVLPAGSAGSGANVLEAAQWDRSEHAGSVMMVQTRBQWQAQEKAGADVVRVRCDDVQAQEAARALRGVSVPLVLAANGQT  
VARYGKLHLGLGAHVAVRDETIGKHE

## SEQ ID 7279

ATGAACACAGAACCGCGATCTGACCCGATCAGCCACAAACCAAAATCGTCCGACCCCTTGGGCGGGCAGCAACAACGTCGAACCTGTTGAAGACATGATCCGCGTCCGCGCCCTGA  
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ACGAGGATATCCGAAGCGCTCAGCACCAACTTACGGAATGCGCGCGCGCGCTTACGCGCAAGACCATCTGCTCCGCTCAGCAAGCGGTTTCGACCGCGCTTTCGACCGCGCTTTCG  
AAATCAGCGCGCAATATTACCTGCGGATTTTCGCGCTGACCGCGAGCGTTTTCGCGCAACGCGGATGCGGATGATACCGGGCGTGGCGCGCTGATTTTGGCAACAGCAGCGGACCA  
CGACACGCGCTTGAACGAAGTCGAACGATGCTGGTGAACACAACATCTGCAATTCGCGCGACGAGTACATCATCACGCGGCTCGCAATGCGGAATCCGTTTCGACCAATACGCTG  
GAACTGCTGCGCGTCAAA

## SEQ ID 7280

MMQTSRDLTRISHNTKIATLPGSGNNVELLEDIRVGLNVVRNFSHGTPPEFHQENARIVREAAKRAGQELAIADLQPKIRVVGKIAGGGIEINKGETLVLDAALEGGETREAVGLDY  
RDLDPDIVAAGDVLWLDGLPLTVESVEGSRITRVENSHILKSNKINKRGGLSAGALTEKDFRDLKTAIAIGDYLAISFVKSAEDLHARAKVESEMKGSRTAVRPLVSKIRVERAI  
ENLDEIILAGDGINVARGDLAVEVGHAAVPALQKRMIRRELRFRSITATQMMESMTNVPVTRAEVSDVANVLDTDAVMCSAETAIVAGYPPFETVSQMAIICAAAEKEQDSINQVABQ  
TEYPEAVSTNLAIAGGAVSVARAVHAKAIVALTESGSTAFEISRHNITLPIFALTSPVSAQRNRMAYRGRPLILATSTDHDTALNEVETMLVEHNILHSGDQYIITSGSQMRSGSTNTL  
EVLVRK

## SEQ ID 7281

GTGAACAAAACCTCATCTCGCCCTTCCGCGCTTTCAGCCTGACCGCGTGCAGCGTGAACGCGTCTCGCTGTTTCCCTCTACAACTCAAATCATCAAGGCAACGAACCTGAAC  
CGCGCGCGCTTGCAGCGCTGCGCGCGGATGACCAAGACCAAGTCTGCTCTGCTCGCGAGCGCCCACTACTGCGCGACGCTTCCATACCGCACCGCTGGGACTATACCTTCAACACCTC  
CCGCAACGGCATCATCAAGAAGCGCAGCAACCTGACCGCTATTTTGAACCGCGTACTCGTCCGACCGAAGGCGACGCGCTCCAAATGCGCGCAAGCGCTCCGCGCGCAACAAAC  
GCAGACAAACAA

## SEQ ID 7282

VNKTLLALSALFSLTACSVERSLFPYSYKLKIIQNELEPRAAALRPGHTKDQVILLLGSPLRDAFHTDRWDYTFNTSRNGI IKERSNLTVYFENGVLVRTEGDALQNAARALRAKQK  
ADEQ

## SEQ ID 7283

ATGATTTACGGCATCGGTACAGACATCGTTCCCTCAAGCGCATCATCCGCTTAAACAAAAATTCGGACAGCGGTTTTCAGGGCGCATACTCACTCCGAGAGCTGCTTGAATTTCCGC  
AGCGCGGCAAAACCGTCACTACCTTGCACAAACGCTTTCGCGCAAGAGCGCTTCGCCAAAGCGCTCGCACGCGCATACGAGGCGCGGTTTCTTCTGCAACATCGGCATCGGCGACGA  
CGCATTTGGCAAGCCGAATTTTCTACGCGCGCGCTGTCGCAATGCTGGAAGAACAGGCATCAGCCGCTCAGCTGAGTATGGCGGACGAGGCGATACCGTGTGGCGTTTGGC  
GTTGCCGAAAAA

## SEQ ID 7284

MIYIGTDFIVSLKRIIRLKKPKQAFAGRIITPEELLEFPQAGKPVNYLAKRFAAKEAFKAVGTGIRGAVSFCNIGIGHDALGKPEFFYGPALSEMLEEQISRVSLSHADEGDTVLAPA  
VAEK

## SEQ ID 7285

GTGTGTTCTTATTTGTTGCTCGGTTTGTGTTTTCGCGCGGAGGCTTCGCGCGCATTTTGGAGGCGCTCGCTTCGCTGCGGACGAGTACGCGCTTTTCAAATAGACGGTCAGTTGCTG  
CGTCTTTGTATGATGCGCTTGCAGGAGGTGTTGAAGGTATAGTCCAGCGTTCGGTATGGAAGCGTTCGCGCATGATGGGCTGCGAGCAGGAGGAGGACTTGGCTTTGCTATCGCG  
GGCGCAGGCGGCAACGCGCGCGCTTCGAGTTGCTTGGATGATTTTGAAGTTTGTAGGAGGAAACAGCGAGACGCGTTCAGCTGTCACGCGTCAAGGCGGAGGCGGAAAG  
GGCGAGGATGAGGTTTGTTCAGCGGAGAACCTTCTGTGCAAAATCGGATGCTAGT



**SEQ ID 7286**

EQ ID 7286  
VCSLLFVCVLPRAEFGGSGILEGVAFGADEYAVFKIDGQVAAPFDDAVAGGVEGIVPAVGMSVAQYGAEEQBDLVFGHAGAQQGNGARFEFVALDDFEFVGKKQDAPDAARGQAEQGGK  
GEDEGFMHGRTFLCKSGCLV

**SEQ ID 7287**

SEQ ID 7287  
GAATTTTTTTCGCTTGCAGAAAAACCATTTTGTATCCTTCAAATAGTGTTCGGTTCGTTCTAAACCGTTGATTATAGCAAATTGTCCCTGTTTCTGTGTTTTACGTTGCAGCGTCGACAC  
GGCAA

SEQ ID 7288

EFFCLAENPFCILQIVFGSP\*TVDYSKLSLFLCFHVAACRRQ

SEQ ID 7289

SEQ ID 7289

GTGCCAAGTCTACAAAGGAGAAGTAGAGGAGAAAAATCAAGCTGCATCAAGCAACTCAAGCGCGGTAAATTATCGCGCGTTCTTATCTGCTGTCAATTATTTTTGAAAAATTACCGGACCGATTCAAAATTTTGCAAAAAACCTGCGCGATGGCTATCGGTAACAAATTCCTCAAAAAACCGTCAATCCGATTATTCAAAAAATCATATGCTTTCATCGTGTTTCCTTTTCGGTTGAACCTCGCCCTTTAGGGCGGTAGAATCAGACTTTATAGTGGAT

SEQ ID 7290

SEQ ID 7280

VPSLQRRSRGKSSCIKQLANGGYPPFLICCCQLFFENLPDRFKFCKKLARNLSGNKFPQKPVNPIIQIKIICPHRVSVETLPFRAVESDFIVD

SEQ ID 7291

SEQ ID 7291

ATGGCAGAAATCTGTTTGATAACCGGCACGCCGGTTCAGGGAAACATTAAAAATGGTTTCATGATGGCAAACGATGAAATGTTTAAGCCAGATGAAACCGCGTACGCCGTAAAGTAT  
TTACGCAACATCAAGGTTTGAAGATACCGCACACCCATAGAAACAGACGCAAGAAGCTGCCGAAATCAACCGATGAACAGCTTTCCGCCATGATATGTATGAATGGATCAAGAAGCC  
TGAAAGACCTCGCGCAATTCGTTATGTGCGATGAGGCGCAAGCGTATGGCCCGCAGCTCCGCAAGTTTCAAAAATCCCGGAAACGTCCTAATGGCTGAACACACACAGGCATCAGGGCATA  
GATATATTGTATTGACACAAGGTCCTAAACTCTTAGATCAGAACTTCGGAACATTGGTTAAAAGCATTACCCACATTTCGGCCCAACAAAATGGGTTTCGGTACCTCTGTTGAATGGAAG  
TATGCGCGGATGACCCGGTAAAAATGGCATCAAGTGCAATTTCCAGTATCTACCACTCGGATAAAAAAGTTTATGACTTGTACGAATCCGCAAGAAATTCACACGCTTAACAAAGTCAAGCG  
TTCAAAATGGTTTATGCAATTGCCCGTCATCATATTATGATTCGCCGTATTGTGCGGTTGTGCTTACAAAATGTTGGGCAGTTTCGGGAAAAAACAGGAAGAACCCGAGCACAAGAATCG  
GCGGCAACAGAACAGCAGGCAGTACTTCCGGAATAAACAGGAAGAAATCGGTGAATACCGGAACATTCGCGCAGATATGTTTGTTCGACATTGCCCCGAAATCCCGAAAGCAAGCCGA  
TTTATAACGGTTGAAGCGTAAAGCACTTGAATATATAGGACCTGTATAGGAAGGCGGAAGAACCCGATGCACCTGCTATTTCGCATCAAGGGACGGCATTGAAGAAGTGACGGAGTT  
GATGTGCAAGGACTATGTAAAAACCGCTTCGCCGTTTAACCCATACAAAGAAGAAAGCAAGGCGAGGAAGTTTCAGCAAGGCGCGCAGCAACATTTCGACAGGGCGCAAGTTGCCACCTTG  
GGCGGAAACCGCAGCAGAACCTAATGTACGACAATTGGGAAGAAGCGCGGAACCGTTTGAAGGAATCGGCGGGGGCGTGTGCGGATCGGCAAAAC

**SEQ ID 7292**

SEQ ID 7292  
MAETCLITGTPGSGKTLKVMSSMANDENFKPDENGVRKVPNTNIGLKIPTHHTIETDAKKLPKSTDEQLSAHMDYEWIKKPENVGAIIVTDEAQUVWPARSAGSKIPENVQNLNTHRHQGI  
DIFVLVTQGPGLLDQNLRLTFLKRRHYHLAANKGLRGLTLELWKCADDPVKNASSAFSSIIYTLDDKKVYDLYESAEHTITNVKVRKSWFPLPVIILLIPLFVGLSYKMLGSGYKKQEPPAQES  
AATEQQAVLDPKLTQEGESVWNGNLNADMFVPTLPKPEPKSPIYNGVRQVTFEYLACGIEGGRTGCTCYSHQGTALKEVTELMCKDYVKNGLPFPNPKYESQGGQEVQQAQHSRAQVATL  
GGKPPQNLMYDNWEERGKPPFEGIGGGVGSAN

SEQ ID 7293

SEQ ID 7293  
ATGCCGCCCTTACTTCATCACCCCTCTTAACGATGGAAAATACAAAAGCGCGCGGAAACGCCCACTACAAATCCAACGGGCTTCATACCGGTCCGCTTTTCGCGCTTCCAAGCGTTTTTTTG  
CCGTTTCGGGCAACCGTCGCTTTGCCTGTGTCGGCAAGCGCGGGCGGCTGTGTACACAGCCAGTTTTCGCGCGTATTTACGGCAGGTGTAAATAAATTCATGATATTTTCCTTCAA  
AAAGTGTTTTGGCGGTAATCGATGGAGAGTTTTTCAGACGACCGCGGAACATCCGAAAATCAGTCTTTCAAAAATCCGAATACGACAAATTCGCAATGGTTGCCGATTTCTCTCCAAACCTGC  
GTTAACCGCTTCTTCGAAGTCGTAGAAATAATCGGCATTGGTAAT

**SEQ ID 7294**

SEQ ID 7294  
MPPYFTLLTMENTKSAKTPITTIQPASIPSFAAASKAFFAVSGNAAFACAASGAAVTTASFAPYLRQVLNFMIFSFKKCLAVMDGEFFRRPPNIRKSVFQKSEYDKFALVADFFQTC  
VNRPFVVEIIGIGN

**SEQ ID 7295**

SEQ ID 7295

TTGTTGATAATATCGAATGTTAGAAAAAGGAGAAAAACATGTCTGAAGAAAAAATTGAAATGAGTTTCGAGCCAAACCGTAATCGAACATTTGGGTGTAAGAGTGTATTGCGACACTGTTCTCG  
CGATTGCCGAGTTGATPAGCGAATGCCTACGATGCAATGCTGCTACGGAAAGTGGAAAGTTAGGTTTATTCGATAAACCGGAGCATAAAATCGTTATTAAAGATTAATGGCATAGGAATGAGCTTCGA  
TGAATTAATGATTATTTATTGTAATCGGTGCGAACAGAAGGGAAGAAAAACAAGCTCCCGTGGCGAAGAAATTCACACGGGTAAAAAAGGCTCTGGTAAATGGCATTATTACAGGCTT  
GGCAACAAAATCGAAATCTCTACTATCCAGGAAACGAACGGGTACTTTTACTTTGGATTATGCGAGAGATTAATAAAAAAGTGAAGCTTATTATCAACCGGAGTTTCAGAAAGAGTCTGTGTA  
AACCCCAATACCGAAAACCGGAACCACTATACTTTAACCGGAGCTGACGAAAAAACAGGATACCCCGTTAGTAAATATGTCGGGGCACTTTCCCGTTATTGTTGATTTCTCCGCTCAGGATTT  
TAAAAATCAAAGTAAGCTTGAACGGCTCGGAACCAAGAATCATPTGACGAAACCTAAAAATTAATCTTATTAATCCCAACCAATTCGAATGGGAATACCGAGGATCAGCAACCAATATTTTCATCG  
TTATCTTCAAATTCGAACAGTATGAAATCAGCGGATTAATCAACAGGTAAGTTCATTACAACGGAAAAACCTTTAAAGATAATATGAAAGGTATTACCTTGTTTCCCAACCGGAGAAATGG  
TAAATATGCCCGAGTTTTCCTACTGATAGCGAATCCAGCCATTTTC

**SEQ ID 7296**

SEQ ID 7296  
 LLITSNVRKGEWSEELKMSFEPTVIEHLGVKMYSHVPAIAELIANAYDACATEVEVRLFDKPEHKIVIKDNGIGMSFDEINDPYLRIGRNRREEKQASPCGRIPITGKKGLKGLALFEL  
 GNKIEISTIQGNERNVPTPLDYABIKKSERIYQPEFQKESVKPNTENGTTITLTELTKKQGYPLDNYVGHLSRLFDFFPAQDFKIKVSLNGSEPRIIDGNLKYNLVTPQFEWEYQDLATNLS  
 LSSKFEQYEGSLIQGKFITTEKPLKNMKGITLFGANGRMVNMEFFTDSSESHF

**SEQ ID 7297**

SEQ ID 7297  
GTGCAAMTCGCGCAACATCGGATAAAATCGAGTGCCTATACTAAAGCGAAACAGGCATTTCGACTGCCCTTTTATTGTGCCACCGTCCGCCCTTTTACGGAAACCGAAATGACCCCTT  
TCACACTGAAAAAACCGCTCTGTCTCGGCACTGCCCTTTCGCCGCCCATCTGTCCACGCATCCGGCTACCACTTCGGCACACAGTCGGTCAACGCGCAAGCACGGCAAAATGCCGCCGAC  
GCGTCGACCATCTTCTACAAATCCCGCCGGCC

**SEQ ID 7298**

SEQ ID 7298  
 VOYTHRIKSSANTKAKOGISDCLPYLSTVRLFTSTETPTFLKPKSCCSALPLPHLSTHPATTSANRSRSTRKARQMPPTRRPSSTIPPA

SEQ ID 7299

SEQ ID 7299  
ATCCGCTCTGAACCGTFTGCCCTGCCCTTACGGCAGCAGCCTTGCCCTGAACATCGCCCTCCTTCATCTGGCGCACGGCTTCGGGAAGTCCGAGGAAGAGGGCTTGGGCAATCAGCGAATGC  
CCGATGTTTCAGTTTCGCGGATGCGCAGGATTTGGGCGACGGGGTAACGTTGTGTATGGTCAGTCCTGTCGCGCGTTGACGACCAAGCCAAATCGCCGGCGAAATGCGCGCCGTTTGGGA  
TGCCTCGAACTGCCTGATTGTTGTCGGCGTGGCTTGTGCGTCGGCATATCGCGCGGTGTGCGAGCTGCAGCAACGGGCGCGCGGACATCAGCGGCGGCTTGGATTGCTCTGCTCGGCATC  
GATAAACAAGGACAGCGCTATTGCCCGCGCTCGGTGTCAGGATTTTGGCGGAATTCGCGCGATTTCGCGGATTTTTCCTGTGGGCCAAATAGCTCCAAACCGCCTTCGGTCTGATTTCTCTGCGCTTTTTCAGGC  
ACGATGCACAGCTCTTCGCGATCACTTTAAGCGCGTTTTCGAGCATTTCTTCGTCAACGCCATTTCAGGTTACGCGCGCTGCGGATGGCGTTTTCGACGGCAAATACATCGCGCTCTT  
TGATGTGGCGCGGCTCTCGCGCAGGTGCATGTTAATCAGGTCTGCACCGCTGCGTTTCGGCAACAGTGCCTCTCACGGGGCTGGGATAGTCTGTCGCGCGCGCTTGCAGCAGGTGGC  
GATGTGGTCGATTTGACACCCAGAAGCATATGTTTCTTTCTCTCGTTTTCCTGTT



## SEQ ID 7300

MPSETVCLPLRQPCPEHRLHLAHGFGKSEEEGLGNQRPMDVQFADGEDLDGDNVYVQSVSGVDDQAOIAGEMRAVLDALELPDLFGVALCVGICAGVQLDNGRADITGGDLFPVVG  
DKQGHAYARVGQDFGEFGDFLLRQYVQTAFRGRDLPFFPRHDAHVFRHFKRVFRHFFRQRHFKVQARADGVFDGKYIRVFDVAAVFAQVHGNQVCTVRFGNQCRLHGAGISRAARVADGG  
DVEDVDITQRHNVSPSLRFPV

## SEQ ID 7301

ATGATACCGCTCAAAATCGCCATCGCCGCGCAACCGCGCATGGGACCGCTCTCGTGAAGCCGCTCAACACCATCCCGACACCGCTCTTCGCGCGCGCTCGAACACTCAGGCTCAG  
AAGCCCTCGGCGCTGGACGCGGCTACCGCGTGGGACTCAAAACCGGCATCGCCATTTTCAGACGAGCTTGACCGCTTCTCGCCCAAGCGCAGCTACTCATGACTTACCCCGCCCGAGCC  
GACCTCAAGCACTTCAAAAATGCGTTGAAAAACAAGTCAACATCATTCGACCAACAGCGCTTCGACGATGCGGCAAGCGCCATCGCGCGCGCGCGCAAAAACAGGCAATCGTT  
TTCGCGCGCAACTTCAGCGTGGCGTCAACCTCACCTTCCACATCTCGACACCGCTCGCGCGCGCTTCAACGAAGGCTACGACATCGAAATCATCGAAGGCCACACCGCCACAAAGTGG  
ATGCCCCAGCGCGCACAGCATTAAGAATGGGCGAAGTCACTCGCGCGCGCTCGCGCGCGCACTCAAAACATGCGCGCTTACGCGCGCGAAGGCCACACTGGTTCGCGCGATCTTCCAC  
CATCGGCTTTCGCCCGCTCGCGCGAGGCGACATAGTTCGCGACACACCGCCCTTTCGCGCACCGGCAAGCGCTGGAATACCCACAAAGCGCGCGCATGACCTTTCGCGCG  
GGTCCGCTCGCGCGCGCTTGGGTAAACGCGCAAAACGGGTTCGACGATATGAGGACGCTACTCGCGCTGAACACCGT

## SEQ ID 7302

MIPLKIAIAGANGRMGRVLVEAVNNHPTVLSGALEHSGSEALGLDAGYAVGLRTGIAISDDVDVLAQSDVLDFTPTPEPTLKHLLQKCEKQVNIITGTGFDAGKAAIRAAAEKTVI  
FAANFSVGVNLT/PHILDTVARVLENGYDIEIEIGHHRKVDAPSGTALRMGEVIALGALGRDLQCAVYREGHTGPRDPSTIGFATVRAGDIVERDIALFATDGERVEITHKAGSRMTFAA  
GAVRAAVVWNGKTLGYMDQDVLGLMNR

## SEQ ID 7303

GTGCTGCCAGCATTCATTATGAAGCAGATTCCGCCACCGACTTTACCGGCTTCCCGTCCAAGGTTCTAAAAACGGCAAAATCACCAAAACCGGTCGCACCCACATTTACCGCGCAT  
ACAAAGTCAACGACATTCGACCTGGGCTTGGGCGGTACGTCCTTCGCGCTCGCCACCGGAATAGAAAAAGATTCCGTTGCGGCCACAACATCAACAACTCGGTCGACAGCAT  
CGCGCTCGAACCTGTGCGCGCGTGGAAACTCAACGAACGCCATTCCTTCGCGCGAGGCATCATGCCCAACATAATTCGCGCACTGCGCAATATGCGCGAC

## SEQ ID 7304

VLPSTHYEADSATDFTGLPVQGSKNGKITRTTVAPHIYGAYKVNNDLTVGLGVYVPGSATFEYEKDSVLRHNINKLGLTSLAVEFVAWKLNERHSFGAGIIAQHNSAELRYAD

## SEQ ID 7305

ATGCTTCTGGGTGTCAACATCGACCATCGCCACCGTCCGCAACCGCGCGGCGACGACTTATCCACGCCCCGTGGAGCGGCGACTGGTTGCCAAACCGCACGGTGCAGACCTGATTACCA  
TGCACCTCGCGGAGAGCCGCCACATCAAGACCGCGATGTATTTGCCGTCAAAACCGCATCCGCAACCGGCTGAACCTTGAATGGCTGTGACGGAAGAAATGCTCGAAAACCGCGCT  
TAAAGTGATGCGCGGAGAGCTGTGCATCGTCCGTGAAAAACGGCAGGAATACGACCGCAAGCGGCTTGGAGCTATTGGCGCAACAGGAAAAATCGCGAATTCGCCAAAATCTCTGACC  
GACCGCGGCATACCGCTGTCTTGTTCGATGCGCGGACGACAGGCAATCCAAAGCGCGCGGTGATGTCGCGCGCGCGCTTGTGCGAGCTGCACACCGCGCATATGCGCGACGCAAAAGCC  
ACGCGCAACAAATCAGGCGTTCGAGCGCATCCAAACCGCGCGCATTTTCGCGCGGATTTGGGCTTGGTGTCTCAACCGCGGACAGGACTGACCATACAAAGTTACCCCGCTCGCCCA  
AATCTCGCCATCCGCGAATGAACATCGGCGATTCGTGATGCGCAAGCCCTCTTCTCGGACTTCCCGAAGCGGTGCGCGAGATGAAGGAGCGGATGTTTCAGGGCAAGGCTGCTCGCG

## SEQ ID 7306

MLLGVNIDHIALTVRNAGRTTYPSPVEAALVAETHGADLITMHLREDRRHKIDADVFAVKNAIRTRINLEMAITREMLENALKVMPEDVCIPEKQEIITTEGGLOVLAQQEKIAEFKILP  
DAGIRVSLFDADRQIQAAADYGAAPVVELHTGAYADAQSHABQIRQFERIQNGAHFAGDLGLVWAGHGLTIHNVTPVAQLLAIRELNIHSLIAQALFLGLPEAVRQMKFAHFRLLP

## SEQ ID 7307

TTTGTCACCGCTCGCGCTTTTACGGAACCGAAATGACCCCTTTACACTGAAAAACCGCTCTGCTGCTCGGCACTGCTTTGCCGCGCGCATCTGTCCACGATCCGCGTACCCTTCG  
GCACACAGTGGTCAACCGCGCAAGCAACCGCAATGCGCGGACCGGTGACCATCTTCAATCCCGCGCGCTGACCAAACTCGACAGCAGCGAGATTTCGCTCAACGCCAATCATCGT  
GCTGCCAGCATTCATTATGAAGCAGATTCCGCCACCGCATTTACCGGCGCTTCCGTTCAAGGTTCTAAAAACGGCAAAATCACCAAAACCGGTCGACCCCAATTTACGGCGCATAC  
AAAGTCAACGACATCTGACCGTGGGCTTGGGCGGTACGTCCTTCGCGCTTTCGCGCAAGATACGAAAAAGATTTCGTTGCGGCCACAACATCAACAACTCGGTCGACACGATCG  
CGCTCGAACCTGTGCGCGGTGGAACTCAACGAACGCCATTCCTTCGCGCGAGGCATCATCGCCCAACATAATTCGCGCGAATGCGCGCAATATGCGGACTGAGGAATCCCAAAAAAGC  
GCAAAATGCTGCAAGCAACACTTCTAATCTACTGCGCGCTGCTCAA

## SEQ ID 7308

FVHRPPFYGNRNDPFTTEKTVLLGTAFAAASVHAGSYHFGTQSVNAQSTANAADASTIYFNPAGLTKLDSQISVNAVIVLPSIHYEADSATDFTGLPVQGSKNGKITRTTVAPHIYGAY  
KVNNDLTVGLGVYVPGSATFEYEKDSVLRHNINKLGLTSLAVEFVAWKLNERHSFGAGIIAQHNSAELRYAD\*GIPKKAQLQATPSNPTAAAQ

## SEQ ID 7309

TTGTCATGCTGCACAAGCAACTTTATTGATATCGCGATACGAAGCGTGTGCGCAAAATGCCGTGGAACAATATCTTTTCAGACGGCATTTTGTATGGGGGT

## SEQ ID 7310

LSCCTSNFIDHPIRSLSAKRLANIFSDGILYGG

## SEQ ID 7311

ATGCTGCAAGCAACACCTTCTAATCTACTGCCGCTGCTCAAAATCAAGGCCGACGGACCGCGATGTCAAAGGCAGCGATTGGGGCGTGGCTACCAACTGGCGTGGATGTGGGACATCA  
ACGACCGCGCGCGCGTGGGCGTGAATACCGTTCCAAAGTTTCACACACGCTCAAGCGGATGCGCGAATGGCGCGCAGACGCGCGCGCGCAACACAGCTGGAATGACATATGCTCAC  
ACCGCTCGGTTACGCGCGAATGAAAAAGCAGTGTCAAAATCGTAACGCGTGAAGTCTTTGTGCGTACACGCGATGTACAAAGTGTTCGACAAAGCGGACTGTTGCGCGACGTAATTTGG  
ACGCGCACAGCGCGCTTCAATAAGCGGGAATGTTTTTGAAGAAAGAAAAATATGCTAATGGCAAAAAATCCGACCGCACCACTACACCCCAACTGGCGCAACACCTACAAAGTGG  
GCTTGGGCGGTTCTTATCAAAATCAGCGAACCGCTGCAACTGCGCGTGGCATGCTTTTGACAAACCGCTGTGCGCAACCGGACTACCGCATGAACAGCTGCGCGACGCGAACCGCAT  
CTGCTTCTCGCGCGCATGAAATACCATATCGGCAAAACACGCTGCTGATGCGCGCTACACCCACATCCATCAACGACACCGAGTACCGCACGCGGAAGCGAAGCGCAACGATGTG  
GACAGCAAGGTGCGTCTTTCGCGACGTTCAAAACACCGCGCATCATCGCGCTGCAATACCTTACAAATTCAAA

## SEQ ID 7312

MLQATPSNPTAAAIKADGHADVKGSDWGVGYQLAWMDINDRVRVGVNYSKVSHTLKGDAEWAADGAAAKQVNDNMLTPLGYTANAKASVKIVTPESLSVHGMKVSADKADLPDGVTH  
TRHSRPNKAELEFFEKEKLIANGKSDRTTITPNWRMTYKVLGGSYQISEPLQLRVGIAPDKPPVRNADYRMSLDPGNRIWFSAGMKYHIGKMHVVDAATTHIHINDTSYRTAKASGNDV  
DSKGASCARFKNHADIIGLQYTYKFK

## SEQ ID 7313

TTGTTTCATTGTTCTTCGTAATTTCTATTTTAGGCAATTGTGCCCTACACCAATTACACAGACTGGGTAAAAATTAATTCAGCAGTTACGCTATCTGAAATTTATCTATGGATACG  
CTACGGAGAACCAAGATAAGATATCGATAATACCTTGGAGCTTGGAGAAATTAAGCAGGATGATGAAATCTTGGATTATGAGAGTGCACCTGGCAATTAATAGGCGTAGGTATATCTCC  
GACCACTTTATCATAGATATAGTTTCCCGGGAATAGAGTGTGAATTTTATGATCAGGAGCTTTCAT

## SEQ ID 7314

LFHLFPVNFYRQLCTPNYNTDVKIKPKQPSYLYKIYGYATERNQDKIDITWLELGLQDDDEILDYGGALALIGRRYNLPTSFIIIDIVCREIELEFLDQESFN

## SEQ ID 7315

TTGCGCAGCTTCAAAACACCGCGACATCATCGCGCTGCAATACACCTACAAATTCAAATAAACGTTACACCGCTTGAATATAAAATGCCGTC

## SEQ ID 7316

LRTFQKPRRHRAIHLQIQINVTPEYKNAV

## SEQ ID 7317

ATGGATTATTTTCCCGAAGCAGCAGCTATTACAAAAAGGGGGAGAAATTGTGATTATGGCACATCAAAACAATAAGTATTTAAGAGGAATTCCAAATGAACAGAACTGGCCCGAATGG  
GATTAAGGTTAAATATAATGGTTCGTTAACTGAT

## SEQ ID 7318

MDYFPEAARITKKGGKIVNGTSNNKYLRGIPNETELARMGLRLKYNGSLFD

## SEQ ID 7319

ATGTCCGAATACCGAGTCAACACCGAACCCTTTTATGCTGGCATCTTCGCCCTTGGCGCGAAGCAGCCTGCGGGTTGAAGCAFTTACGCCGCCGTACGGGCGTGTGGCTTTGCTGGCGC  
GCAGCGCGCGCAACCGCAGAGCGAGCTGCGCGCGTATTGGTTCCGTTCCCTGCCAGCGTGTCTGGTACGGCAGTCAGGAACCTCAAACCCCTGCACCGCGCCGGAATGGATGGCGG  
ATGGCGGCAGCCGCGCGGCGGCGTGTTCAGCGGCTGTATGTGAACGAGCTGGTGTGAACTGACCGCGCGCGAAGACCCGATGCTCCGAACCTGACGACCGGTTGGCAAAAGTGATG  
GAGGCACTGTGCCGTGAAGCAACCATATTGCCGATTTCGCCCGCTTCGAATGAAGCTGCTCAATGCCCTTGGCGGTGCCCCCGATTGTCACGCGCAGCGGCAAGCGCGCGATATTTTG  
CGGCAAAACCTTACCGCTGATGCCGAAGAGCGGCTCATGCCCCGATGCGGGGACACAGCGCGCTTTGCGACGAAGCGCGCAATTGTGGAAGGCGAGCGCTGATGATTTGCGCGA  
AGGCACTTCCGCGACCGCGGAAAGCTGCAACAGGCATTGAAATCACAGCGCTGCTAATGCGCACGCTGCTTCCGAAGGCTTGAATCGCGCGAGGTGTGGAACAGATAAGGCACTTC  
GACCGCAATACCGCG

## SEQ ID 7320

MSEYRVNHEPVMFLASSFWRESSLRVEAFRRYGRVALLARSARKRQSELRGVLVFPVPASVSWYGSQELKTLHRAEWMGGWRQPGRALFSGLYVNLVLKLTAREDPMSLYDALAKVM  
EAVCREANHIALRRFEWKLNALGVAPDLHADGTGGDILADKTYRLMPEAVMPVCRDTGALSHEAGATVEGQSLIDLREGSFRTAESLQALIKITRLLIGTLLPEGLKSRQVLEQIRQF  
DRNTA

## SEQ ID 7321

TCTCGGTATTCCGGGAGAAATATATACAGAACCTCCTTCATATCAAAATGGTAGGAGCGCTCGGCGAACAGGACGGCGGCGAGGACGCTTGGTGATGCCGTTCAAACCGCGCGGGAACAGCGCA  
ATCCGCTCTTTGCCCTTTTCCGATAATCTGCTTTGCGGTTGTGGATGGAATCTACTTCGCGATGGCGGTAAGCAGCGGTTCATTTCGATATAGGCTTCGTTGTGGATGGCTGCCGACT  
GTTTCGCAACACGTCATCTGCTGTGAGCTTGTCTGCTGGCTTTCATCAGCCTGTTGAAGAAGCAGCGTTGCTCCTGCACTTTGGCGGTACAGCCTTCGATACTTTCCGATACCGGCC  
GAACCTGTCGAGGATTTTTCAGACAGCTTTTCCAAGTCGCTCAGGACCGCGCATCTTTCGCGGAAATCTTCTTCAGGCTTCCCTGCCGAATGGACAA

## SEQ ID 7322

SRYSGEYIQNLHLIKMVGTLGGQDGGRLGDVQTAREQRNPLFALFRIICFVVDGNYFAMAVQRVHFHDIGFVVDGCRFLQHVNLVPELVVGFHQPVERRLLQFGGTGDFTFYRYP  
ELFEVFFQTVFQVQQAAGHLAKGFFFRSLPNGQ

## SEQ ID 7323

TTGTATATCCACTATATGTGGGAGCAGACGAATATGTTGATAAAAAAGCCCTTTGATTGCCGTGCTGTCGGCGAAGCGTGGCGGACCTGTTGGGCGCGCACCTGATACGCGCCATCC  
GAAAGCGTTGCCCGCAGGACCGTTAACCGGCATCGCGCGGAACTGATGAAGCGGGAAGTTTCGAGAGCCTTTATGATCAGGAGCGGCTGGCGGTGCGCGGCTTTGTCGAAGTGTGTAG  
GCGGCTGCCGGAATTTTACGATACGAGGAGCTGTGACGGGATTTGCTGCTGTTGAAACCTGATGCTTTGTGCGTATCGATGCGCCGATTTAATCTGGGTGTGGCGGAAAGCTG  
AAACGGCGCGGCAATCCGACCTGCAATATGTGAGTCCGCTGTTGGCGTGGCGCGCGAAGCGGTGGGCAAAATCGTGATCAGGTCAACCGCGTGTGCTGCTGTTCCGATGGAGC  
CGCAGCTTTATCTGATGCGGCGGACGTGCGGAGTTTGTGCTCATCCGATGGCAGCAGCTTATGCCCTTGGAAAGACGACCGTGAAACCGGCGCGGAAACCTTTGGGCGCGGATGTGCGCAT  
CCCCGATTGCCCTGCTGCCCGCAGCGCGCTCAGCGAAATGCACTATATGGCGCGGTGTTTTCAGACGGCATTATTTGTTGTTGGAACGCTATCCCGCGCGCGCTTCTCTGCTGCT  
GCCGCAACGAGGCGGACGAAGCGCGCTTTGGCGGAAGTTTTCAGCGCGCGGAGTTTCCCGGATTGGCGCTGACCGGTAACCGACAGACAGTCTGAACCGGTGTGACGGCGCGGATGCGG  
TGCTGTGTAACGAGCGGTACGCGGACTTTGGAGGTGCGCTGTGCAAGCGTCCGATGGTCACTACAGTACAGATTTCGCCGCTGACCTATGCTTATGTGAAACGCAAAATCAAAGTGGCGCA  
TGTGCGGCTGCCGAATATCTGTTGGGTAAGGAGCGCGTGGCGGAATTTATGCAATCTGAAGCAAAACCGGAAACCTGGCGCGCATTTGGCGGACTGTGACGAACCCCGATAGGTT  
GCCGCGTGAACAGGATTTCGGGCGTTCACCTGCTGTTGAAAGATACGCGGATTTGGCGCGCGCGCGGTTTGGAAAGCGCGGATGT

## SEQ ID 7324

LLIHYMGTQNMVKKSPLIASVGEASDILLGAHLIRAIRKRCQARLTGIGGELMKABGFESLYDQERLAVRGFVEVVRRLPEILIRRELVRDILLSLKDVPVIGIDAPDNLGVAEKL  
KRAGITPLHYVSPVWAWRRERVGKLVHQVNRVLCLEFMEPQLYLDAGGRAEFVGHFMAQLMPLEDDRETAGTKLADVGIPVFPALLPGSRVSEIDYMAPVFFQTALLLLERYPAARFLP  
AATEATKRRLLAEVLQRPEFAGLALTVDROSETVCRADAVLVTSGTATLEVALCKRPHVISYKISPLTYAYVKRKIKVPHVGLPNILLGKEAVPELLOSEAKPEKLAALADWYEHDPKV  
AALQDDFGALHLLKKDTADLAARAVLEAGC

## SEQ ID 7325

ATGGTAGGAGCGCTCGGCGAACAGGACGGCGGCGAGGAGCTTGGTGATGCCGTTCAAACCGCGCGGGAACAGCGCAATCCGCTCTTTGCCCTTTTCCGATAATCTGCTTTGCGGTTGTGG  
ATGGAACTACTTCCGCGATGGCGGTAAGACAGCGGTTCATTCATTCATATAGGCTTCGTTGTGGTGGCTGCGGACTGTTCGCAACACGTCATCTGCTGCTGTGAGCTTGTGCTGCGCT  
TCATCAGCCTGTTGAAGAACGAGCGTTGCTCTGAGTTTGGCGGTACAGCTTCGATATTCGATACCGGCGCGGAACTGTTGAGGATTTTTCAGACAGTTTTCGAAGTCGCTCAG  
CGAGCGCGCATCTTCGCGGAAATCTCTTCAGGCTTTCCTGCCGAATGGAACATATACGCGATTAAACAAAATCAGGACAAGCGGACGAAGCCGAGACAGTACAGA

## SEQ ID 7326

MVGTGGQDGGRLGDVQTAREQRNPLFALFRIICFVVDGNYFAMAVQRVHFHDIGFVVDGCRFLQHVNLVPELVVGFHQPVERRLLQFGGTGDFTFYRYPPELFEVFFQTVFQVQ  
AAGHLAKGFFFRSLPNGQYSLFKIRTRRRSRQYR

## SEQ ID 7327

GGACGCGACATAGGCGCAGCCTTATGTGCCCTCCTGTGTGTTGAACATCAGCATAGGAAACACAGGAAAGCGCGCTGTTTGGCGCTGCGTACCGATTGGTCAAAATGCCGCTGAA  
ACCGACAACAGGCTTCAGACGCGATTTCGCTCAA

## SEQ ID 7328

GRHIGRRFMCRRPVC\*NISIGNTGKAGCFAPAYRIGQNAV\*NRQGFRRHFRQ

## SEQ ID 7329

TTGATGTTAGAAATGACCGCAAAATTACCGTTTCAGCGAAATATGTCCCAAATATGACGAACTCCTCATCCCGCAACCGCAACCGCATCGACACCATCGATGCCGAAATCTGCGGCTGC  
TCAACGAACGCGCGCAACATGCCACCGCATCGCGGAGCTGAAAGCGCGCGGCTGTACCGCCCGCAACCGGAGGTGCGGCTGTTGCGCGCGCTTACGATTTGAACAAAGGCCGCT  
GCCGACGAATCGGTAGCAGCGCTGTTTCGGGAAGTGATGAGCGAGTCCCTGCGCGTGAACGTCGCTGACCATCGCTATCTGGGCGCGCAGGCGCATTTACCAACAGCGCGCAATC  
AAGCATTTTCGACACGCGCGCATACAATGGCGTGTCCGACCATAGACGACTGCTTCAACAGGTTGAACCCGTCAGGCGGATTATCTGCTGCGCGCGCTGGAACAACTCGACCGAAGGCT  
CGGTGCGGCGCACATTTGGATTGCTTGGCGTTACCGCGTTGACGCGTGGCGGCAAGTCTTTTCGCGATCCACCAACCACTGTTGCGCAAAACAAAGGCGACGAGGATTCGCCAA  
AGTATTTTCGACGCGCGGCGTGGCGGAGTGAACGACTGTTGGCGAGGCGTTCGCCAATGCCGAACGATTTGCCGTGTCAGCAATGCCGAAGCGCAAGGCTGTTGCCGAATCG  
GACGACGCTACGCTTGGCGCATCGCGGACGACGCGCGGAAATTTACGAGCTCGATATGGTTGCGGATGATCGAAGACGAACCGAACAACACCGCGCTTCTGCTCATGGGAC  
ATCAGCAAAACGCTGACGCGGACGCAACAACTGCTGCGCGTTTCGCGCGCAACCGCGCGCGGCTGCTGCTGCTGCAACCGCTGACCGAATCGGGTATTTCCATGACCAA  
GTTTGAAGCGCTGCGGAGCAATCCGTTTTCGGGAATACCTGCTTTCATCGACATCGAAGGACACCGCGGACGCGCAGATTGAGACGCTTGGCGAAGCGCGCTTGG  
TTTGTCAAAGCATCGTTTCGATCCGACTGCCGTTTG

## SEQ ID 7330

LMLECTANYRSGETMSQTTIDELIIPHRNAIDTIDAEILRLNRAQHAHAIGELKGTGAVYRPEREVAVLRIQDLNKGPLPDESVARLFRVMSSECLAVERPLTIAYLGPQGTFTQAAI  
KHFPHAHTMACPTTIDCFKQVETROADYLVAPVENSTEGSVGRTLDLAVTALQACGEVVLRIHNLRLNNGSTEGIAKVP SHAQALAQCNOWLGRRLPNAERLIASVSNBAARLVAES

DDGTVAALAGRATAAEIYGLDMVABCEIDEPNMTPLVMGHETGASGSDKTSLAVSAPNRAGAVASLLQPLTESGISMTKFESRPSKSVLWBYLFFIDIBGHRRDAQIQTALERLGERAS  
FVKALGSTPTAVL

## SEQ ID 7331

TTGTTTATGTTTCGGCACGGCGTTTCGGGCAAGTGGCCGGCGCGGTTGCCGACATCAAAGGGCGCAAAACCGCTGCGCCTGACCGGTTTGATTTGTATATGCTTGCCTTGCCTGCGCCATCG  
TATTTGCTTCGAGTACCAGACAGCTCCTTAACCTGCGTGCCTGACAGCGCTTCGGCGCAGGCATGGCTGTAGTTCATCGTGGTGGCATGGTGGCGGATTATTTATTCGGGACGCAAGGCCG  
GCAGATGTTTGCCTTATCGGCATCATTTGATGGTTGTGCGCTGGCCGACCCATGCTGGCGCATTTGTTCAGGGATTGGCGCGATGGCGGGGATTTTCGTTTTCGGCGCGGTAT  
TCGCGGCTGCTGCCCGGTTTGGTACAGTATTTCTGCGCAATCCGCGCTGCGCGGCAAAATCGCAGGGATGTTTTCGCGCTGGTGGCGGGGCGGTTCAAGCGCGTATTTGAAACCCGCTG  
CCGCGATGGGTATCTGTTTTCAGGCATTGAGCTTCGCTTCGATGTTTCGCTTCTGACCGAATCTTCTTTCGTTGATACCGGAGCTTACCAACGTTACCGCGCACCGGTACGCATGGGT  
GTTTGCACTCAACATCATCAGATGATGTTTTCAGCGCGTTTACCGCTGCGCGCTTAAACCGCGCGCATCGCAAGCATCTCTGCTGCGGGGATTGTCGTTCAATTTGCGGCCAAC  
CCGTCACACTTCGCGCGCTGCTGTTTTCGCGTTCGCCCGTTTGGCTGCCGCTGCGCTGCTGATGTTTTCGCTGCTACGCGGCGCTGGTGGTGGGACACGCGGATGCTTTA  
TGTCTTATTTCAAAGAGAGGGCGGCGAGCGCAAGCGGTGTCGGGTGATTCGCTTAAATCGCGCGGCGCTGGTTCATGGCGGCAACCGTGGTGGCGGCAACCATGACCGCGTCCG  
CTCTTCGCGCATTCGCTTTTGTGGCTCTGCTCGCACAGGCGTGAAGGAAACGAAAAAGCGAATACTTGTAAACCGATGCGCTCGGAAACCGCTTCAGACGGCATTTGATGTTAGA  
ATGCACGGCAAATACCGTTTCAGGCGAAATTTATGTCACAACTATCGACGAACTCTCATCCGCGACCGCAACCGCATCGACACCATGATGCGGAAATTCGCGCTGCTCAACGAAACG  
CGCAACATGCGCCACCGCATCGCGAGCTGAAAGGACGCGCGCGGTGATCCGCGCGCAACCGGAGGTGCGCTGTTGCGCGCGATTGAGGATTTGAACAAGGCGCGCTGCGCGACGAAT  
CGGTAGCACGCTGTTTCGGGAAGTATGAGCGAGTGCCTCGCGCTGCAACGCTCGCTGACCATCGCTATCTGGGCGCGCAGGCGACGTTTACCAACAGCGCGCAATCAAGCATTTTCG  
ACACGCGCGCATACAAATGGCGTTCGCGACCATAGACGATGCTTCAACAGGT

## SEQ ID 7332

LPMFGTAFQVAGGAVSDIKGRKPVALTGLIVYCLAVAAIVFASSTEQLLNLRVAFAGAGMAVVIVGAMVRDYYSGRKAQMFLIGIILMVVPLAAMPVALLQGLGGWRAIFVFLAAY  
SPVLPGLVQYFLPNPVGKIGRDVFLVAGRFRVLKTRAMGYLFPQAFSGSMFAITESSFVYRQLYHVTPHRYAWVPALNITMFMFSRVTAWLKTAHPQSILLRGIVVQFAAN  
PSQLAAVLPFGLPPFLVACVMPFVGTTQGLVADTQACPMFYPKEGGSANAVSGVFRSLIGAGVMAATVMAATMTASASCGIALLHLCSHKANKENEKRLILVNRCPKPLQTAFFDVR  
MHGKLPFRNVPVNYRRTFHPAPQRHHRHRCNSAPAQRTRATCPRHRAERHGRGVPRTGRCRVAPHSGFQRPAARRIGSTPVSGBSERVPRRRTSADHRLSAGAGHVYPTGGQAFR  
TRRAYNGVSDHRRLLQTG

## SEQ ID 7333

ATGAAACCGCACGAAATAAGCAAAGGTTTCGGTACGCTGATAGGGGTTGCCGAACATGAGGCGGGTCAACGCCCTTGATACTATCTGATAAAATCTCAAGGCGTGGCCAAAGGCTATA  
TCCACCGCATTTATCCGCGCGCGGAGGTGCGGTTGAACAAGAAACGCTGCAAAACCGCACGCGCTATGCGGAGGAGATACGGTGGGATTCGCGCTGTCGCGTGGCGGAGAGGAAAF  
GCGGTCTGAAGGGCGTGGCGCGTACCGCGCGTGGCTTTGAGGTGGTGTATGAGGACGACGCGCTACTGGTGGTCAATAAGCCTTCGCGGTGGCGGTACACGGTGGCGAGCGCGTGGT  
TTCGGGCTTATCGAACAGTTCGCGCGCGCGCTGCGGAGGCGAAGTATTTGGAGTTGCTCCACCGTTTGGACAAGGATACGAGCGGCTGTTGATGTTGGCGAAGAAACGACGCGCGCTCG  
TCAAACCTGCACGAAGCTATCCGTAACGACACCCCAAAAATCTACTTTCGCGTGGGGTGGGCAAACTGCGGACGACAAATTTCCATGTCAAACTGCCCCCTGTTCAAATATACCGCGCGC  
ACAAGCGGAAAGAGTGTACGCGTACGCGAGGACGCGGCGTGGCGCATACGGTGTTCCTGTGTTAAGCGGTTTCTCAGACGCGCATTTTGCACGCGTGTGCGGCTGTGCGACCTGACTTTG  
GTGCGGCAACCGCTGAAACCGGCGGTACGACCAAAATCCGCGTGCATCTGCAATCTCAAGGCTGTCCGATTCGCGGCGACGAAACGCTACGCGCATTTACGCGGAAACCGCGGTTTCGAGA  
AATGGGTTTGAAGCGCATGTTTTCACCGCTGCGAGCTGCACCTGAACCATCGCTCAGGCGTGAACCGCTGCTGTTGAGGCGGAGCCCGCGGATTTGGCGCATTTGCGGTGAT  
GTTGGAACCGGCGGCAAAATG

## SEQ ID 7334

MKTHEISKGSVSLIGVAZHEAGQRLDNYLIKILKGVPKYIHRITRAGEVRLNKKRCKPDSRIABGDTVRIPPVRAEKEMPSERRAAVPARAFEVYEDDALLVNVKPSGVAVHGGSGVS  
PGVLEQLRRARPEAKYLELVRHLKDTPSGLLMVAKRSALVVKLHEAIRNDHPKIYALGVGLPDPNHFVKLPLFKYTGAGGEMVRVSEDGQSAHTVFRVLSRPSDGLLHGVLGSLHLT  
VRATLKTGRTHQIRVHLQSQGCP IAGDERYGDYQANRLQKLGKRMFLHASLHLNHLPTGEPVLKLAEPDPAQFAVMLENGTKH

## SEQ ID 7335

TTGGCACATCTCTATTGAATGTGTGCATTTTATCTGAAGCAACAAGCCTCTGTGCGTGATGTTGTTATGTTTCATTTAGATGTCAAACCGCATACCGCGTCTGAAATATTCATCCAA  
ATCCAAACCGGATTTCTT

## SEQ ID 7336

LAHLLHVCIFLYLKQASVRDVVMFHLVDPKPTRSEIFNPNKPDFL

## SEQ ID 7337

ATGAACATCATCCGCGCTCTCTCATCTCTCGCTGCTGCGCGCGCGGCAAAACCGCGTTTCTTAGCAGGCATCAAACCTGCGCGGCGCATCGTGGCGATGGCGGTGCTGTTTGGC  
TTTTGACAGCGGGTTGGGTCAAACGCTTTCGCTGCAACAGCTTACCGAGCGCGTGAAGGCAACCTGACGCTGTCTCTGCTGCGCGCTGCGTGGCGGTATCATGCTATTTGGATTTGAT  
TGCGCAGCATTTGGTTTTCGATGCTGTTTCCGCTCCGCCAGCACTTTGCTGCTACTGCTGTTACGGGCAAGGTTACCGCTGGATACGGAGCATTTATC

## SEQ ID 7338

MNIRALLIILGCLAAGETAVLAGIKLPGSIVGMVLFALLQAGVKTSLWQLQDLMANLTLFLVPPCVAVISYLDLIADWFSILVSASASTLCVLLVTKVHRHRSII

## SEQ ID 7339

TCCCTCGGTGCTCAAGGCATTAATGCTGTAACCGCGCTCAACATAAGTGATTTGCGCGGTAATCGCGGACGACAGGTGCGGACAGCAGGAAGCGGCGATTTCCGACTCTCTCGATGGTA  
ACGTTGCGCGCGCAGCGGTTGTGGGCGCGGACGCTGCCAAGAGTTTGCGGAAATCGCGGATGCGCGAGGCGGCGAGCGTTTGTATCGGGCGCGGAAATCGCGTTCAGCGGATGCCCT  
CTTACCAGACAGCGCGCGGTAAAGCGGATGCTGCTCAAGCTGCTTTTGCATPACCATCATCGTTGTAATTCGGAATCGCGGTACCGCGCCAGTAGCTAAGGCGGACGATGGC  
GGAATCTCTGCGCGCATCATCGGACGCGCGCTTTTGCAATGCGGCGAGGCTGTATGCGGAAATTTGCTGCTGCTGTTGAACGCTTCGCGGCTGATGCTGTCAGGAAGTCGCGGCTC  
AAGGCTTCTTTCGCGCGAAGCGGATGGAATGCACCAACCGTCAAGCCATCCAATGTTTGCTTAAGTGGCGGAACACTTGGTTGATTTGCTGCTGCTGCGGACATGCGAGCGGAATA  
CGAGTTCCGAATCTAATTCGCGCGCATTTTTCGCGAGCGCTCTCCAGTTTGTCCACACGTAGGTAAACGCCAGTTCCGCGCGCTGTTGCGCGCAGGCTTTGCGGATGCGGTAAAGCGAT  
GGAACGCTCGGAAATCATGCGGTAATCAGAAATTTTTCGCTTCGAGAAACCCAT

## SEQ ID 7340

SLGAQGINAVTAVNISDPAGNAGRQVGGQEGGSIPTDFDGNVAAQRVVGDDVSQFAEIGDAGGGERFDRAGGNVAAADALPTQGGGKADACLAGFCHTHVIRNRAYRAQVAKGDDG  
GVPAAHRTGGFCQCGQAVCGNFVCGVERFAADAVEVAAQGFFRREADGMHQVQALPMFA\*VGEHLVDFVVGADIAAEYFEGI\*FRHFADALPQFVHNVKQRFALFAAGFGDAVSD  
GTLGNHAGNQNFALQKTH

## SEQ ID 7341

TCGCGCAACAGGTTGGCGATATTTTCCATCTGTTCTTCAAGTAAACCGFTTTCGCGCAATCTGGCGGCAACTGCCCAATTCGCGCGCAAAACCGTGGTCCGACCGAGCTGCCCGCAATTT  
TCGACTTTGGCTTCGCGTGTGGTTTTCGCGGCGCGGTTTGAAGGAAATCTGCTTTTGGGGAGCGGTATTCAT

## SEQ ID 7342

SAEQVGDIFHLFPKTFVPAQSGGNCFFARQTVVRTELPPFFDFGCGGTFQRPDGNPAPGDGIH

## SEQ ID 7343

TTGGGCTCCGCTGCCGCTTACTTCCGCGCGCAACCGCAAAATCAATTCAAACTTGACTACGTTCTGCGCTGCCGCTGGGAAACAGGCGCAGGCAAAATGCTTTGCGGAGTGGCTTT  
TAATA

**SEQ ID 7344**

LGLRCRLTSAPKRQNFKLDYVLRLPAGNRRRENALRSAFLI

**SEQ ID 7345**

ATCGATGCGAATAGCGCGGAAGATACGTGATCCGCTCGCGCGTCAACCGCGTGTGCGCATTTGGAGCTTGAGGTATTCGCGGTATTCCTGCGCGGTCTGCCTGCGCGGGCGGCTTGTGCGGCAGTTG  
 CTGATTTTTTCTCGCGCCCACTTGCCTGTTCGCGCGACCAACTCTTTTTGCACGTCGATATCGAGTCTCCCCAAAGTTTGGTAATTTTCGGAATTCGCGCATGTTGGTTTTGTACGCGCGCCT  
 CTTCACACTTTCGCCCCGTGATACGGTAACGGTATCGGCACGCTCGAGCTGCTCGGGATCGAGGATTTTCGGGTTCGGGTGCGCCTTCTCGCGCTTCGGGGTACGCCCGCATCGCCCGCGCGCGG  
 ATTGTGTTTCAAAATGCTCTCGGGGTGGGTTTGACACGGTCTCTTCTTCAACGGGCTTTGCGCGCTCAAAACCCCTGACCGCGTCTTCTTTTGTACCGCCTTGCCTCTATCATCAGATGCTC  
 TTCACGCGGTAAAGCAGCAACGCGGAGACAGCGTTTGCCTGCCATACCGACCGTGTGTGCGATAAATCGCGTCCGAGCGCTTTTGGCGGGCAGGAAGCGAGCGCTGCCCTCAATACGC  
 CGTCTTTAACTCGACATGTTCGCCCGCGCTTCTGCTGTCAGATGCTCTCGCAAAGAGTCTTCCCCATACGAGCGCTGTTCCTCGGCATCGGCAAGCGTTTTCAGAAGCGCATCGGTAAAT  
 GTTCAAACTGGCGCATCAGACAGCTGCGCCGCTCTTCTGCGATCTTCGGAACGGTGTCCAAAGAAACGCGCAACCGGTAGGCGGCGCGGATTAATTTTGTGCGCATCGACAACTGCCTGCGG  
 TCTTTCTCGCGCGGAAGACGCGCTTCTGCGTGAGCGTTTCTGAATACTGCGCGTATGCTCTGCAACACGCGGCGGTGTGGCGCATTCACACGCTTGGCGGTTCTTCTCTGCGCGCACG  
 CTGCAAGCAGCAGGCGAAACGGCAGCGCAATGAGTTTCCGATACAT

**SEQ ID 7346**

IDGIAAKILYLPFAKHPRVALELEVGVFLVCLRGGLSAVADFFLRPLALFADQLFLHVGIESPFGKGNFGFRTLVLVYARLFHFAP\*YNGIGTLDVVGNQDFGPGCAFCGLGYARIAAGG  
 VOIGNVFGGGGRFFFTGFAAQNPDVRVFFCHRLAVYHHDALHAVRQQRGRRLRRHTDRVVDKCRPSVFGQGEADGCRQYAVFKLDIAARLLHLDVCCRFPFIQOGAVCLGIGKRFPRHGN  
 VIGDTERAPAFILRFRSVFORKROTGVGGDNFVGDIDKLPAVFAKERTRFLRERFLMTAAAYVLQHGCVGAFORLGRFFPAARCKQQGKRQNEFPTH

SEQ ID 7347

SEQ ID 7347  
ATGCCGCTCGAAGCGGTTTCGGGCGGCATATCTTCGGGTTTTGCCCCCGCTCCGATATGTTAAACTTGCGCCCGTGCCGACCGTCGTTTGCGACGGTTTCTTTATTATGATTGAACGGAA  
AAACCATGTCTCCGCCCTTCCTCCGATGAGCGGAAAACTGATGGCGGTTTGTATGGCGGTACTGGTGCCTGATGCCGTTTTCATCGATGCCCTACCTGCCCGCATTCCTCGAAATGCC  
GCAGCGCTGAACCGCGATATCCACCGTATCGAA

**SEQ ID 7348**

MPSEAVSGGI SFGFAPPSDMLNLRPCRPSFATVSLFDLNGKTMSPPLPPMSGKLNVLNAVLVALMPFSIDAYLPAIPEMAQPLNADIHRIE

**SEQ ID 7349**

SEQ ID 7349  
TTGAAAATCCGCAGGGATGCACGTTCCGGGGAAACCGTGTCCGGGAAGGTCGGAATAAGAAAGGCTATAAAGATCGATCGCGCGGTCTGCCTGCCCGCTCCGAAACGCTCGGTCGGAAAAAT  
GGCGCCCGCGCTTCCTCTGTGTATCGTCGATGCCGTGTGTTTTCGGGCGGTTTCGCTTCGGGGCTTGGGGCTCCGCTGCCGTCTTACTTCCGCGCGGAAACGGGCAAATCAATTCAAACCTTGAC  
TAAGCTCTCGCGCTGCCGCTGGGAACAGGCGCAGGGAATAATGCTTTCGCGGAGTCGGTTT

**SEQ ID 7350**

I KTRRDARSGEPACBGSDKEGYKDRCGGLPAAFRTLRSSEKNAPASSCYRDACVFGRAFANGSAAVLLPRRNGKINSNLTTFCACRLGTGAGKMLCGVRF

**SEQ ID 7351**

SEQ ID 7331  
TTGAATAACATTCCTTTTCATGATCACCTCGTGACGGGCGGCATTCCGGCGCGCCGGTCCGGTTCGGCATTCCGTAAGGCTGGGTTTCCGATGCTCTCCGGATAAAACCGGTAATCAGTTT  
TGAGT

SEQ ID 7352

LNNILFMITSWTGGIRARRSGSAFRKAGFPMSSDKTGNQFLS

**SEQ ID 7353**

[illegible]

SEQ ID 7354

SEQ ID: 7534

VTHKRLFNATQAEEKLVAVDGNLLDLDETFLGKEQRKGNITKGIITRIEPSLEACFVDYGTDRHGFLPPEKVSRSYFLGTEGGRARIQDVLKBEFMEIVQVEKDERGNKGAAITPIS  
LAGRYLVLMPPNNRGGGVSRRIEGGERQELKAAMAQLDIPNGMSTIARTAGIGRSAAELEWLDNLYLKQLWQATEAGAKAHDPPYLLFMESLLIRAIRDYPRPDIGELVDNQEVIDQVAB  
FMSYVMPGNAGRIKLKYEDHTPLFSRQPIEQHTESAFERSVSLPSGGAIVIDHTEALVSIIDVNSARATFGADIEDTAFKTMNEAAEVARQMRRLDGLGVVDFIUMENPKHQDQVENVLR  
DALKKDRAVRVQMGKLSRFGLLIELSRQRLKPALGESSHAAACPRCAGTGVTIRGESTALHVLRMVQEEAMKNTGVEVRAQVPVDVATFLINAEKRAELFAMEERLDVNVVLIPIHLENPHYEI  
NRIRTDDEVEDGEPSPYKRVAEPEEDESAPFGGEEKAKAARPEPAVGKVRHTSPAPTAAPKEKTSWSDSKFAMLKRIPGGSETQVAPAEATESEKRSSTANRSGSRRANRRQNPSSRKREGSKI  
EVREAAGKTAGQKARADKATERNNGHRRNRNERGDRATERANEAEITQSRNVQPAAPVADAAPFETEBGTQKRRNRSNREGTQVAPAEATAEVAQTVAATEPPEPTVEKDGSKSEKSRN  
REARDSRAKERERNNQRRDQKGRKNIPSAAKIBQYLNLIHDTADKRVSAAHVFGETDANAPITFVSIADPLIATVPQTQASSAVSNGDALIYTAQAEKIRRAAADILPEGAAPKAAAQEMP  
SETATPTAAABQARETAQTGGLVLIETDPAALKAWAAQPEVQAGRGLRRSEBPKPSEAAITVPAEMIQVETROG



**SEQ ID 7356**

**SEQ ID 7357**

**SEQ ID 7358**

**SEQ ID 7359**

**SEQ ID 7360**

**SEQ ID 7361**

**SEQ ID 7362**

**SEQ ID 7363**

SEQ ID 7364

SEQ ID 7365

TTGTTTGGAGCAA

SEQ ID 7366

**SEQ ID 7367**

**SEQ ID 7368**

SEQ ID 7369

TTGGCCGAGGTCAA AAAATCAGCGCTACCGAGTATTACTTGAATCAGGCACATGGCCGGA AAAACAACACTTCTGCCGGCGTGGCATCTCCGCCACCGACATCAAAGGCAAAATATGTTC  
AAAGCGTACGGTCGCAAAAGCGCTCGTTACCGCCGAAATGAAATCAGACGGCGTAAACAAAGAAATCCAAGGCAAAAGACTCTCCCTGTGGGCCAGCGCTGAAGCCGGTTCGGTAAAAATG



GTTCGCGGACAGCCGGTTACGCGGCCCAAGCCAAAGACGCCGACGCTTACCAGCAGCGCGCACCGGACAAACGGCGGCAAGGCAAAATCGACACCAAGCACTGCCGCTCAACTGC  
CGCGATAAATCAACTGCCAAA

## SEQ ID 7370

LAEGQKSAVTEYLYNHGTWPEMNTSAGVASSATDIKGYVQSVTVANGVVTAEMKSDGVNKEIQKRLSLMARREAGSVKWFQGPVTRAKAKADDVDDAGTDNGGKIDTKHLPSTC  
RDKSTAK

## SEQ ID 7371

AATATGAAATTCCTGGTCTTCTGTAGCATAAGTTCGATGATATGCCAAGTAAGATTACGTTTGTCTGTAGCAGATTGTATCTAGCTTCACATCACACCAACGTCGCCAAACATCA  
TCTGATAACCGCTTAGATTTCACCATATTTCTTCATCATCAACGAAATATATTTCAAATCAAATAGGCTATCCAAGGTACGACTTAATAGCAAGCGTTATTTGGGTCGTATGCTTCG  
TATCATCCGACAGGATGAAAGGCTTAATATGACTGGCAATCAATACAGGATAGGCAAGTTTTCAGCATATATTTCACATTACCGTAATGTCTTCATCTTCTTGAAGTGGTTTTT  
GTATAGGCGATGTAATAAGGGTCGGTTTCTTACAGTAATTTTATCCAAATACCAAAATACGTTGGGCATCCTCAGCAAAATATAAGTCATCACCTACTCGTTTAAAGTCGTCTAAT  
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TTTTAAGTCTACTAATCATCATGCGCGCAATTTCTTTTATTTAGCTTGCCTTGTGGATGCTCGACAGCGTTTAAATCAGGAAATTTATTTGTCGAATATTAGAGTTTTCAGTTACTGA  
ACGCTGAAAGCCAGAGTGGCTATATACGATTTTGGAAAGTAGGGTTTGTCTGTTTTCGTTAGTACGAGCTTGTACATAATCTCGTGATAAAGGTGTATAGCTTGATAAAGCGGTTCTATA  
AATCCCAT

## SEQ ID 7372

NMKFLVFL\*HKFSMICQVRFTFVVEQIVI\*LHITPTSPNII\*\*PLRPHHSPIIKRNIFQIK\*AIQGT\*\*QAVIWWVFCGIIRQDERLANMTGNQYRIGKFFQHTFHTVMFPTFFFLKLVF  
V\*AM\*IRVAPPYSNFIQITKNWILGILSKI\*VITYSP\*VV\*FV\*\*VP\*ITYLIVFSPNKS\*FYSLLKILIIQPCFG\*IILLKGP\*VY\*HGGNFFFI\*LALWMLDQRFNQEITLNSIRVPSY\*  
TLKARVRIYDFGK\*GLSPSVSTSLYIIS\*\*RCIA\*\*KRFYKSH

## SEQ ID 7373

TTGGCTGATTATTACTCATCTCTGTCTCCAAGAAATTCGATACCAATATTCTGTTTGTGATTTAAGTAATATCTATCATTCATGATTTTCTAC

## SEQ ID 7374

LADYSSLSRIFDNLFLYLSNIVHSCIFY

## SEQ ID 7375

ATGAACGAGAACTTACCGAATGGCTGCAACGGCTGGGTGCGGCCCATCAACGATCCGATGTGTCATACTTGTGTTTATATGCTTTTGGGTACGGGGCTTTTCTTCACCGTAACCAAGGGCT  
TTGTCCAAATTCGCGCTGTTTCGGCGCGAGCATCAAAGAAATGCTCGGCGCGGCCCAACAGGGGGACGACCTTCACGGCATCACCGCGTTTCAGGCATTGTATACCGCGCTTGCCAGCGCGGT  
GGCGGTGGGCAATATCGCGCGCTGGCAATCGCCATCAAAGTGGCGGGCGGGCGCGGTGTTTGGATGTGGGTAAACCGCTTAATCGGCATGAGTTCGGCGTTTGTGCAATCTTCGCTG  
GCCAGCTCTTTAAAGTCCGCACTGCGACAACCACTTTCGCGGGCGGCCCTGCTACTACATCAGCAGCGGTTCGGGCAGAAATGGCTGGGCGTGTGTTGCGCGCTGAGCGCTGATTT  
TCTGTTTCGGTTTGTGTTTGAAGCGGTTTCAGACCAATACCATCGCCGATACCGTCAAAGCGCGGTGGGCTGGGAGCCTCATTTATGTCGGCGTCCGCTGGTGAITTTAAACCGCGCGCAT  
TATCTTCGGCGGCATCAGCGCATATCCAAAGCGCGGAAATCGTCGTGCCCCCTGATGGCGGTTTGTACCTCTTTATCGCGCTTTTCATCATTTTGACCAATATTCGATGATTCCGGAC  
GTGTTGCGTTCAGATTTTTCGGCGCGCTTCAAATTCGACGCGCGAGCGCGGTACTCGCGCGTCTGATTTCCGAAACGATGATGATGGGCATCAAACCGCGCGCTGTATTCCAACGAGG  
CGGGTATGGGTTCCGCGCGCAAGCGCGCGCGCGCGGAAAGTGAACACCGCTGTTTCGCAAGGATGATTCAAATGCTGGGCGTGTGTTGTCGATACCATCATCGTTTGTCTTCACCGC  
CTTCATCATCTTGATTTACCAACAGCGCTTATGGCGATTTCAGCGGTGCGCGCTGACGCGAGCGCGGATTGTCAGCAAGTGGGCAATGGGCGCGGGTTTCTCGCGCTCATCTGTTT  
ATGTTTGCCTTTTCCACCGTTATCGGCAACTATGCGCTATGCGGATGCAACGTCGCAATTCATCAAAGCCATTGGCTGATTACCGCGCTTTTCGCTATGCTGGTTTGGCGTGGGTCTATT  
TCGGCGCGGTTGCCAATGTGCGTTTGTCTGGGATATGCGCGATGTCGCGATGTCGCGTGGATCAACCTGTCGCGCATCTGCTGCTCGCCATGGCGTTTATGCTGCTGCG  
CGATTACACCGCAAGCTGAAATGGGCAAGACCCCGAGTTCAAACCTTCGCAACATCCGGCGTGAACCGCGCATCAAATCCGATGTTTGG

## SEQ ID 7376

MNENFTMLHGWGAINDFMNSYLVMLLGTGLFFVTGTFVQFRLFGRSIKEMLGRRKQGGDPHGITTFFQAFVGLASRVGVNIGVIAIAIKVGGPGAVFWMVWTALIGMSSAFVSSSL  
AQLFQVRDCDNHFRGCPAYYITHLGGQKWLGLVFLALSILPCGFVPEAVQNTYIADTVKAANGWEPHYVGVVALVITAPIIPGGIRIRISKAETVFLMAVLYLFIALFIIILNIPMLPD  
VFGQIFSGAPKFDAAAGLLGLLSQYMMMKIKRGLYSNEAGNSAPNAAAABEVKHPVSQMIQMLGVFVDITIVCSCFAPILITVQPPYDLSGAALTQAATVSQVQWAGFLAVILF  
MFAFSTVIGNYAYAESENQVFKSHWLITAVFRMLVLAWVYFGAVANVPLVMDMAMGIMAWINLVAILLLSPLAFMLLDYTAKLKMGKDFEFLKSEHPKLRRIKSDVM

## SEQ ID 7377

GTGTTTAAACGGGTGGCAATGAGGCACATGACAGGCGCTTGAAGCCAAATCGATATATTTATTTCCACCGGAACGGACGACCCCGCGCGCTTGCAAAACCTTAAAGACAAGCCCGCGGGT  
TGATCCGGCGCGCGTGGGAATCACTTACCGTTTGAATTTATTTAAAT

## SEQ ID 7378

VFKRVAMRHMQLRAQSIYFHRNGRFRPPCKPLKDKPPGLIRAAGVNHLPFDLFKI

## SEQ ID 7379

ATGAGCGAAATCCTCAGGCAGCCAGCGTTCTGCTTTTCTCAGCGCTTCCGCTGTACGCGCTTGGATTATCGTGGCGACGCGCAGGGCAATATCTTCTGCAACCCCGTACTCGTCAGCA  
CTATCGTGTGATTGCTTACCTGAAATCTCGGTATCGATTATGCGGTGTACCAACAGCCCGCGCAATTCATTGATTTCGGCTGAAACCCCGCGTCTGCTTCCGCTGCGCGCTCTA  
CCAAACCCCGCTGAAATCTTCAACAGTGGCTGCCGTCATCGTTTCGACGCTTTCGGCGAGCGTTACGGGCATTGTTACGGGATGATTTTCCAAAGTGGCTGGCGCGGCAACGGAA  
GTGCTCTCCCGCTCGCGTCCAAATCTGTTACCAACCCCATCGCATGAAATCACCGCTCCATCGCGGCAATCCCGCCATTACCGCGCCACCGCTCATCTTCCCGTCTGGTGGAC  
AGATTGCGGTTACAAATGTTGAAGAACAGCGTCTCATGCGCTCGTCCGTGGGTATGTCGCTCGGCAGCGCTTCGCAACCGATGGGCATTGCGCGCTCGCTCGAACCGAGCGCGCGCAT  
GGCGGCATACGCGGGATGGGCTGACGTTCAACGGCGTCTGACCGCGCTGATTGCGCGCTGCTTATCCCGGTTTGGGGTTT

## SEQ ID 7380

MSEILRQPSVLLFVTLAVYALAIIVRTGTENIFCNFVLVSTIVLIAVLIKILGIDYAVHNAQFIDFRLKPAVVVLAVELYQNRKI FNQMLFVIVSQLAGSVTGTIVTGMVFAKWLGAERE  
VVLPLASKSVTFNPIAIEITRSIGGIPAITATVITAGLVGQIAGYKMLKNTVMPSSVGSLSGTASHAMGIAASLERSRRNAAYAGMLTFNGVLTALIAPIILLIPVLG

## SEQ ID 7381

GTGCTCATTTGCCACCGGTTTAAACAGGTTTATCTGACAGGCGCGCAATCCGCCCCCTATTGTTAATCGCCATATTGATTGAACACCGCGCGGAAACCGATATAATCCGCGCT  
TCAACATCAGTGAAATCTTTTAAACCGT

## SEQ ID 7382

VPHCHPFGHYLTGAQSAPSPVNPPICTETPPGTRYNPPFNISENLFITG

## SEQ ID 7383

CAAATTGATTAATAGCTTACGAACCGAGGCAAAATTCATGGCTTGTCTTCTCTCGGAAGCCATAACGGAATCTTGGGCAATGTTTGTGCAATGCTTCATATAGTTCGTTGCTGTAT  
GGCTGGCTTGTATCGCATCAATAAGTCAAGACAAATATGAGTGCAGTACAAATTTTGTATCGTTATAATTTGTAAGGCATTGGTAAACGCCCAATAATCTTCATAAATTTGCGCTGT  
TTGGCTGATTATTAATCAT

## SEQ ID 7384

QID\*\*LFRNQIHLACSLRSHNGILGNVLQCFI\*FVAVLVLIRINKVKTNIECSTKFLIVIIICKGIGKRIIFINLAVVLIITH



**SEQ ID 7396**

SEQ ID Y3936  
 MTHMTIDVTDDIVVVGGHAGTEAALAAARMGACTLLITHNIETLGMSCNPSIGGIGKGLHVRELDALGGAMALATDKSGIQFRRLNASKGAAVRATRAQADRILYKASTREMLNQNEM  
 DLFQQAQVEDVTLFEGERI.SGVITAMGVFVKARAVLITAGTFLSGKITHIENYEGGRAGDPAKSLGGRLRELKLPQGRLLKTGTPPRIDGRTIDFSQLEQPGDTPVPMVSMGRNAEMHPRQ  
 VSCWIHTNTQTHDIIRSGFDRSPMTFKIEGVGPVKYCPSIDKINLPADKDSHQILFEPGLTTHEYYPNGISTYSLPFDQIALVRSVMKGLENATHIRPGYALIEYDFYDPNKLASLET  
 TIGLFFPAGQINGTGYEEAAQGLLAGANAQVVRGQDPLLLRREQAYILGLVDDLLITKGLNEPYRMFTSRAEYRLQIREDNAIDRLITGDKYILGLVEAQWRYMFDNREAVREIEQRLK  
 TTWYTPQKLADEQIRKVPQGLSREANLHDLRRFPNLDYALMTLEGANPSENL.SAEVILBQVEIQVKYQVILDRQWREIDSRRDITETLKLPGDIDYGRVKGLSAEVQQLNQHKEPTWGQA  
 SRI.SGVTPAAVALNLVHLKRGFDKAM

**SEQ ID 7397**

SEQ ID 7397  
TTGGAGTCGATGAATCGGTGGGGCTTCAGTCCGCCATTCCCATCAATCCAACATTTCTACCGTTTTCATCGAATCCATCGAATCCGGCTCTTTGACCACCCGGCCCTATGCAAC

**SEQ ID 7398**

LESMNRWASVRHSHQSNISTVFIESIRASFDHPALCN

**SEQ ID 7399**

SEQ ID 7399

ATGCAACTGAACCGTCATCCCAAGGAAGTGGGAATCTAGGACGCGGGGTTTGGGCAACCGTTTATCCGATAAGTTTCCGTGCGGACAGGTCCGGATTCCCGCCTGCGCGGGAATGACGA  
GTTTCAGATAGTCGGTGTTGTGCGGAATGACCGTTCGGGTATTATTACTGCGCCGCCCGCGCCTGTAAACGCGGGCGATTAAAAATGCCGTCTGAAGTTCTAGACGGCATCGGTATCGG  
AAATACGAGAAGCGGTAGCGCATGCCAACGAGGCTTCGTGGGTTTGAAGCGGGTGTTTTCGAAGCGTCCCAAGTTGTGTAGCGGTAGCCCGCGCTCAAGGTACAGGCGGGCGCGACGTC  
TATGCCACGCGCCGCATCGCGCGGAAGGCCAAGCGCGCGCTCGTGTGCTTTTGTAGTAGGTGTTTTTTCGGGATGTCCTGTCAGGATAAACCCGTAACCTGCTGCGTCAGCATCACTAGGG  
TAGCGCGTAAGAGTACCTGTTATTTTATTAGTCGAATCGATGCTGTGTCGACGATGTCCTGAGGCAACCGCGCCACCGATAACCGTTTGAATTTGTGCTTTGAAATCGGTAAACCG  
CGGACAAGCCGAGAGAAGAACGCGCGTGAATGTGCGGTTTCTCGATATGTCGCTGTTTGGTATTATTGATTAAAGCTGGTTCGCCGCAAAAGTTTATTATTCTTCTTCCAACTCTTT  
TATGTCGCGGAATATTATTATTGTTGTGTCGCAATTTCTGTTTACCGGGCATAATCCGCGCGATGCGCGACGCCGAAGTCGTAGCCGACCGACACCTTGGGTGGATGGAATCGGTACGGATG  
TTTCTGAATAATCGCTTACCGTGCTTATTTTGTTTTCCTGGAGCGGTGCTTCCGGATAATCGTGGGTAAATGCGTTCGCGCGCGTAGGC

**SEQ ID 7400**

SEQ ID 7400  
MQLNRHSHSGNLRGRVWATVLSDKPCGVQVRI PACAGMTNFEI AVLSCMTVVRVFCARPAVPVNGRLKMPSESGDIGIGESEAVAHARGVFVGFAGVFPQASPVVVA VAVAGVQGAQRD V  
YAHARHRAEAQAAA VAFLLVFLRMSVRINRNCVSVITRVGGKSTCYFFSRIDA VSDVSVGDARTDIGEFVVFVEFVINGGQAEERRNGVECAVFLMFLRLVTVVKLVAARSFII LSPQLF  
VYHGFIPIVVPFVTGIIRGDAPAAEVVADRHPGVDGMRTDVS EIIATRAYFVFANSWGFR IIVGNAPGGVG

**SEQ ID 7401**

SEQ ID 7401

TTGAAATTCGTCATTCCTCGATAACACCGCAATCTCGAAACCCCGTCATTCCTCGCGCAGCGCGGAATCCAGACCCCCGACGCGCGCGGAATCTATCGGAA

**SEQ ID 7402**

LK F V I P D N T A I S K P V I P A Q A G I Q T P D A A G I Y R K

**SEQ ID 7403**

SEQ ID 7403

ATGCCGCTGTGAACCACTTTTCAGACGGCATCGTACCATCCCGACAGGAAACATCATGCACATCTGACCGCCGGCGTGGACGAGGACGAGACGCGGACCTTTGGTCGGCAGCGTGTGTTGCGG  
CGCGCGTCACTCTTCGGGAAACATTGCACTGTCCCGGACTGACCGACTCCAAAAATCTCAGCGAGAAAAACCGGACGCGCTTGCCGAAATGATTAAAGAACACGGCGGTGCGCTGGCAGCT  
CGCCGCCCTCCACGCCGAAGAAATCGCAAGCTCAACATPCTGCAAGCCACCATGCTCGCCATGAACAGTGGCCGTTTACGGTTTGGCTGCGCGTCCCGAAAAAATATTCTACGACGGCAAC  
CGCATTCCCGAACATTAGGCACTCCCTGCCGAAGCAGTCGTCAAAGGCGACAGCAAAATCATCGAAATCTCCCGGCATCCGTTTGGCAAGACGCGACGCGATCGGAAATGTAGCGAC  
TGGCGCAACGCCGTCCTCCCAATACGGTTTCGACAACACAAAGGTTACGGCACAAAGCAGCATCTGGAAGCGCTCAACAAATACGGCGGTGCTGCCCGAACACCGCCGCGACTTCGCCCCCGT  
CAGAAACCTGCTCGCGCAGCAGCCCTTGTTT

**SEQ ID 7404**

SEQ ID 7404  
MPSEPTFRRHRTIPTGNTIMHLTAGVDEAGRGLPVGSVFAAAILPETFDLPGLTDSKKLSEKKRDALAEIMKEQAVAMHVAASTPEETIASINILHATMLAMKRAVYGLAARPEKIFIDGN  
RTPEHLTGPAEAVVVKGDSKILKEISAAVSLAKTARDAEMYALAQRRPQYGFDDKHKGYGTKOHLALQYGVLPPEHRDFAPVRNLLAQQALF

SEQ ID 7405

[illegible]

SEQ ID 7406

SEQ ID 7406  
PQLQKKRIRHRRIGRAVVALGFAAGCPFAAAVFRRHFMFCARFVVIQAHGQORDAFACGIDGFQHFHFHEHVAGFHHFARVLDLIRQGGDVHQAVLMDADVHERAEVGDVGDMHLEYHADLQ  
VADFVDAFGKRCRLKRTARVAAGFPQLGQDVNSRQTEAFVGEVGCPLDLHTLAVADEFGGNGALLRQHPGDDGIGFGVGDGARVQLFAAVNPQKACCLLEGFPFAQARYP\*QFSSAVERAV  
FITVGDDVLGKGLI\*TCNPRQERGEGGVRVHADGVHAFVDPHVRQFPEALVHVLIILPHADGFGVDPTDLGKRVLPAGDGHCAAGQNI\*VGKLARRQFGRIRNRAGFGNDDFVQAAPG  
HSAHQFARDFVDFAGAGVADGDELHTFVLPFQARQCRQHLVFLMQIDNDRIQQFARVVHGHAFHAVAVAGVESQSQSQPPGGRGEQQVFEIAGEHGNRVSGVSFPQTIESTFQRQKDFRAP  
GQAHGVAQFPFAV\*NLBAAGDILLV FALLNRNRVVG L VFERDVQHA FVATAQNRQRAVAGHGANGFAA V E I A E F A P G F P A N D L R V D F G F P V L V A Q R A D E F V F G K L I L H Q N R A I Q R  
SFGVGVDVQVALRGGFHVLR L F G Q H V R Q R L Q T V F R D L R F G A A F G F V G Q V Q F R G F V V G G F D L R P E V V \* K L A L L F N A F \* H N G L A L F Q L A Q V L Q P I K Q I A Q L R I V Q P A R G F T T V F R D K G  
DGRAVVQKLDGSDGLHSGGEFLGDSGDVHKLPP\*CR LNSRRRN VGNRLERKMIILYFARYNLKGMFVYDRPOTYRRHRYFAH

## SEQ ID 7407

TTGTTTATGACCTGCTGATTACCGGCGGCAACGGCTTTATCGGTTGCGACACCGCGCTGCTGCTCCAAATCCGGTTACGATGCGGTGATTTTGGATAATCTGTGCAACTCGTCTGCGG  
CCGCTCTCCCGCGGCTTCGGCAAAATTAACCGGCAAGAAACATACCGTTTATCAGGGCGACATCCGCGACTGTGAGATTTTGAGGCGAGATTTTTCAGAACATGAAATCGAATCCGTCATCCA  
TTTTCGCGGTTTGAAGGAGTGGGGAAAGCGTTGCCGAGCGGACAAAATATACGGCAACAATGTTTACCGGAGCTGGTGTGCGGGAAGAAATGGCGCGCGCGGCGGTGTGAAATC  
GTATTCAGCTGCTGCGCAACCGTTTACGGGATGCGGAAAAGTCCCTATACGGAAGATATCGCCCGGCGGATACCGCTAATCTTACGGTGCCTCAAAGCGATGCTGAGCGGATGT  
TGACCGACATTCAAAAGCGGATCCGCGTGGAGCGTGATTTGTTCGCTGTTTCAACCGGATCGGCGCGACGAAAGCGGACTTATCGCGGAACAGCCCAACGGCGTTCCTCAACATCT  
TTTGCCCTATATCTGTCAAGTGGCTTCGGGCGAGGCTGCCCAACTGTGCTGATTCGGGCGGCGACTATCCGACCCCGAGCGTACGGGAATGCGGCGACTACATCCATGTGATGGATTTGGCA  
GAAGGGCATATCGCGCAATGAAGGCGAAAGCGCGCTTCCCGCGTACATTTGTTCAACTTGGGTTGCGGACGCGCTATTCGGTTTGGAAATCATCCGCGCTTTGAGGCGCGCATCG  
GTTTGCACATTCCTTACCGAAATCCAAACCCCGCGCGCGGCGGACTTGGCGTGTCTTATGCCACCCGCTCCCATACCAACAAACAAACCGCGCTGGGAACCAACCGCGCTTGCAGCAAT  
GATGAAGATTGCTGGCGTGGGTGAGCGCAACCCCGGAGATATGGGAT

## SEQ ID 7408

LFMTVLTGGTGFIGSHTAVSLVQSGYDAVILDNLCNSSAAVLPRLRQITGRNIPFYQGDIRDQILRQIFSEHEIESVHIFAGLKAVGESVAEPTKYTGNNVYGLVLAERMARAGVLKI  
VFSSSATVYVGADEKVPYTEDMRPGDTANPYGASKAMVERMLTDIQRADPRWSVILLRYFNPFIHAGESLIGECPNGVFNLLPYICQVASGRLLPQLSVFPGDYPTPDGTGMRDYLTHVNDLA  
EGHIAAMKARGVAGVHLNPLGSGRAYSVLEIRAFEAASGLHIPYRIQPRRAGDLACSADPSHTKQQTGWETKRLQQMEDSWMVSRNPRGYSD

## SEQ ID 7409

ATGGTTCAAAATGGGCAATTTGTGTAACCGTTTTCGCAAGTGCCCGCATGTPAGCCTATCGCGGAATATGCGCAAGTTCGCGAGGAAAAGGAGAAGAAATGGCAAAATCAGAGTTG  
CCGCGGTGCAGATGGTGTGCGGCGGTGTCGCGGAAACCAACGTCGCGCCATGAACGCTTGTGCGACGGGCGCGGAGCAGGTTGCGGATTTGGTGTCTGCTGCCGAATATTTGGTGTCT  
GATGGCGCAAAAGATACCGGCAAACTGCGACTTTCGCGAGCCTTTGGCGCGCGGACGCTTTCAGACGCGATGAGCGAAACGGGAAAGATGCGCGCTGCTGCTGCTGCGCGGAACCGTG  
CCGCTGCAAGACCCGAGCGCGGCAAGGTCAATGAACTTTATTTGTGTATCGGTCGACGCGGTAAAGACGGGCTGTACCAAAATGCACTCTTCGCTTTTTCGCTTTTGGCGGAAC  
GCTATGCGGAAGCGGATACCATCCGCGAGGCGGGAAGTCCCGCACTTGTGCGCAGAAAGGATGCGCGTGGCGCAGGTATTTGTACGATGTCGCTTTCCCGAATTTTTCGCGCGCA  
ACTCGGTTTTCAGGTATTTGATGCTGCGCGCGCATTTACCATACGACGCGCAAGCGCATGCGGAGCTGCTGCTGCGCGCGCGCGCTCGAAACCAATGTACGCTGCTGCGCGCGGCA  
CAGGCGCGTTTTCAGCAAAACGAGCGCGCACTTCGACACAGTATGATTTGTCGATCCGTGGGCGGACGTGTGACGCTATTACCGAAGGCGAAGGATCGTTACGCGCAGACATCGATG  
CCAACCGCTGACAGCGCTCGCAACCGCTGCGCGCTTGAACACCGGTTTGGATGCGCTC

## SEQ ID 7410

MYQNHLCRKRFSQSAAMVAYRRNMPQGRQEKGEEMDKIRVAQVMVSGVSPETNVAAMKRLVARAAEQGADHVLLPEYVWLMGANDTGKLLAEPLGGGRFQTALSETAKECGVVLPFGTV  
PLQSPFAGKVMWTLVLYGCDGVRGTGLYHKMLPGFSGLGERVYAEADTIRAGREVPHLSAEGMPVAAGICYDVRFPFRRQLPFDVLMPLPAATHTTTGKAHWELLRLARAVENQCYVVA  
QCGHENGRRRTFGHSMVDVFWGDVLDVLPGEIGTADIDANRLNSVRNRLPALKRVLDV

## SEQ ID 7411

TTGCGGCATATTCGCGGATAGGCTACCATGCGCGCACTTTGCGAAAACCGTTTACACAAATGCCATTTGAACCATATTCGCTCATCGGTGTAGGGCTGATCGCGGTTGCTTCGTPC  
TCGACCTCAAAGGCGAGGATCGCTCCGACCGTTACCGGTATCGACACCGCGGACCACTCGAACGTCATTTGGAACGCGCGGTGATTTGACCGTGCCTCCGTCGTCATCGACCGGA  
CAGCATCGCGGTGCGGACTTGGTACTGATTGCCACGCGCTGCGCACCGTTCCCGCGCTTTTAAACCGCTGCGCGCGGCTTTGCGGAAACACACTTGGATTTCCGATGTCGCGAGCACC  
AAATCTTCGCTCATCGAAGCTTTCGCGGCTGCTGCGCGCGCTGCGACCGCTGCTGCGCGCAACCGGTTTTCGCGGTTTCGACAGAAACCGTTCGCAAGCGCGCGCTTTCGCGGCTGT  
TCCGCCACAGAAACTCATCATCACGCGCCACGCGCGGAGATTTGACAGCGCATCGCATTTGTAGAAACCTGTGCGCGCGGCTGCGGTGCGGACATTTTACGATGGACGCGCAACACCA  
CGACGCGGTTTTCGCGCGCTGCTCCATATGCCCACTGACCGCTTCGCTATGTCACAGATTTTCGACACCGCGCGGCGGAGAAATATCTGAATTCGCGCGCACGGGCTTTCGCG  
GACTTCAACCGCATCGCTCCGCGCATCCGCGCTGTGGCGGACATTCGCTTCGCAACAAAGACAGCGCTGCTGCACTGTTCAAGGCTTGGGCAACAGTTGACGTTTTCGCGAGACA  
TCCTGACCGCGGACGCGGAGCGGAGCGCTGTACCGCTATTTTGAAGAACGCAAAACACCGCGGACCGCTGCTGCGGCGCAAC

## SEQ ID 7412

LRHIPPIGVHGTLRKPTQMPILNHIALIGVLIIGSFVLDLKRQGLVTRVTGIDTDRDNLERALERGVIDRASVVIDADSIGGADLVLIATPVATPVAVLTALRPVLPHTWISDVGST  
KSSVIEAFRRCLPGRHLRCLAAHPIAGSDRNGAAQPGFLFRHKLITTPHGGEDSDGIALVENLWRAVGADIFTMDAQHHDVFAAVSRMPHLTAFAYVHQILDHPDQBYLKFATGFR  
DFTRIASGHPAVWADICLANKDSLLQVLQGLKQLDLVLDLITADREALTRYFEAKTTRDRHLDGN

## SEQ ID 7413

ATGGCGTTTGGAGGTACCTGAAATTCAAAAAAACCGGAAACCGGACGCGATTGGATTCGCCCTGCGCGGGAATGACGGATTTAGGTTTTTT

## SEQ ID 7414

MAVMKLPETQKKNRTDWIPACAGHTDFRFF

## SEQ ID 7415

ACCTACGCGGGCAATTCGAATCGCTGACCGACATTCGCGATAATCCCGCTACGCTTTTGAAGCAAGTGATATTTGCGACCGCGCGGAACCTGACCGCGTGTTCGCGCAATACCGCGCG  
ATGCGGTGATGCACTTGGCGGCGGAAAGCCACGTCGACCGCGCATCGGTTCGCGAGCGGAAATTTATCCGAACCAATATCGTTCGCGCATTCGACCTGCTGGAAGCTGCGCGCGCTATTTG  
GCAGCAATGCGCTGTAAGAAACGCGAAGCCTTCGTTTCCACCATATTTTACCGATGAAGTCTATGCGGATTTGACGCGCAGACGATTTGTTTACAGAAACCAACGCGCATACCGCGCG  
TCCAGCCCTTACTTCGCGCTCCAAAGCGCGCGCGGACCACTTGTTCGCGCGGTGCGCGGACTTACAGCGCTGCGCTCCATTTGTGAGCACTGTTCCTAATTAATACGGCCCCGCAATATCC  
CCGAAACCACTTCTTTGATGATTCTGAACGCACTTTTCGCGCAACCACTGCTGTGTACGCGACGCGGCGCAAAATCCGCGACTGGCTGTTTGTGCAAGACCAACGCGCGCGCTGTGTA  
TCAGGTGTTACGAGGTGTTGTCGCGGAAACCTACAATATCGCGGACAC

## SEQ ID 7416

TYAGNLESITDIDNPRYAFQVDICDRAELDRVFAQYRPDAVHMLAAESVDRAIGSAGEFIRTNIVGTFDLEAARAYWQMPSEKREAFRPHIISTDEVYGDHGDLDLFTETTPYAP  
SSPYSASKAADHLVRWQRTYRLPSIVSNCSNNGYPRQFPPEKLIPLMLNLNLSGKPLPVYGDGAQIRDLFWEDHARALYQVTEGVVGETYNIIGGH

## SEQ ID 7417

TTGTTAATCCGCTATATCGTCATTCGCCGAAAAACAAAAAATCAAAACAGAAAACTGAAATATCGTCATTCGCCGCGAGCGGGAATCTAGGTCTGTCGGTACGGAACTATTCGGA  
AAAACGGTTTTTCAACCTCGAGACTCCGATTCCTGTTTTTCGCGGGAATCCGGTTTTTTTGTAGTTTACGTCATTTT

## SEQ ID 7418

LLIRYIVIPAKTKIKRNLKYRHSRAGGNLGLSVRLIKGNKFSNPETPDSCFRGNPVFLSPSHF

## SEQ ID 7419

ATGGCTGTCAACTGACCGAAAAACCGCGAACAACGCGGACATCGACGGCATTCGCCCTCTACACCGCCAAAGCAGCGGTGAAGAAGCCGCGGACATACCGACTGACACTGATTCGCG  
TAGCCGCGCGGACGACCGCTGCGGTGCGCTTTCAGACCAACCGTTCTGTGCGCGCGCGCTCCACATCGCAATCGCACTTTTCGAGCAAGACGCGGTGCGCGCGCTGCTCATCAACAC  
GGGCAACGCGCAACCGGCTACGGCGCACAGGCGAGAATCGATGCTTTGCGCACTGTGTCGCGCGCGCGCGGCAAAATCGGCTGCAACCGAACCAGGTGATGCGCTTCTCCACCGCGGTG  
ATTCTCGAACCGCTGCGCGCACAAAAATCATCGCGCGCTGCCAAAAATGCAAGCTGCTTTCGGAACGAAGCGCACGCGCATCATGACCAACGACACCGTTCCCAAGCGCGCTGCG  
GCGAAGCAAGGTGCGGACCAACACACCGCTCCGCGCACAGGCTTTCGCAAGGCTGCGGATGATTCATCCCAATATGCGGACCATGCTCGGTTTCATGCCACCGATGCCAAAGTTTC  
CCAACCGCTCTCAACTGATGACGCGAGGAATTCGCGGACGAAACCTTCAACACCATACCGTTGACGCGGACACGACCAACGACGCTTCTGTCATCATGCCACCGGCAAAACAGC  
CAAAGCGAATCGAACAATCGCGACCGCGTTACGCCCACTCAAGAAATTTGTGTGCGAGCTTTCGCTGCACTTCGCCACTGCTCAAAACCGCTTTTTCGCTCGACCCCAACCTTCGCGAGGCT  
TCACCGTCCGCGTGGAAACGCGCAAACTGCGACGAAGCCGCGCAAGCCGCTACGCGCGGACGCTTTCGCACTGCTCAAAACCGCTTTTTCGCTCGACCCCAACCTTCGCGAGGCT



GCTCGCGCCATCGGTTATGCCGACGTTGCCGACCTCGATACCGACCTCGTGGAATGTATCTCGACGATATTTGGTTGCCGAACACGGCGGACGCGCGCAAGCTACACGAGCACAA  
GGGCGCGCGTGATGTCGAAGGACGAAATCACGTCGCGATCAAGTCGATCGCGCAAGCGCGGCCACCGCTATACCTCGGACCTGTCGACGAGATCGTTCCATCAACGCCGACT  
ACCGTTCC

## SEQ ID 7420

HAVNITEKTAELPDIDGIALYTAQAGVKKPGHTDLTLIAVAGSTVGAFTTNRFCAPVHIAKSHLFDEGVRALVINTGNANAGTGAQGRIDALAVCAAAARQIGCKPHQVMPFSTGV  
ILEPLPADKIIAALPKMQPAPWNEAARAIMTDTVPKASREKVGVDQTVRATGIAGSGMIHNMATMLGFIATDAKVSQPVQLMTQELADETFNTITVDGDTSTNDSFVLIATGKNS  
QSEIDNIADPRYAQLKELLCSLLELAQAIVRDGEGATKFTTVRVENAKTCDEARQAAYAAARSPLVKTAFASDPNLGRLLAIGYADVADLDTDLVEMYLLDILVAEHGGRASYTEAQ  
GQAVMSKDEITTVRIKLRGQAAATVYTCDSLHGYVSINADYRS

## SEQ ID 7421

GATGCCGCGCAAGAGTTCGTTACGCTGGTTTGGCGCGGGTTTGGCGCTCCACGCGTTTGACGATGACGGCAGTAAAGGCTGTGGCTGCCGCTTTTGAAGGCAGGCTGCCGGACAG  
ACGACCGAACCTTGC CGGTACCGCGGCTTGGTAGATTTCGCTGTGGTACGCTGCAAGATTTTGGTGGATTGACCGATGAACACGCCCATCGAAATCACGCTGCCCTTCTTCGACAAATCGCGC  
CTTCGACGATTTTCGAAACGCGCGCGATGAAGCAGTTGTCTCAATGATGGTGGGCTGCGGCTGCAAGGCTTCGAGTACGCGCGGATGCCGACACCGCGCTCAAGTGGACGTTTTCGCC  
GATTTGCGCGCAAGAGCGACGGTGCCTCAAGTATCGACCATCGCGCTTCGTCGACGATGTCGCGGATGTTGACGTAAGACGGCATCAGCAGCGCGTTTTCGCAACAAAGCTGCCGCGT  
CGGCAACCGCACCGGAACTGCGCGGAAGCTGCGTTTGAATCTGCTTCAGACGATCGGCAATTTGGTGGCAGCTTTGTGCAAGTATTGTTCACGCGCTGTTGAGGACTTCGT  
TGTCTGGATGCGGAAGGACAGCAACACGCGTTTTCGCGCATTCGTTGACTTTCACCTGCCCCACGCCAAGCGTTCGCGACGCGCAGTTTGGCTGAATCGAGTTGGCGGATGCTTC  
CAACACGCGTTCTTTCGCTTCGCGGCAACGCTGCGGAGTATGTCGCGCGGTTTTCAGGCGGTTTCGATAATGTTTTCGAAAGACATAATGTTTCCTTGGTTCGAGATATTTCGG  
GACGCTTGGCGGTATTGTTTCAGACGGCATGCGGTTGGAACAAACGCTGCTATTGTGCCATACAAACGCGCGCGCTCAGCGCGCGCGCAGGCTTGCGBATGCCGCGCTTCGGAATCGGG  
CGGCGCGCAGGATATGCTTTTTCGCGCGCGCAATCAATACAGAAAGCGCGGTACTTTTATGCGCGACCGCGCGCTTTCAGACGCGCAT

## SEQ ID 7422

DAAQEFVHAGFGAGLRVHAFDDGTGKAVAAVFGRAAGHDDRTCRYAALVDFACGTVEFGGLTDEHAHRNHAAPFDNRAFDDFGRADAEVVFNDGGGLQGFYAADADTAQVDFVA  
DLRARADGRPSIDHRAPVDVADVDVRRHQHGVFNGKAAASGHRTRNCABCFELVFRPVGKPRGRFVFEVHVAVDFVFLDAEGQQHGFPRPFVDFPLAHQAQFDAQFA\*IELADGF  
QHGFFDFGNGGRSDVRAVFKGGFDNVLQRHNVSILRDISGRLEFVLFRHGWGNKRAIVPYKRPVSRAAGLPDAGVSESGRQAYVFFRANINTERRYFAAPPFFRRH

## SEQ ID 7423

TTGCTTTCCTCAATTTACTCTATTGTTTAAATCAATAAATAACAAAGTAAATCCAAATGAAGAACTAGATAAAATCGATTTCGCGCATCTCAAAATTCCTTCAGCAAAATGCCCGTA  
TCCCGATGACGAGCTTGC CGAGAGAGGTAGGTTTCCAGCACGCCGTTTACAGAGAGGATGCGCTTTGGAGCGGGAACATTATATTTCCGGCTATCAGCTCCATCTCAATCCCATCT  
GTTGGGCAAAACCGCATGCTTTTGTGAGCTGAAGCTGCAATCCAAATCGGCAATATTTTGAAGATTTCAGAAAGAGTCTGAAATTCGCAATATGAGGATGCCATCTGGTG  
TCGGCGAATACGACTACCTGATTAAGTACGTTTCCCGATATGCTGCTATCGGATATGCTCGGCAATATCTTATGCAACTGCTGCCGCTTCGAGAGTAGGAGTTATGTTGTGA  
TGGAGGAAGTCAAGAAATCCGGTTTGGATTGGAT

## SEQ ID 7424

LISQIYTLFVKINKYVIMKELDKIDFRILKILQONARIPTMTELAEKVGLSTPVTVERVRLEREHYLSGYHVLNPHLLGKPLVFLVFLKLSKSNIFEDFKKEVLKIPQIMECHLV  
SGEYDYLKVLRLPMSAYRDMNLNILLQPAASESRSYVMEVKENPVLDD

## SEQ ID 7425

ATGCAAAACCGCAGGCAAAAAAATCCTCGTTACCGCGCGCGCGGTTTATCGGCTCGGCGATGCTCGCGCATATATCCAAAAACCCGAGATTCCGTCGTCAACCTCGACAAGTAA  
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TGCGGTGATGCACTTGGCGCGGGAAGCCAGCTGACCGCGCATCGGTTGCGGAGCGCAATTTATCCGAACCAATATCGTGGCACATTCGACCTTCTGGAAGCTGCGCGCGCTTATGG  
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CCAGCCCTACTCCGCTCCAAAGCGCGCGCGACCACTTGTCCGCGCTGCGCAGCGGACTTACAGGCTGCCCTCCATTTGTCAGCAACTGTTTCAATAATACCGCGCGCGGACAAATCCG  
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CAGGCTGTTACCGAGGGTGTGTCGCGGAACCTTACAATATCGCGGACCAATGAAAAACCAATCTCGAAGTGATCAAAACATCTGCCGCTCTTGAAGAACTCGCGCGCGGAAAAAC  
CGCGCGCGGTGCGCAGGTATGAAGATTAAATACCTTTCGTACAAGACCGCGCGCGCATGATGCCGCTACCGCGTGCATGCGCGGAAATCAGCGCGGATTGGCGTGGCTGCTTTGGA  
AACTTTGATATCCGCGCTCCGCAAAACCGTGCAATGGTATTGGAACAACAAACCGCGCGGCAAAACGCA

## SEQ ID 7426

MQTAGKKNILVTGGAGFIGSAVVRHIIQNTDRSVNLDKLTAGNLESLETDIADNPYAFQVQIDCDRAELDRVFAQYRPDAVHMLAESHVDRAIGSAGEFIRTNIVGTFDLLEAARAYW  
QMPSEKREAFRPHISIDEVYDGLHGTDDLFTETTPYAPSSPYASAKAAADHLVRAWRTRLPSPVSNVSNYGPQFPKLIPLMILNALSGKPLPVYGDGAQIRDWLFVEDHARALY  
QVVTBGVVGTEYINIGHNEKTNLEVIKTI CALLELAPKPAAGVARYEDLITFVQDRPHGDARYAVDAAKIRDLGWLPLETFESGLRKTQVWYLINLKRQNA

## SEQ ID 7427

ATGATTCGCTTTTTCGCGCAATATATTAATGATAAACAAGGAACACACATGAAATTTACCAAAACATCCGCTCTGGGCAATGGCGTTCCGCGCGTTTATTCAGTGGCGGCACTGTACGCGG  
CATTTGTCGATTTGCTGTGGGTTTTCGCTACACGGGAACGACGAGCTGTCCGCTTCTATTGGCAGCGCATGAGATGATTGGGTTATGCGCGTCTGCTCATCGCTTCTGCT  
GACCGCGCTGCCACTTGGACGGGACAGCGGCCACGAGGGCGGCTTCTGCTGCGCTTACCGCTTTTGGCTGGCTGCGCGGATTCGCGCTTATCCGCGGTGGGCTGCGCGGCA  
AGCGGCATATCGGTACGCTGTTTCTGTTACGCGCGGCTGTCATGGCTTTCGCGCTTATCCGTTTCGCAAAACCGCGCGCAATATGTCGCGCTATTCGCAATATTGTCGCGGCTA  
CGCATGCGCGCTTCCACGCTCCAGCTGCACAACGGCAACCTAGGCGGACTCTTGAGCGGATTCAGTGGCGCTGTTATGTTGTCGCGCTTATCGCGCTGATTGGGATGAGGATTATTTC  
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CGCGCTCGGTATACGCGCAATTCGATTATCCGCGCGCAAGCGCTTCCGCTTGGCTTTGGCTGATGATGCGCGCAACCGCGCTCGGTATGCTGCGGTATTTCTTCCGCGCTGCT  
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## SEQ ID 7428

MIPPCKGYINDKQGTMKFTKHPVWMAFRPPYSALYALSVLLWPGYTGTHLSGPYWHHEMHWYAGLVVIAFLLTAVATWTGQPPTRGGVLVGLTAFWLAARIAAFIPWGAA  
SGILGLFFWYGAVALPVLIRSONRRNYVAVPALFVLGTHAAPHVQLHNGNLGLLSGLQSLVMSVGFILIGMRIISFFTSKRLNVQIPSPKVAQASLWPLMLTALMAHGVMPW  
LSAFAFAAGVIFPVQVYRWYKPVLEKPEMLWILFAGYLTGLGLLAVGASYKPAFLNLGVHLIGVGGIGVLTLGMARTALGHTGNSIYPPKAVPVAFWLMMAATAVRMVAVPSSGTA  
YTHSIRTSVLFALALLVYANKYIPWLIRPSDRPG

## SEQ ID 7429

ATGAGTGGCAACATCTTGCATCGCCAAATCAGAAGGGCGGTGGGCAAAACGACGACGACGGTAAATTTGGCGGCTTCCGCTGCGCATCGCGCGCAACCGGCTGCTGGTGGTGGATTGG  
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CAGCCATTTCGGGGATTTCCTTTTGAACCCGCAATCCCGCGCAATATCCGCTTTCGGAAGCGCGAGCCACGGTATGCCGGTATGGCTTACGACGGCAGGCAAGGGTGCCAAAGGC  
TATCTTGCCTTGGCGGACGAACCTGGCGCGAGGGTGTCCGGGAAA

## SEQ ID 7430

MSANILAIANQKGVCKTTTTVNLAASLASRGRVLDVLDPPGNATTGSGIDKAGLSGVYQVLGDADVQSAAVRSKEGGYVILGANRALAGAEIELVQRIAREVRLKNALKAVAEDYD  
FILIDCPPSILTLTLNGLVAAGGVIVPMLCEYALEGISDLLIATVRKIRQAVNPDLITGIVRTMYDSRSLVAEVSEQLRSHPGDLLFETAI PRNIRLAEP SHGMPV MAYDAQAGAKA  
YLALADELAARVSGK

## SEQ ID 7431

ATGGAACGTAAAGAACGCTCGCTGCAGGCATTGCCGCGATGGGCGCGATATTTCCGAAAACGGCGCAGGACAGGCTTTTGGCCTATGTGGATTGTGTGAAAAGTGGAAACAAACCTACA  
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GCCCGCATTCGGCGCGCGGTGTGCCGTCCGATGTGCAGATAACCTTTGTTGGATGCCAATACGAAGAAAACGGCTTTTTCGGCGAGCGGCTATCGAGTTGGGGTTGCAATGTGGC  
GTGGTGTCCGGGCGCGTGGAGCGGTTCGCGACGTGCGTCCGACGTGTGTACAGCGCGTGGTTTTCGGAAGTGGCGGATTGTGTGTGTGGAGCGCGCACTGTTGAAAGACGGCGCT  
ACTGGCGCGCATGAAGGCGGTATATCCGACGGGGAAATCGCGCGCTGCCCGAGGATGTGTGCGTGAAGAAAGTCCAAAGGCTCGACGTGCCGGCTTGGATCGGAACGCCATATCTGT  
CATCTGAGCAAGCGT

## SEQ ID 7432

HERKERLRAGIAAMGPDISETAQDRLLAYVDLLKWNKTYNLPALRDEEKIVHLLDSL/LLPYIEGAQTMLDVSGGGQPGIPAAVCRPDVQITLLDANTRKTAFLRQAAIELGLONVR  
VVSGRVEAVSDVRVVTSRAPAEALDFVSWTAHLKIDGGYWAAMKGYVPGIEGRLPQDVCEKVRQLDVPGLDAERHIVLSKR

## SEQ ID 7433

ATGCCGTCTGAAGCGCGCTCAACGCTTGTCTCAGGATGACGATATGGCGTTCGCATCCAAAGCCGCGCAGCTGAGCGCTTTGGAATTTTTCGACGACACATCTCGCGCAGCGCGCGGATT  
TCCCGCTGCGGATATACGCGCTTCATCGCGCGCCAGTAGCGCGCGTCTTCAACAGGTGCGCGCTCCACGACACAAAATCCGCCAGTTCCGCAACGCGCGCTGGTAACCGCTCGGCAC  
GCACGCTCGGAAACCGCTCCACGCGCGCCGACACACCGCGCATATGTCCAACCCCACTCGATAGCGCGCTGCCGCAAAAAGCGGTTTTCCTGATATCCGATCCAAACAGGTATCTG  
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CGCAATGCTCTGACGCGCGCGTCTTTACGTTCCATATCTGCTTCTGCTCATATTCAGGCGTAATGTAGCGGAAAACATGCGCTGTAAGAACCGGTATCGGTTTCAGACGCGATT  
CGGTTCGCTCTATTTTTCCTGTGGAACACACAGGCTGCACCGCGCGCGCTCAGCGCTTTCCGCGCGCTCAGCA

## SEQ ID 7434

MPSEARSTLAQDDMAFRIQARHVEPLDFFDAHILRQADFLIRIYALHRRPVAAVFQVRRPRHKIRQFRKRTAGNHVQTHVRNRLHAPRHHAHVOPQLDSRLPQKSRFLIRIQQGYL  
HIRTAAHRRNRAGLAARATDIQHELCAFDIGQQRQAVQKMDNHFPLVAQGGQIVGVPLFQQIHIGQKPVLRFRNIRPHRGNACTQAFPTFFHICPLSIFRNVSGKTCRLKPRIGQPTAF  
PFRPIFCGTPQAAPARASGVSAASA

## SEQ ID 7435

ATGGTATTTGGACAACAAACCCGGCGCAAAACGCATAAACGGCAACTGCCGTTCGGAACGCTTAGGTACGGGCAAAATAGTTTTCAGACAGCATCCGACGCAATGCCGCTGTGAAAAC  
CATGCGCAAGGAAGAAAGAAAGATGAAAGGCATCATCTGCGAGCGCGCAGCGGTACGCGCTTATATCGATTACGCGCGCGGTATCCAAACAACTGCTGCCCGTGTACGACAAACCGAT  
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AACCCTACGGCAATACCTGCTGCGCTGATCGGCAAA

## SEQ ID 7436

MVFGQONPAKRIKRLPFGTLRYGQIVFRQHPDAMPSENPSQRKKEKMKGII LAGSGSTRLYPTITRGVSKQLLPVYDKPHIYYPLSLVLMLAGIRDILVITAPEDNAAPQRLLDGSDFGI  
RLQYAVQSPDGLAQAFIIGEEPIGNVCLILGDNIFYGQSFTQTLQAAARTHGATVFGTRVKDPERFVGVEVDENFNALSTIEEKPPQPSDWATGLYFHDNRNRAVEFAKQLKPSARGH  
LRIIDLNRMYLEDGSLSVQILGRGFANLDTGTQESLHEAASFVQVQNIQNLHIACLERLAHRNGWLTKKDVTETRAKPLEKTATGYVLLRLIGK

## SEQ ID 7437

ATGCCGCTCGAAACCGGATATCGGGTTTCAGACGCGATTTCGCTTCCGTCTTATTTTTCCTGTGGAACACCAAGGCTGCACCGCGCGCGCGCTCAGCGGTTTCGCGACGCTCAGCATAG  
ACACGAGCCACAGCGCAACAGCATATTCGACACCGCGCTCCCGCTCAGCGCGCGCAAGCGCGCACTGCCCAACACAGCTTGAAATCCAAGCCACCGCGCGCAAGCGCGCACCGCGCA  
CAGAAACAGCGCG

## SEQ ID 7438

MPSETAYRVSDGHSVPSTFPLMNTTGTGARVRRFGSVSIDSHTANAYSDTASPLSPPKAALPNNSLKIQATAAQAATPDRNSA

## SEQ ID 7439

ATGAACCGGTTGAAACGACATTCGCGCTTGTGCGGCTTTTCGCGGCAACACCACTCGCTTTCCCTGTGCGTGTGCTATGTTTCGGGACGCCCGGGGACGACCATGTCGCGCACTCGAGC  
TGCATTTTTCGCGAAGTGGAAACCAATTTTCGCGAAGAAAGCAAGTTTTCGCGCAATTTGCGCAAGATGTCGCGCTGAGTTGAAACCGGTTTGAAGCGGATCAGCGCAACTCGCGCA  
GATGATGCGAAGCCCGAATCGGTAACGCGCGTGAATACCGCTTTTTCACACACCTGCGCGACCAAGCGCGCTTTGAAGAACGCGAGCTGTTTCCGCGCTGCAACCGTTTTCGCG  
GCA

## SEQ ID 7440

MKPLKRHSALVGLSREHHSLCVRMLRTPGADHRAELHFAELETHFREERKAPATHQNVAPELKTRFEGDHAKLRQMHASPECGNAANNATFATTLRDHARFEERELFAVEPFLP  
A

## SEQ ID 7441

ATGATATATATAAAGGTTGTGTTGCAACTTTTCGGCGCGCGCGCAAGCGGTCGCGGTATATGCGGCTGCTTCGGAAGAGGGGGACGCGCATGTTGTGAACGAGAAATATCTT  
ATGCGACCGCTGTTTGGCGGCTGTTGTTTTCGACGCTGCGGTTTTCGCTTGGCGGTCATGATGCTTTTGCATGTGCGTTGCGACGGCGGGCTGCTGTTGCTGCTGCGGACGCGGATT  
CGCGCGGCTGCGGCTTGGGACGCACTGTTGTTTGTGTTGCTGTTTTCGCTTTTGAATGTGTTGTGTCGCGCGGCTGACGAACTTGGCTACAAAAGATGATGCGCGGCT  
TCGCGTTACGCGCTGTTTCTGCTGCGCGCTGCGCGCTTTCGCGCGCGGCTGCTGATTTTCAAGCTGTTTGTGGGCACTGCGCGCTTGGCGCGGCTGAGCGGGAGCGGCTGCGGAATATG  
CGTTTCCGCTGTTGCTGTTGCTATGCTGACGCTGCCGAAACCGCTGACGCGCGCGCGGTCAGCGCTGTTGTTTCCACAGAAAAA

## SEQ ID 7442

MIYINGCLNFSGGRGGARYNAACFGRGGTAHFVNEKYPYATLPAGLVFLTLPLALAVHDAFACAFGRAGLLVSVSDGGFGRRGGWGTGVFVGVFAFLNVVVSAGLTKLAKKMRHH  
SRYALFLSGVAACAAVAHIFKLLLSAALGSLGSAVSEYAFVHLVSMILPLKRLTRAPVQVVFVRRK

## SEQ ID 7443

ATGGACATCATCGACACCGCGCTCCCGACGTAAACCTTTTAAACCCGCAAGTCTTCACAGACGGCGCGGTTTTCCTATGGAACATTCGCGACGCGGTTTCAAGAAAAATATGCGG  
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CGTGGCCGTGATATGCGCGAAGGTTCCGCGACTTTCGGCAAAATGGGCGGGCGCAACCTTGTGGCGCAAAACCGATACAGCTTTGGATACCCGAAGGCTTCGCACACGGTTTTTGGGTT  
TTGGCGGACCGCGCGAAGTCGTGTACAAATGCACGACTATTACAAACCTGAAACCGAACAGGTTTAAATATGGAACGACCCGGCAATCGGCATAGCTGGCGGCTTCAAAACCGCGCGC  
TACTTTCCGCGCAAGACCTTGCCTGGCAAAACGTTGGGCACAAGCCGAAAGCTCCGCTTACGCTTTCCCGA

**SEQ ID 7444**

MDIIDLTPDLVLLKPVQVTFDGRGPFMETFRDGFKNIAIDRTFVQENHNSXKGLRLGLHYQTENTQGLVRIIVGVEFVAVDMREGSPTFGKNAGATLSAQNRYQLWIEPFGAHGFCV  
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**SEQ ID 7445**

ATGTATCTGACCCAAACATACGACTACGGGCTGCGGCTCTCATCTACACCGCGCTCAACGACGACGCGTGGTCAATATCGCCACCATCGCTCGACCTACGGCATTTCCAAAGCCATT  
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CCTCGAACCGATGACGCTGGTGTATGGGCCGAACAGATGCTGATTACGCGCTGCGCGGCTGACGGGCATCTCGCGGTGCAATGAAGTGGTTTTTACGCTATCTGGAC  
GGTTTACGCTGCAAGACCTGCTCAACAGCGGACCTACGACCTGCTTTATGAATCGAAAAATCCGATTCGGGTGCGA

**SEQ ID 7446**

MYLTQHTDYGLRVLIYTAIVNDALVNLIATISTYGISKSHLAKVVTALVKGGLFHSVRGKGGGLRLAAPPERINIGAVVRHLEPMQLVECMGPNNECLITPSCRLTGILGGAMKSFPTYLID  
GPTLQDLNKPFTYDLYESKIPIAIVR

**SEQ ID 7447**

TTGCACAAACACCGTTTATATATATACATAACGAAAAACCGGCTGTAGCTCAGTCGGTAGAGCAGCGCATTCGTAACCGCAATGTCGGGGTTTCGATTCCCTTCTCCGGCACCAATACCA  
AGCAGACACCTCCCTCGGGAAGGCTGTGCTTTTTCACATTTTCGCTTCAGACGGCATTCGATATGAACCTCTCGCAACGCAAAACGCTTTCCGGCGCTGGCTCAACTCTACGAAGCGT  
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CGCGCGCGCATCGCATCGACCGGCTCAACCGGAACTGGAAGCGCTCGCGCAACCTCACTACCAATGCGAGGCTTCTCTGGCTCAGACCAATATGCGGTGAGGAATTTCC  
GCCCTGCTATCTGCTGCAACGCAACCGCGCAAAATGGCTGGATGCCCGCAAGCCAAACCTGCGCGCAAGCGCTGCT

**SEQ ID 7448**

LHKQFFIYIITKNAGVAQSVQRIRNANVGGSIPIPSGTWTKHRPSLGPVLFHISASDGIRYELLATQTPFRPLAQLRLTLPPLPHTCRAARRNRFVRHRTPATPPPTRRMDRDLRR  
PRHAPVPRDLIQGGGTARYGHARGFGRFMAEPALPRQPLPDLPHRHGKTRLRGGGRQRLRYPYAGADDVHAHRQRQRMARQRPDARDERPHRRHRHCRQTAABEIHDTVAF  
HACRQPRGLQNDNRNQRQAYDARTFGAEYQNAAPNORTHGQKPPRRHIGRKHPOPLHDGSHAARPQNRQHRAAPDHRRAAISQTRQRNPAARPLHTAPNRPATNRRPHQRQT  
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**SEQ ID 7449**

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CCAAACACGGCGAATGGATAGGATGACCGTCTTCTGCTCTCGCATGCTCCAGTTTCAAGGCGCGATTACTCCAAGCGGTGGAACGTATGCTCGGTACGGTCATCGGGCTGGCGCG  
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AAACACGGGAACACGGC

**SEQ ID 7450**

MSGVRFPSPAPIPSTDPSPGSLCPTTFLQATSDMNSSQRKRLSGRWLNSYERYHRLITHAVLGGTVLFATALARLLHLQHEWIGMTVFVVLGMLQFQAIYSKAVERMLGTIVIGLA  
EGVLWLNQHYPHGNLLPYLTIGTASALAGAAVGNKGVVPLAGLTMCMLIGDNGSEWLDGLMRMNVLIIGAAIAIAAAILLPLKSTLMWRPMLADNLADCKMIAISNGRRMTRERL  
BQNMVNRQINARHNSRSHLAATSGESRISPSMMEAMQHAHRKIVNTPELLITTAAKLQSPKNGSEIRLLDRHFTLLQTLQDTAALINGRARRIRIDTAIPELEALEHLHYQWQ  
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**SEQ ID 7451**

ATGCCGCGCGTATCGCGCCCGGTGGAATATCCGTTTGAAACGGCAACAAATGCGCTCCGAACCGGGTTTGGCGGCAATTTGATGCGTTATCGCACCGCAATCGGGATTTTCGATT  
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**SEQ ID 7452**

MPARIAPGRNIRLKRQTKCRPNAGLGGILMRYRTAIGIFDS

**SEQ ID 7453**

CCTACCGGCTTTCAGTACGCGCTGTGCAAGAAACATCCCGGTAAAGCAAGACGCGCAAGCCCAACCAAGAGCGGCGCATCCAGTTTTCGAGATTCAACGCGAGCGCGCATCCGAG  
CCGCGCTTGTGTACAGAGAAGGCAATAAAGCCCAATATACCAATCAGGCTTTCACCGCAATCAGGCTTCCGCGGCAAAAGCTACCGATACGCTCGGCTTTTCAGACGGGCTT  
CGCGGTTTTCCGCTTTCGCAATGATGTGTTTCAACACCGCGCAACACCGCGCTGCCAGATAGCGGCAATATGACGCGAGCGGCGAGATAATGCGCATACCGACCGCAAGGACGG  
CAGGCAAGTTTACCGCTGATGATTTTTCAACACCAATCGACGAGATTAATACCGCTTCCAACTCGCGATACCGGTAAAGATGTACGCCATTTCGAGGTTGTGGGCGAAATGCCCGAC  
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AATATTGCTGCCTTTGAAAAATTTTAAACCGCCATCGAAATCACCAGCCGCCGAATCGACAGGCAAGGTCAGCCGACTTTCAAACCGAGGTAACGCTAGACGCAGTAAATAATPACA  
GTGATCAATGCGCCGAGTATCAT

## SEQ ID 7454

PTRLQYALCKEHPGNEERQAQPRSGGIPVLQIQERRIRAAVGHREGNNKRHNYTNQAFDTNQAQREKRTDVGVPQTAFVFRLLANDVQHRHQHACHDGHIDGRRQINAHTRDKOG  
QKQFTA\*\*FFQHQIDDD\*YRNRDITGKDVRFPEVVGENARRNGRHQSRLKGCQSLRRIHAFARHCAGKAVGVFKQFQHGRRNQRTNDTADNGDLLPPRRSFQVAGPQVILQVVVGNRSHA  
DYCRSAKKRQRO\*EFAVGLIRQOTSGFAYQQNQ\*\*NNDGDHDAHAGNRAGRRADQCHITAGGGDQKADDQSQRANRHOKEPRHAARNVRIADKVVKRHA\* NKHHRQHPEHNGFRQILFG  
APCSGRTAARTLERHLIAFHHLLEQHQRPNRRDTYGSRTDKTHFFLPQLHRKRRHFHIGRLRN\*GEIRHGNTPSNRNAQDGDAAARQSDQITRAQQGQ\*KAYRQLENCRTAFKPIITRAI  
GNHTQTSGARAHQSRQRAAGRLFDYAAALTVIPFMTAHFQNFSSRHTFRIQLAFHHHVPQNRNGENHPQNPAGAT\*KRRLPKRETAFAVHQBQTDQDEDDG\*KRTSRGLGLHHVVFQ  
NIAAPEKP\*NRHRNRNRNRNRGKQDFDQTEVNVRRSKNYSQCAEYH

## SEQ ID 7455

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ACGTGAAAAACGACTTCATTCACCGCCGAGTATGCGCGTCAGCGGCGAGGCGGTAATCAGGCATTCGTTGTTGCGGCCATACACTCGACGAGCTGCATCGGTTTCAGGTCGCGCGAC  
GACCGCGCGGATTTGATCGGTTTCGGGCGCGCGCGCGCTCAGCGCGCGCGCTTTCGCGGTACGCTGTGCAAGAACCCGCTTTGACGAGCGCGTAACCACTTCATCAAAATGGCTT  
TTGGAATGCGCTAGGTCGAGCGGATGTTGGGATATTGACACGCGCGCTGCTGTGACGCGGTTGATAGGAGCGCGAGCCCGTAGTCGGTATGTTGGGTCAGATACATGATTTCT  
CGGTATGATCGCTTATCTTATCGGTACGTTTAACTTTCACGGAATAACCTTAATGTTGAAACCTGTCGCTCGGGCGGTAGAATGAGCTGTCTGCGCGGTATGCGCTCGAAA  
CATCGCGCTACCGCTTGATAATTTGTTATTTGTAACCTAAATTTA

## SEQ ID 7456

MPSEASAVQTASRALPAAARNAGAYRARSEYFETANKMPSEGFGRHFDALSHNRDPRFIQVVGRLVEQVLRQRTVQIREKRLHCTAEYARQFAGRRNQAFVVRATLDQLHRFEVAD  
DRADIDAFGRGQFPAAFPAYAVQEPAFDQGNHFMQAFNAVGRGDDGIDQVVDVGGVDEDAQPVVGLGQIHDPLGMDRYSTRYGLSFTENTLMVETLSVGAECCLSAVAVCLK  
HPRYRLIICYCNLNL

## SEQ ID 7457

ATGCCGCGAGCGTCAGTTCCGCGTATTTTCTACCGAACCGGATAAGATTATTCATTATTTCTTCTTGCACACAGCGTTACATATTTGTTGGCATCAGCCATGATGTCAAGTTT

## SEQ ID 7458

MPRSVSSRYFSTEDKDLFIILPI/PTDVHILLASRHDVFP

## SEQ ID 7459

TTGGAAAGCAATATATCAGAAAGCAAAACCGCTTCTACCTGAAAACCTGCTCTGCGCTGAAGACACAAGGTTCTTTAATATTT

## SEQ ID 7460

LGRQLYQEKQTAFLPENCSSGLKQGSLLP

## SEQ ID 7461

TGTTTCGCGGTTTTCGCGTCAGGTTGACAGCCATAACGGTTCTCTTTCGAGTGTGTGCGGCTTCAGACGCGATGGGTTGAAATGCCGCTGAAACCGGTTCAGAACCCCAAAACGGGG  
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TGCGAGCGCATATCCACCGAGCAGGGGATGACGACCGTGTCTTCAACATTTTGAACCGCAATCTGTCCGACGAGCGCGCAATGATGACGCTGCGCGCGTAAATGCGCGGAATGCC  
GCCGATGAGCGCGGTGATTCGATGCGCGTGGGTTGGTAACGATTTGACGCGAGCGCGGAGGAGCAGCTTCGCGTTCCGCGCCAGCCACTTGGCAAAATACATCCCGTAACAAATGCC  
GTAACGCTGCGCGCAGCGTCTGCAACGATGACGCGCAGCCACTGGTTGAAGATTTTACGCGGTTTGTAGACGCGCAGCGCAAGCAGCAGCGCGGTTTTCAGCGGAAATCAATGA  
ATTGCGCGCGGTTTGTGTACACCGCATAATCGATACCGAGGATTTTACAGGTAGGCAATCAGCAGATAGTCTGACGAGTACCGGGTTGCAAGATATGCGCGTGCAGCGAT  
AATCGAAGCGGTACACGCGCAGCGTGAAGAAAGCAGAACGCTGGGCTGCGTGAAGATTTGCTCATCAGATAATGCTCCGTATCCAGCGG

## SEQ ID 7462

LFPGFFGQVDSHNGSPCECVGQTAWVEMPSETGSEPQNGDKQRNRQGHQHAVERQPHPRVCRHAAAFERGGNAHRVRSRAERETHGRGHDDRVLQHFVTGNLSQDGTGNDGGGGNGNA  
ADGAGDFDGDGVGNRFRGEREDDFAPRAQPLGKHPRNNARNAARKLRNDGQPLVEDFTAVLWERHGHKDDGGFPKINELRGVVVRIIDTDFQVGNQHDSAEYGAEDTARARAHD  
NRKRVHGRKREKQNAAGLPEDFAHQIMLRIGR

## SEQ ID 7463

ATGAACATTAATCGATGCCATCATCAATTTGGCTAACCAACCTGTGTGCGGGTCACTCCCATTTCTCAAAGCAACATCGTGCCATCAGGCAAGTGATGCTTTGGAAGAATATGTAAG  
ACTTGTTCGCGGAGTTTCAACCTAAATGAAACCAACGATAGCCGACGCAAAAGTATTTCTCATATTTGGGCAACATCCAACTCTGTATGCCAATGTTGCGAAACGGGATGC  
CATCGAAGTAAGAAAATGAAAGTAAAGATTCCGCACTGGCGTGAATAGCAGCCACCAAAATCAAAGCTCTCTGTTGATGACAGCATGCTTCAAAAGCCTGCAAGATGCGGAAAAA  
TGGGAAGAGAAAGACATTATCTATAATTTGTCGCGCTCGT

## SEQ ID 7464

MNIIDAIINLANNPVVGNWSHQSNNRANQAGDALEETVKDLFGSPNLNETQRIARHAKVFSYLGNNSNPDMANLNGDAIEVKIESKDSALALNSSHPKSLSVDDSMITAKCKDAEK  
WEEKDIIYNCRRR

## SEQ ID 7465

ATCAAAACAAATCGCGAGCTTGTCTAAAAACGATTTCTTTCGCGCGGTTTGGTTTTCAGCCCGTAGAAATCCGCTCAAAATCTTCCAAAAGCTCTTTTTCAGCGTTCGGTCAAAATGACA  
GGCGTTTCGACAAACATATGGCAGTACAAATCGCGGTCGCGCTGCTGCGTAAAGATTGACACCTTACCTTTTCAGCGCATCTCTGCGCGTTTGGGTTCTTTGGGACGGTGAGCT  
TGACTTTGCGGTCGCAAGGTCGCGACTTCTAATCCCGCCCAAGCAGCCATGCGCAAACTAATCGGAGTTCGCAATGCAAAATCCAAACATCGCGTTGAAAAATCTTATGCGCCGGAAT  
GCGGACGGTTACATACAGGTCGCGGCGAGCGCGCGCTGCATACCGCGCGCGCTTACCGCTCAACCGGATACGCTGCGCGTATCGATACCGCGCGGAATATTGACTTCCACCGTCTTG  
ACCGCTTATTTCCGCGCCAGCGCAGGCAATTTGACGCAAGGTTCTTTAATATGTTTGGCGCGCAGCGCGGCGAGGTCGCAAGTCTGCTGCATACGGAATATGCGCTGCGATGTCACCG  
TACCGCAACCTTTGCAAGTTCGCGAGGTTTCCGCGGATGCGCCGCTTTCGCGCGCTGCGCTGCGAGACATCACAGCTTCATAAGTCGAATATGATGCGTTTTCACACCTTTTCG  
GGCTTCTCAAGCGGATTTGATACCGACCTGCGAGCTCTCACCTGATTAATCAGGCTGGCGCGCGCCGAAACCACTTCCAAACATTTGGCTGAAAAATATCCCAAGTCAAAACCTGCG  
GCACCGCAAAATCCGCAACCTTCCGAGCGCGCTTTCGCGCGCTTCAAAACCGGATGACATACGCTGCTGATGCGCAAGCTTTTCTTTCGCGCAAAAGTTTCATACGCTTTT  
GTACTTCTTTAACTTCTTCTTCCGCTCTTATTTGTCAGGATTCGCGTGGGATGATTTTCATCGCAATTTAGGTTAGGCTTTTAACTCATCATCGGTAGCTGCTTTCGCCACAC  
CAGCGTCGCAATAAATCTGATTACTCATTTTTCATCTAAAAATAAATAC

## SEQ ID 7466

IKQIAQLV\*KRFLARRLVQARRNPLKFFQKLFITVGGIDRRFDNNMAVQIAGRAAA\*RFDTLTFHAHPAGLGFPGDGLDFAVQGRHF\*LPQSSHGKTNROFAHQIQTIALENLHFPN  
ADGYIQVAGRAVHTRPAPTAQTDTLFVIDTGNIDFHLRLDRIIPHATAFDARFNNMARTAGRTSLHTENRLLDVHRTTFASRAGFRGCPFRFAAAVADITFISRNIDAFHFFC  
GFFKRDPDTHLVTLIRLGAPRTTSKHLAENIPKVTLLRTAKSAKPSAPLSAAPKREMTILVHGTFLVWGQSFIRLLYFFKILLRFLIVRIAVGNVFRQFVGVFNLIIGSCSCHT  
QRRIKLITHPFI\*K\*NH

## SEQ ID 7467

ATGACGATAAGGAAACAAACTATGGCACAATTTTGGCCGTTTATCCCGACAAATCCCAAGAACCCCTCATCAAGCAGGCAGTGAATATCAATCAAGGCGGCGTGGTGGTTTATCCGA  
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GTTGGGCACATACGCCCAAAATCGACAACTGACAGTTTCGTGAGCTTAAAGCCGCGACGCGCGGCGCTTATACCTTTATCTTGCAGGCGACGAAGGATGCGCGCGCGCGCTTCACCCG  
AAACGCAAAACCATCGGGCTGCGTATTCGGATAATGCCGTTCACAAAGCCCTGCTGAGGAGTTGGCGCGGCGCTTTAAGCTGCACCTGTATGCTGCGCGAAGACGGCGAACCATTTGA  
CCGACCTTTATGAAATCCGCGAGCGTTTGAACACGCGCTGATTTGGTATTGACGGCGCTGGTGGGAACCGATCCGACTACCGTATCGACATGACCGACGGCAGGAACTGGTGG  
CCGCGGTTCGCGGATACGGCGGTGTTCCGTTG

## SEQ ID 7468

MTIRKQMAQFFAVHPDNPQERLIKQAVEIINQGGVVVPTDSCYALGCKLGDKAAMERILSIRKIDLKHHLFLMCADLSELGTAKIDNVQFRQLKAATPGPYTTFILQATKDAPARALEP  
KRRTIGLRIPDNVAVALLEELGGPLLSCTLHLPEDEPLTDPYERIRLEHAVDLVDGGWCGTDPTTVIDMTDGTGLVRRPGDTAVFGL

## SEQ ID 7469

ATGAGCACCTTCTTCGCGCAAAACGCCCAAGCCATGACTGCCAAACACATCGGCCGCTTCCCGCTATTTGGAAGTTGGACCGGTGATTGATTGGCAGCCGATCGAACAACTACCTGAACCGTC  
AAAAAACCCGTACTCTCAGAGACCGCGCGCGCGCGCGCTATCCCTGTCGTCATGTTCAAAGCCGTCTCGCCGCAATGGCACAGCCTCTCCGATCCCGAATCGAACACAGCCT  
CATCACCCGCATCGGTTTCAACCTGTTTTCGCGTTTTCAGGACCGGGCATCCCGGTTCAGCAGCCTTATGCCCTACCGTAAATTCGCTATGCGCGGACGCTTATTCGGCTGCTC  
AAAGTGGGTGCGCAAGCCACCTGAAGCGGATGTGTTGAACCTGTTGAAGCCGCGCAACAGCCTAAGTGGCGCCGCTGCGCGC

## SEQ ID 7470

MSYFRQTAQAMTAHIGRFPILLELDQVIDWQPIEQVILNRQKTRYLDRGRPAYPLSSMFKAVLPQWHSLSDEPEHSLITRIGFNLPCRFDGPGIPGCTLCRYKFRYARAAYFGLL  
KVGAGSHLKAMCLNLLKANRLSAPAAA

## SEQ ID 7471

TGCGAATGGTTACGGAATGACTGCTGCGCGATGCCGAATGCTATTTGAAGATAAAAAATCAAATTAAGGAAGGAATCGGCAACATCGCGCGCATACAGTTTTCAGAAACCAAGAGC  
TGGCGAGGTCACCGCACTGATCCGCTCAACATACTATCTGAGAGTACGGGTATGTTGGGGAATCGAAATCCATGTTTGTCTTACAACTATATTTACCAACGGAATATGGAAGAAAG  
TTTCAATTTTCAATGCGCATATCAACGAAGACAAATGGAACAGTTTAAACAATACAGACAAGCTGCTTGCCATACAGGATTCCAACTGCGCATTTCCGACATTAATAATTAATAATCCCAAC  
AACCGCGCGATTAAGAAATGCAAACTCATCACTACCACTTA

## SEQ ID 7472

LAMVYIDYCADAEYLKIKNQIKEGIGNIGGIQFAETKELGRVNRIDPLNITLVRVMWGIENPWFVFNITQYRNMEKSFNFMALINEDKWNFPNTDKLLAIQDSKLAISDIKIKNP  
NPARLENAKLITPHL

## SEQ ID 7473

TGCGCGGAAACAGCTGAAACCTGTGTTGGGTTTCGCGCTGCGAAGGAAGGCTTTTTCGAAAGGTCAGAAATGCCAGCTTCAAACTGAAACGGAATACACTTTTCAGATATG  
CACGACACAAAACCTTAGATAGGTATAAAACCAACCGCAT

## SEQ ID 7474

LGRKQLKTCVWVSABGRAFLQRSQATAYKLKRNILFRYARHKNLDRYKTNRH

## SEQ ID 7475

ATGCAAACTCATCTACCTTATATCTATGAAATCATTAATTTGTTTTCGCGGTTCGCGCGTTTGGATTGGGTTTCGAAAAAGCGGATTTGAATCCCGCGCGCAACGAAT  
ACGATAAAACCATTTGGGCAACCTTCAAGGCAAACTTCAAGAGCCATTTGATAGAAGCGGATACGCAAGATTAAAGAAGAAGATTCCCTGAAGAAATCGACGGGATTATCGCGG  
CCCACCTGCGCATCTGCTGTAAGCGGAGTTTTCGCGCGCATCGAGTTCGCGCGGACAGTTGTTTTCGACTACATCCGTATTTTGAAGCAAAACAGCCAAATTTCTTTTAGCG  
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TTGGGATTTCGAGGACACAGCGTACCTTTCGCGCGCAAAACGAAGCAACCGCGAGCGATCAACCAACGAATATTTTACCGCGAGTTTTCCTTATTTTATGAGCGCGGAACCGA  
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AAGAAACATATATCGAGGATGACGCTACGGAAGTGCAGAAATCCAGGCTTTCGCGCAACTTCAATTCATCTATCAAAATGTCACAGCGCATCAAAATGATTGGCAACGCGCT  
CCCGCTCAACCTTGCTACGAAATTCAGCGCGCAATTAATAAACCTTAGAAAG

## SEQ ID 7476

MQNSSTPTYNPMKIIISLFGCGGLDLGFEKAGPEI PAANEYDKTIWATFKANHPKTHLIEGDIRKIKEDFPERIDGIIIGPPCQSWSEAGALRGIDARGQLFFDYIRILSKQPKFFLA  
ENVSGMLANRHGAVQNLKMPDGGYDVLTMANAKDYGAQERKRVYIFGFKDLEIKFSPFKSGTVDKDKITLKDVTMDLQDTPAVSPQNKTPDVAVINNNEYPTGSPSIPMSNR  
VKAWDEQGTVOASGRQCQLHPQAPKMEKHGANDYRFAAGKETLYRRMTVREVARIQGFPDNFKFIQNVNDAYKMIIGNAVPVNLAYELAAIKKTLER

## SEQ ID 7477

ATGTCGACCAACTCATCTTGTCTGAACTGCGTCAGTTTCATCGCTCAAAGCGCGCTTATCGACCGCAAAAGCGGACGCTCGCTTAAAGTGCCTCGGGGAACGCTGACTACGCGG  
AAGCCGTCAATACCTTCAACAAAGACGGCAACAAAGCCAAAGTTCCTTCAGCGCGCGCACTGCCACGCGCGCGGCGGTGGTATGCTGTTGAACGAATGGAAGAACAGGATGACGCA  
CCGATCAAGGCCATCGCGCGCGCATCGCCACGCGCGCGGAAAAATATCACGAGTCCGCTCATCGACCAAGACGCTCTTGACGAACCTGAAGCGCTGCATCCCGTTCGCCCGCTGCAC  
AACC CGCAACATCAGCGCATCTCGCGCGCGCAGGAACACTTTCGCGCGCTGCCAACGCTCGCGCGGTGATGGACACTCGTTCACCAAAACCATGCGGAGCGGGCTACACTTATGCGG  
TGCGCGCGCAATTGCGCAAAAAATACGCTTCCCGCGCTACGTTTCCACGGTACCGGTATCGGTTACGTCGCCCTGAAGCGCGACGATCTTGGGCAAACTCTGGAAGACATCCGAT  
GATTATTGCCCACTTAGGCAACGGCGCATCTATTACCGCGCTCAAAACCGCAAACTCCGTCGATACCGGTATGGGTTTCAGCGGATCGAAGGTTTGGTAAATGGGTACAGCTTTCGCGGAC  
ACCGATTCGCGCGCTATACGCTATCCGACTTTCACGCGAGGATGATGTTGCCCAAGTTGATGAAATGCTGAACGAAAAATCAGTTTTCGCGGTATTTCCGAACCTTCCCAACGACTGCC  
GCACCTCGAAATCGCGCGCAGGAAGCGCGCGAGCGCGCGCTCGCCCTCGAAGTCATGACCTGCCCGCTCGCCAAATACATCGCTCGATGGCTGCGGCTGCGGCGAGTTTACGCG  
ACTCGTGTTCACCGCGGTATCGCGGAAACCTCGCTAATATCCGTCGCAAAACCGTTTCTTATCTTGAATTTCTTGGGTCTGCACATCGACACCAAGCCAAATATGGAAGAAACCGCTACGCG  
AATTCGCGCATATACGCGCGACCGATTTCTTCCGCGCTGTTTGGTCTGCCGACCAATGAAGAACTGATGATTGCTGCGCACTGCCGAATTCGCGCATCTTG

## SEQ ID 7478

MSDQLILVLNCSVSLKGAVIDRKSQSVVLSCLGERLTTPAEVITPNKDNKRQVPLSGRNCAGAVGMLLNELEKHGLHDKAIGRRIAHGGEKYHESVLIDQDVLDELKACIPFAPLH  
NPANISGLIAAQEHFPGLPVNGVMDTSFQTPPERAYTAVPRELRKYAFRRYGHGTGMRYVAPEAARILGKPLEDIRMILAHLNGASITAVKNGKSVDTGMGPTPIEGLVMGTROGD  
TDPGVSYPTPHAGMDVAVQVDEHLEKSGFPGISELPNDCRTLELADEBREGARLAEVMTCLRAKYIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDLFLGLHDTKANMEKRYG  
NSGIIISPTDSSPAVLVPTNEELMIACDTABLAGIL

## SEQ ID 7479

TTCATCGATTTCATTCGCCGATATAGCGAGGCTTCTTCCAGCATTTCCTTCCAAACAAAGAACAAAAAGCGCGCGCGGACGCGATGCCCTTCTTACAGGTTCCCTTATTTT  
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AGACTGAACGCGCGCTTTTGGCGCGGTATTCGCAATGGCTTCGCGCGGCTATGCGCGCGCGCGCTCCAGCTCTGCTGCGAAGCGCATTTGATGTTTACCGCGCGCAAGGAGAG  
GCGCAGGAGACAGCATACAGAACATACAAACATTTTTCATGTTTTCCTTTAAGGGTTGCAACACAAACCGCATCTTGCAGCATATGCGGGATTAACAAAAACCGGTACGCGG  
TTGCCCGCGCGCGCTCAAGGGAACGATTCCCTAAGG



SEQ ID 7481

**SEQ ID 7482**

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SEQ ID 7487

SEQ ID 7488

SEQ ID 7489

**SEQ ID 7490**

**SEQ ID 7491**

**SEQ ID 7492**

**SEQ ID 7493**

SEQ ID 7494

SEQ ID 7495

ATGTTCCCAACCGCAATTTTGGTCGACGAATTTGATGTGCCGAATATAGGTCGTCTGAAAGCCACGCTCATCAACGCGGGCATTCCGACCGGTTTTCTCTGAACGCGCGGACATTGGGCTACA  
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CCGCGCGCGCACGCGGAAACCCGCTTCGTGCGCGCCCGCGGATTACACCGCTCCAGCGGCAAAACCGTAAACCGCGCGACATCGATTTCGCGGTACGCGCCCTGAGCATGGGCAAA  
CTGCACCAACGCTATGATGGGATCGGCTCGGTGCGCATCGCGCGCCGCTGCTCGGTACGCTGCTCAACCTTCGCCGAGCGCGCGGAACGCGTAAAGAGTTCGCGCTTCGCGGCATCGGTACG  
GTACGCTGCGGTGCTGCGGTGCTGCGCGGAATGTCAGGACGGAATGAGACGCGCGCAAAACCGGTGTCAGGCGCGAGCGCAGCGTATTATGGAAGTTCGGTTCGCGCTTCGCGATGATTG  
TTTT

## SEQ ID 7496

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LHHAMGIAASVAIAAAVLGTLVNLAAAGGTRKEVRFGHPSTGLVGVAAAECDQGMATAKAVMSRSARVIMBGWVRVPDDCF

## SEQ ID 7497

TCCTGCCCACTGTGTCGGTTTCGGGTACGGTTCGATTCAAACCTGAAGCTTAGTGCTTTCTCGGAAGCGTGTATCGGTGCTTCGTGTCGCTAGACACTCGTCATCAC

## SEQ ID 7498

SCPVSVCCTVRFKLKSFGSWKRGIGCFVSVDTREH

## SEQ ID 7499

ATGCTTGACATCTTCAATTAACCTTCGGCACCGGCGAGGCGTCACACCTTATACCTTCTCGTGTGGCAGAGTCTGTGTTTTAATAACAGTCGACGCCACCTATTCTCTGG  
ACCTTCGGGGCTTACGAGCAAGTCTTAACCTTAGAGGGCATACTTCTCCGAAAGTACGGTATCAATTTGCCGAGTTCCTTCGCCGAGTTCCTCAAGCGCTTAGAATCTCTCATC  
CTGCCCACTGTGTCGGTTTCGGGTACGGTTCGATTCAAACCTGAAGCTTAGTGCTTTCTCGGAAGCGTGTATCGGTGCTTCGTGTCGCTAGACACTCGTCATCACTTCTCGGTGTTA  
AGAAAACCGGATTTCGC

## SEQ ID 7500

MLAHLQLTFRRHAGVTPTSTFVLAECVFNKQSQPILCDPPGLTEQVLNLRGHTFSRSGINLPSFSRVLSSALEFSSCPVSVCCTVRFKLKSFGSWKRGIGCFVSVDTREHFSVL  
RKPGFA

## SEQ ID 7501

ATGCGCTCTGAAAACGCTTCAGACGGCATCCGGTATAAGTTATCTCATTATGACACCAGATCTGACCATATTAGGCAGTACCGGCGAGCATAGGCGAAAGCAGCTGGAGTTGTCT  
CCCGCCATCCCGAAAATTCGCGTATTTCGCGTGGCAGGGCATAAGCAGGTGAGAACTGGCGGCTCAATGTCAAACGTTCCGCCGGAATATGCCGCTGTCGCGATGCCGAACACGC  
CGCCCGGCTTGAAAGCCCTGTTGAAACCGCAGGCGACGCGGACTCAGGTTTTACACGGCGCGCAGGCATTGGTTGACGTTGCGTCTGCCGACGAAGTCAGCGGCGCTCATGTGCGCATGCTC  
GGGCGCGCGGGCTGCTTCCCGCTCGCAGCGCGCAAAAAGGCAAAACCAATTTATCTGGCAAAACAAAGAAACGCTGTTGTTTCGCGCGCTGTTGTTATGAAACCGCGCGCGCAAAAG  
CGCGCGCAGTGTTCGCGCTCGACAGCGCAACCAACGCAATTTTCAAGTTTTCGCGCGGATTACACAGACCGCTGAAACGAACACGCGCATCGATTATCTGACCGCTTCGCGCGG  
CCGCTTTTAAACACCGATTAAACACGTTTCGACAGCATACGCGCGGAGCAGCGGTCAAAACCCCAATTTGGCGTATGGGCGCAAAATCTCCGTCGATTACGCACTATGGCAACAAAG  
GGCTTGAAGTGAAGCGCATTTGGCTGTCAACTGTCGCGCGCAAACTCGAAGTCTCATCCATCCCAATCCGTCGATACAGTATGGTGGCTACCGGAGCGGCTCCGCTGCTGG  
CGCAACTGGCGCAATCCGATATGCGAAGCGCCCATCGCTATTGTTTGGGCTTCGCGAGCGCATCGATTTCGGGTGTCGCGCAAACTCGATTTCGCGCGATTTCGCGCGTGAACCTTCCAAAA  
GCGGACTTCGCGCGCTTCGCTGCTGAAGTTCGCTTATGAAACCAATAAACGCGAGCGGAGCGCGCGCTGCGTATTGAAACGCGCGCAACGAAACCGCGCTTCGCGCGCTTTTGGACGGA  
CAGATTAAAGTTACCGCATTTGCCAAACCGTCGCGCCACTGCTTGCACAAGACTTTTCAACGCGCATGGGCGATATAGAAGGACTGTTGGCGCAAGATCCCGGACACGCGCACAAAGCG  
GGGCATTATCGGCACACTGCGC

## SEQ ID 7502

MPSENADGIRYKVLINTPQVLITLSTGSGIGESTLDVVSRRPEKFRVFFALAGHKQVEKLAACQCTFRPEYAVVADAHAARLEALLKRDGTATQVLHGAQALVDVASDEVSGVMCAIV  
GAAGLPSALAAAGKGTIYLANKETLVVSGALFMETARANGAAVLVDSEHNAIPQVLRDPTDRINEHIDSIILTAGSGFFLTDLSTFDSITPEQAVKHFMNMRKRI SVDSATHANK  
GLELIEAHWLFNCPDKLEVVIHPSVHSMVRYRDSVLAQLGNPDMTPLAYCLGLPERIDSGVGLKDFGALSALTQKPDFGRFPCLKPAYETINAGGAAPCVLNAANETAVAAFLDG  
QIKFTDIKTVARHLAQDFSNMGDIEGLLAQDARTRAQARAFIGTLR

## SEQ ID 7503

ATGCCGCAAAATCAAAATCCCGCGCTTACTACCGCGCGGTACATCTAAAGGCAATTTCTTCAACGCAACCGATCTGCCGCGAGCTGCCGAGGAAGCAGCGGGGCGCGGCAAAATCC  
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CGATTACTTGTTCGGCAAGTTTCCATCGCAAAACCAATTTGTCGATTGGAGCGGCAACTGCGGCAACCTTACCGCGCGCTGGGCACTTCGCCATCGCAACAGGCGTTGTGTCGATAAATCC  
AAATCCCTTCAGACGGCATCTGACGGTCAAAATCTGGCAGAAACCATCGGCAAAACCAATTTATGCGCATGTCCGATGCAAAACGAGCAGTGTGGAAACAGCGGATTTTCGAGCTTG  
ACGGCGTAATTTTCGCGCAGCGAAGTACAAATCGAATTTT

## SEQ ID 7504

MPQIKIPAVYYRGSTSGKIFPKRTDLPAAQEAAGARDKILLRVLGSPDPYKQIDGLGNASSSTSKAVISDKSERADHDVDYLPQVVSIDKPFVDSGNGNHLTAAVGTFAIEQGLVDKS  
KIPSDGICTVKINQKNGKTIIAHVPMQNGAVLETGDFELDGVIFRPQPKYSNF

## SEQ ID 7505

TTGCTTAAGTCTTCCACTACCGCTTAAACAAGCTATTCCAACAGCTTGCCAACTAACCTTCTCGCTCCCAACATCGCATTGAAATCAAGTACAGGAATATTAACCTGTTTCCCATCGA  
CTACGCTTCTTCTGCTTCGCTTAGGGGCGAGCTCACCCTACGCGGATGAAGCTTGGTAGGAAACCTTGGGCTTTCGCGAGCGGGCTTTTACCGCTTTATCGCTACTCATGTCAACAT  
TCGCACTTCTGATACCTCCAGCACATTTACAATGCACCTTTCATCAGCTTACAGACGCTCCCTTACCATGCGCGTAAACCGGCACTCGCAGCTTCGCTTATAGATTGTAGCCCGCTTACA  
TCTTCGCGCAGGAGCACTCGACCATGAGCTATTACGCTTTCTT

## SEQ ID 7506

LPKSSTYRLKQAIPTACQFNLLRPHIAPESSTGILTCFPSTTHFCLALGADSPYADERCVGNLGLSAGLPTFRFIATHVNI RTSSTLYNAPSSAYRTLPYHAGKPASAAVSIDLSPVT  
SSAQDDSTSELLRFL

## SEQ ID 7507

TTGCGCTGGATTATTAATTCCTCCCAATTGATTCTTAAATTTGCTAATAAACACTTGTTTGGTAAGGAATGAATTTATGCGGCTTTGAACGTGCAGATCAGGTTGGGCAACCTTAGGCACA  
ATTATCGGATTTTGAAGGAATGACGAGGCAAGCTGTGCGGTAGTGAAGGCGGACGCATACGGAACAGCGTGGGTGAGATGCTTTTCGCGCTGGCAGACTTGGCAGACGCGCTTTCG  
CGTGGCGCAATTCAGCAGGGAATCAGGCTGCGGGAGAGCGGCATTACCCATCCGATTGTCTTTTGAAGGCGTATTTGAAGCATCAGAGTACGAAGCGGTGCAACAACTACTCGCTTTGG  
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ACACTTCGCGCATATGCGGCAATGAAACAGTTCGAATATGTGGACAGTATTGTCAAGTCTCGCATTTCTCTGTGCGGACGAACCTGAAGCGGTATGACGGAATACAGATGGAAGCAAT  
CGATTTGGGTACGAAGGCGTGAAGCGGAAGAAAGCTTGCCTTTCGCGAGCTATTTTGAATATCCCGAAGCAGCGAGGATTTGGGGCGCGCGGCTTTCGCTTATACGCAATTTCC  
CGGTCGAGGCGAGGATGACAGGCTGAAACCGGTGATGAGGCTTCAACCGGTATTTTCGCGCAACCGCTTTTACAGCCGCACTCCCTATCGGTTATGGCGCAACATTTTATACAGTA  
AATCTACGCGCTCGCTGATTGCTGCGGTATGCGGAGCGGTATCCCGCGCGCGCTCCAAGCAATTCGCCGTCGCGGTAATTAACCGGCTCATCGCAGGATCTCTAT  
GGATATGATGACTATCGAGCTGAGCGCTTCGCAAGAGGTTTGGGACAGAGGTGCAACTGTGGGCGATACGGTCAATATCAATACCGTTTGGCAAGCGCGGCAACCACTCCCTTACGAA  
TTGATGTCAATATCAACAGTCGCAAAATTCACCTATATCGAG

## SEQ ID 7508

LPLDYNPIDFLILLINTCLVRNEFMRPLNVQIRLGNLRHNYRIKEMHGKLLAVVKADAYGHGAURCAALADLADGFAVATIDEGIRLRESGITHPIVILEGVFEASEYEAVEQYSLW  
PAVGNQWLEALLSRHWKPKVVKLMDSGMHRGTGFPFHDYTSAYAAKQSEVDSIVKFSHPSCADEPESGTEIQMEAFDLGKLEGEESLANSAILNIPEARRDWGRAGLALYGIS

PFGGSDRLRLKPVMLSTRIPGGERVLQPHSPIGYGATFYTSKSTRVGLIACGYADGYPRAPRSPSPVAVDGKLRVVGIRISDMMTELDASQEGLGHEVELWGDVTNINVTVAEAAAGTIPTYE  
LNCNIAKRAKFTYTE

**SEQ ID 7509**

TGCCGACC GCCGCGCTTTTCAGACGGCATTTCGCGGTAAAACGCCATCAGCCCTTCGGTGCAGGCATCTGTACGGACGTGCCGCTTCACAGTTCGCGGAGTAGTGTTTTTGCACACTGTTTG  
CCGTACTCAACCCCCCACTGATCGAAGGGGTTGACGTTTCCATATCGCGCTTGGACGAAGGTTTGTGTCTCGTAAGCGCCATCAGCATACCCAGATTGCAGGCGGTGAGGCGGTGAGCA  
GGATGCTGTTGCTGGGGCGGTTCGCGGGGAACCTTTTGTCGGGCGCGAGGCGTTCGCGTTCGCGTTTCGGGCAAAATCGCCAGTTCGGGCGGTGCTCGTCTAAGGTTTACCTTTCATCAG  
GGCTTCGCGTTGGGCAAGGCGTTGGCAACCGTATAAACCGCTCGTCTCGCTCGCGCGCTCGCGCGTTCGCGCATCGGAAGATAAAGTCGAGGGAATCAGGCGCGTCTCGTGTGAGGACGT  
TGAAATAGGGCTGTGCGAGTTGACCCCTCACCGCGGAACAGGTCGCGCGCTTTGTCAGCGCGGGACATCGCGCTCGAAGCGCGGCTTTGCCCAAATCTCCATATCGAGCTGGT  
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CGGGGCGGTGTGAAAAAAATGGCTGTCCATCGCGTGCGCCGCCCTAGCAGTTCGCGGAACCGCGCCCGCCAACCGCAACCATCAGGGGCAACCGAGCGGCGGACCGAGCGGAATAGCGT  
CCGCCACCCAGTCGTACATCGCAAAACACGCGTTCGCGCGCAATGCCGAAACTTTGCGCGCTTCCTGTATCGGAGACACCGCGCAAAATATGTTGCGCGCTTTCGAGTTCGAGAAACCCG  
CACCGGATATACCAACCGCTTGACCGCTTCGATTCGAGCAGGGTTTTCGGTGTTTTAAAGGACTTGCTGGCAACGCAAAACATTTGTTTTCGGGGTTACAGACGCGATAGAGACTCATCCAG  
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GCAATCGGTTTTTCGGTTATCCCTGATATAAACCGTCGTTCAAATCTGTGTGCAAACTTCAACGACAGATTAACATTCGCGCGGATTTTCGGGCAACACGTCCTCGCGCTCGCATAAACCG  
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AAAAGGATGTGGCAGCTATCTGTATATGGCTTCGAGCGCATACCATGCAGCGGTAAAAGCATCCATCTGTTTTCTTGATTTTCAGAACCGGATTAATAATATAGCAGAACTGATGCTA  
ACAA

**SEQ ID 7510**

CRTAAPQTAFAVNRKHQFPFGRGIVYGRAAPQADDFGQCLFAVLNPLIEGVDPVYRALDEGVVFSVRHQHTQIAGREAVEQDQAVAGAVAGELFVRREAFAPFPGQICQFACFV\*GFTLHQ  
GFLRLKGKGVNGKTAASVILRALRRHRDQKVGNGQARALVQBLELIGLVAFTAEHDAARFARGGTAV\*SAAPQTLHLIELVQPRRQQAQVAVNRGGLPVRVLEIVI PHGNQCHONGNVAT  
RGRVEKMAVHRVRP\*QFAETPRANRHHGQYDPRDGLASAPVVRHKHFAETLRPRIRGRHAKVRRPFGFRRPTAIPRLDRICI EQGFRCFKGLAGNAKHCCFCGVQTA\*DLIQ  
AGRVGERNNKMDNLPSERLERLHAHCRPEVQSAJDRDNLNRPFGSGYPLI\*TVVQTCKLQRTI\*LAADPGHVAQVNRGGLRTVGAQSQMRGFTPLAADVDFTRPQSTHFPFQIRRLRK  
TABQLQRIFAKTVFAVIBQHPVQTLMHTLKTVPFGSKAVAQKDVARILIMAFERICTGCKSHLSPLIFQNRKIK\*QNVV\*Q

**SEQ ID 7511**

AGTAAGCAAAC TTGAAATCCCTACTTTGATAAAGCTTACTGCTTTGTTGTGTCCTTAATCCCGCCCTTTGTGTTTCAGGATTAAGTCGATACAA

**SEQ ID 7512**

SKQT\*NPYFDKAYCFVVS\*SCLLCFRIKSIQ

**SEQ ID 7513**

GTGGGCGGTTTTGAAGCGAAACCGTGATGCTGGGACGCGCTCCATGATGCGCCTGCCGATATTGTGCGCGTGGAGCTGACGGGCAACCGCAGCGGGCATTACTGCCACAGACATCG  
TGTTGGCACTGACCGAAATCTTTCGCTAAAGAGCGCGTGTCTGGGCGCTTTTGTCGAAATTTTTCGGCGAGGGCGCGAGAAGCCTGCTATCGCGGACCGCGGACCAATTTCACACATGACCGC  
GGAATTCGGCGCGACTGTCGCCATGTCAGCGGCAAACTATGATTATTTTGAAACTGACCGGACGTGACGACGCGCAGGTGAAATTTGGTGGAAACCTACGCCAAAAACCGCAGGC  
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CGCCGCGCAGCTGTTGGCAGCAATGCCAACCGCTCCGCGTTGAAACCGCAAACTCTGGGTGCGGCTGATTCGTTTCGCCGGGTTCAAAGTACCGCGGAACTTTTGAAGAAAGCAGGCTTG  
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CACCAGCGGTATGTGACGGCAACCGCAACTTCGACGCGCGTATCCATCCGTATCGGAAACAGGCTTTCTCGCTTCGCCCTCTTTGGTGTGCTTACGCATTGGCAGGTAGCATCCGTTT  
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GAGGGGAAGCTACATTAAAGAGTATGAGCTCCGCGCGGATTTGGCCGACAACATCAACGACGCCATCTCGCCCATTCAGTGCGGATTTCGGCCGGCAGTGCCCGCAGGTGAAATATTGCG  
GAAAATGGGTTTGCTGAAGAAGACTTCAACTCTTACGCAACCCACCGCGCGACCACTTGACCGCCCAACCGCAACCTTCGCCAATCTTGCCAAATGTTTAAACGAAATGTGAGAAAGCA  
GACGCGCAGCTACGCCAAGTTCGTTGGCACGCGTTGAACCAAGAGGCCAAACCATGCGCATGTGGGAAGCCATCGAAAOCTATATGAACCGCAACAGCGCGCTTATCATCATTTGCCGGTG  
CGACTATGTGTCAAGGCTCAAGCCGCGACTGGCGCGCGAAGGGGCTGCGGCTTGGCGGGTGTGGAAAGCCATCGCCCGCGAAGGTTTCGACGCGCATCCACCGCAACACCTCATCGGCATGG  
CGTCTTCGCCCTGCAATTCAAACCCGGCACCAACCGCCATACCTCGCAACTGGACGGTACGGAAGACTACGACGTTGTGCGGGGAACGACACCGCGCTGCGGCTCGACCTCGTGAATTCAC  
GTGTAAGAACGAGGAAACCGTCAAGTTCGCGGTACTTCGCCGCCGATACCGCAGAAGAAGCATTGATATGAAGCCGCGCGCTATTGCAACGTTTCACAGGACTTTTGGAAAGGGA  
ACGCGGCT

**SEQ ID 7514**

VGGLEAEFTVMLGRASMRRLPDIVGVELGKKGAGITATDIVLALTEFLRKREVVVGAFVEFFEGGARSLSIGDRATISNMTPEFGATAAMFAIDAQHTIDVLIKLTGRDDAQVKLVETAYKTAG  
LWAGGLKTVAVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAGLAKPYEEDSGQMPDGAVIIAATTSCTNTSNPRNVVAAALLARNANRLGLKKRPWKSSFPAGSKVAGIYLKEAGL  
LPEMEKLGFGIVAFACCTCNMGSGALDPKIQQETIIDRLYATAVLSGNRRNPDGRIRHPYAKQAFLASPELVVAYALAGSTRFDIENDVLGVADGREIRLKDIPWTDEEIDAIVAEYVKPQOF  
RDYIYPMSDTGTATQAKPSPLYDWRPMSTYIRRRPYWEGALAGERTLRGMRPPAILPDNITTDHISPNAILAGSAAEYILAKKGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVRNE  
DGSVRQGLSLVAREPEQGTTHMRWAEITVYNNRKKPLIITAGADYQGSRRDWAAGVRLAGVAEIAAEGFERIHTNLIGMGLVLPQKFGPCTNRHTLQLDGTETYDVVGERTPRCGLTLVTH  
RKNGETVEVPVTRCPDTEAEALVYEAGGVRPFAODPFLGNAA

**SEQ ID 7515**

TTGTGTCCTTAATCCTGCCTTTTGTGTTTCAGGATTAAGTCGATACAAATCATCACCCAAATACATGTTTGTGTTTCTTTTCTCTTGCAGAAAGGTTTTATCCTTTGCCAAGAATAAAAAATC  
AAAACAAACATATGCTCTTTGTTTGT

**SEQ ID 7516**

LCLNPARCVSGLSRYNHHPNTMFVFFSLAGFYPLQRIKNQKLIIVVC

**SEQ ID 7517**

ATGCGCGACACGCGCACAAAGCGCGGCATTTATCGGCACATCGCGTGATACCGTCGGAACACCGTTATCAAAGGAAACCAATTTCGAAACCCCTCTAGCTTTTATCTTCGCCATCTCTGA  
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ATGGTGGCTCGCCCGGATTCGTTGGCGCGCTAGCTCAAAATGGTCGATACGCGCGAAGGCGAAGTATCAGAAGCCGATTATACCTTACGCTTTTGACAAACAACCTCCGCCAAGCGCATC  
GCCATCGTCGCGCGCGGTTCGCTGACCAACCTTCGACTTGGCGGTTTTCGTGTACGGACTGAGCTTTTCCTTTCGGCGTAACCGGAAGTTCGGGCCCTATGTGCGCACAGTCGAACCCGACACCA  
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CGTGGCGCTTCAGACGGCATCGGCGCGCGCAACCGCTCCGACCATCGATGTCGCGCAGGACGCGCGGAAGCGGTAAATTCGCAAAAAACCAAGGCTACATCGGCATGATGCCCTTTAAAAATC  
ACAAACCTTCGCGCGCGGTGGAAAAAGGACCGCCGCGCAAAAGACGGCTGTAAACCGGCGCAGAGCTGACTCGCGCGGACGCGCAAAACCCATCGGCTCATGGCAGGAATGGGCAAAAC  
TGACCCCGCAAAAGCCCGGGCAAAAAATCACCTTGACCTACGAACGCGCGCGGACAAACCAATACCGCGACATCGTCGCCCGGATCTGCTGCAAGACGCGCGGACCAACCTGATCGGGCGCT  
CGGCTTCGCTCCGACGCGACAGGCGGTGGGACGCGCAAAATCGCGCGAGCTACCGTCGCTGTGTGTCGCGCATTCGGCATGGGCTGGGAAAAAACCGTTTTCACCTTCGTGGCAACCC

CTCAAAATTTTTCGGCAAACATATCAGCGGCAACGCGCTCTGTACGCCATATTTCCGGGCGCGTGACCATTCGCGACATTCGCCGACAGTCCGCCGAATCGGCTTGCAAAGTATTATTGGAAT  
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TGTCCAAAAATCGGTTTCGCGCTTCGGGCTCGCCCTGATGATGCTGATGATGGCGGCGCGCTTCTTCAACGACGCTTACCCGCGTGATCGGT

**SEQ ID 7518**

MPGHAHKRGHLSAHCADTVRTPLSKENHLQLLAFIFAILLVLSLHEFGHYTVARLCGVKVVRFVSGFGKPPFFTKRGDTEWCLAPILGGYVKMVDTRGEVSEADLFPYAFDKQHPAKRI  
AIVAAGPLTNLALAVLLYGLSPFGVTETLPYVGVTEPDTIAARTGFGSGDKTSVNGVSVQDNSSAQTEIVMLNLEAGKVAWGVQTSAGAQTVRTIDAAGTPRAGKIAKNQGYIGLMPFKI  
TTVAGGVKSGSPAEGAGLPGDRLTAADGKPLASQWENANLTROSPGKKITLYERAGQTHADIRPDTVQPDHITLGRVGLRPQPDRAWDQAIRRSYRPSVVRPFGNGWERTVSHSWT  
LKFPGKLISGNASVSHISGLPTIADIAGQSAELGQSYLEFLALVSLGLVNLPLVPVLGGHGLVYTVVETIRGKPLGERVQNTIGLRFGLALMLMLMAAFAFPNDVTRLIG

**SEQ ID 7519**

TTGTGTTTCAGGATTAAGTCGATACAATCATCACCCAAATACTATGTTGTTTCTTTTCTCTTCGCGAAGGTTTTTATCCTTTGCAAGAATAAAAAATCAAAACAAACTCATTTGTCCTTT  
GTTTGTGTGATTTTCGGCTTTCCAATTTGTTAAAGATCGATGCGTCGTTATTCTACTTTCGCAATCAAAA

**SEQ ID 7520**

LCFRIKSIQSSPKYYVCFLPSCERFLSPAKNKKSKQTHCLCLLISAFQFVKDRCVVILLRKS

**SEQ ID 7521**

ATGACTGCCAACCAAAAGTTACCGCAAAACCCGTCGCCGGTACGGATTGGAAATACTACGACGCGCGTGGCGCGTGTGAGGACATCAAAACCGGCGCTTTACGACAGCTGCCGTACACGAGCC  
GCATTTTGTCTGAGAACTTTGGTCAACCGCGCGGACAAGTCGATTTGCGCGATGCTGCAAAAGCTGGCTGGGGCCAGTGTATAGAGGGGAAGCAGGAATATCGATTTTCCGTGTATCCCGCGCG  
GGTGGTGTGCCACGATATTCTGGGGCAGACCGCGCTGGTGGATTGGCAGGCTTGCGCGATGCGAATTGCCGAAAAGGCGGCGATCTCTGCAAAGTGAATCCGGTGGTGACAGCGCAGCTT  
ATCGTCGACCACTCTTTGGCGGTGGAGTGGCGGGGTTTACGATCTGATGCCTTCCGCAAAAACCGGAAATCGAAGACAGACGCTAACCAAGAGACCGTTTCCACTTCATCAACTGGACAAAA  
CCGCAITTTGAAATGTGGACGTGATTTCCGCGGGGCAACGGCGATCATGCAACCAATAAATCTGGAAGAAATCGCGCGCTGCCAAGTCAAAAAGCGGCGTGGCTTTCCCCGATACCTCGCT  
CCGACCGGATCTCGCATCCGCGCAGCTTGATGTCCTGGGCGCTTTCTCCGTGCGCTGGGCGGTTTGAAGCGGAAACCG

**SEQ ID 7522**

MTANQSYRKLPGTDILEYYDARAACEDIKFGSYDKLPYTSRIIENSLNVRADKVDLPLMQSLWGLQIEGQKQEIFDPWYPARVTVCHDILGQYALVDLAGLRDAIAEKGGDPAKVNPFVQYQL  
TVDSHIAVECCGYDPAFRKNREIEDRNRDRFHPDWWTKTAPENVOVIPAGNIGMHOINLEKMSPVVQVKNQVAFPDTCVGTDSHTPHVDALGVISVAMAVWKRKP

**SEQ ID 7523**

GTGCGCGATATGCGAGTCCGTGCCGACGCGAGTATCGGGGAAAGCCACGCGGTTTTTGACTTGGACGACGGGGACATTTTTTCCAGATGATTGTTGGTGCATGATCGCGTTGCCCGCGGA  
ATCACGTCCACATTTTCAAATCGCGTTTTTGTCCAGTTGATGAAGATGGAAACGCTCTTCGTACGCTGTCTTCGATTTCGCGGTTTTTCCGGAAGGCATCAGGATCGTAACCGCGCACT  
CCACCGCCAAAGAGTGTGTCGACGATTAAGCTGCGTCTGCACCAACCGGATTCACATTGGCAGGATCGCGCGCTTTTTCGGCAATCGCATCGCGCAAGCTGCCAAATCCACAGCGCGGTCT  
CCCCAGAATATCGTGGCACCAACACCGCGCGGATACCAACGAAAAATGATTTCCTGCTTCCCTTCTATCAACATTCGCCACGCCAGCTTTGCAGCATTCGGCAATCGACTTTGTCCGCGCG  
TTGACCAAACTTTGCAGACAAATCGCGCTCGTGTACCGGCATTTGTCTAAGACGCGGTTTGATGCTCTCACACGCGGACGCGCGTGTAGTATTTCCAAATCGCATCGCGGCGCGGT  
TCGCGTAATTTTGGTTGGCAGTCATGTCGGTTCTCTCTGTGATCTATTTTTCTGTGGTTTGGGTTTCAGCCGATGTTT

**SEQ ID 7524**

VRMRVRADAGQIGESHAVFLDDGRHFQQLDLVHDVARRNHVHIFKCGCFVDFEVETVFVTSVDFDAVFAEGIRIVTAAHLHRQVRVDDKLRLHHRHIFGRIAAFVGNRLAQACQTHORGL  
PONTIVANHPRGIPRKIDFLFPFYQLAQPALOHROIDFVRAVDOLRONAAVRQOLVVRAGFIVLTRRTRVVVPQIRTGQRFAVTLVGSVHGVSPVDLFLVHFGQPMF

SEQ ID 7525

TTGCTCTTGTTGTTGTTGATTTCGGCTTCCCAATTGTGTTAAAGATCGATGCGTCGTTATTCTACTTCGCAAATCAAAATAAGCTGTAAAAACAGCAAACCTTGCTTTTCATTGTGTTAAAGTTTTG  
GTGGAGGCGAAACGGGATCGAAACCGATGACCCCTGCTGTGCAAAAGCAGGTGCTCTACCAA

SEQ ID 7526

LSLFVDFGFPIC\*RSMRRYSTSQIKISC\*KQOTCFHL\*SPGGGKDRDTPDLLAKQVLYQ

**SEQ ID 7527**

ATFGAACTGAAACAGATTGCGCTCCGACATGATGTTGGGCATATCGCCTTTGGCATTTCGCCACTTACCATCCAAGACATCCGTGTGGAAGGCTGCAGCGTACCGAGCGAGCACCG  
TATTCACTACCTGCCCCGTCAAAGTCGGCGACACCTACAAAGCACACACGGCAGTGGCAATCATCAAAGACCGTGTACGCCACCGGTTTCTTTGACGACGTACAGAGTCGAAATCGCGGACGG  
GCAGTTCTGCTGACCGGTTATGGAACGCCCCACCAATCGCGCTGCTCAACATCACCGGCGCCAAAATGCTGCAAAACGACGCCATCAAGAAAAACCTCGAATCGTTCCGGCTGGCGCAGTGC  
CAATACTTTAATCAGGCGACACTCAACGAGGCAGTCCGCGGCTGAAAGAAGAATACCTCGGGCGTGGCAAACCTCAATATTCCAAATCAGCCGCCAAAGTAAACCAATCGCTCCGAACCGCG  
TCGCATCGACATCAGATTGACGAGGGCAAAATCCCGCAAATCACCGACATCGAATTTGAAGAACCAACCAAGTCTATTTCGACGCGCAAACTGTGTCGCGGACAGTGTGCTGACCGAAGCGG  
GATTTTGACACATGGCTGACGAGGACCGGTTGCAGCGCGAAGAAATCGCCCAAGACATGGAAAAAGTAAACCGCATTAACCGCATTTTACAGAAACACGCGTACTTCGATTTCGGTATCTCGATACC  
CAATTCGCAAAACACGAGACAAAACAGGCGAGACCATCAAATCACCGTCCACGAAGCGGGACGTTTCCGCTGGGGCAAAGTGTGATTTGAAGGCGACACCAACGAAGTCCCCAAGGCGG  
AATCGGAAAACTGCTGACCATGAAGCCCGGCAAAATGTTAGCAACGCCAGCAGATGACCGCGTTTGGTGAGATTGAGAACCAGATGGGCTCGGCGAGGCTACGCTACAGCGAAATCAG  
CGTACAGCGCTGCCGAACGCGGGAACCAAACCGTCGATTTCGTCTTGCACATTCGAACCGGGCCGGAATACTTACGTCACAGAAATCCACATCACCGGCAACAAACAAACCCGCGACGAA  
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CAAAGGCTGCTGTACAAGGCAACGCTCGGCTGGGGGCGCAACAGACCGACAGCGCTCATGCGCGACGCGCGCTACTGTACCGGGTAAATGCGGAATCGCCTGCGCGGCGAGCAAA  
CTGCAATFACTATCGCGCACCCACAAACAAACCTGTCTTCCCTTAAGCAAAACCTTCACGCTGATGCTCGCGCGGCAAGTCGGCATTCGCGGCGGCTACGGCAGAAACCAAGAAATCC  
CCTCTTTGAAAACTTCTACGGCGCGCGCTTGGGTTCCGTGCGCGCTACGAAAGCGGACGCTCGCGCCGAAAGTGTATGACGAATACGGCGAAAAAATCAGCTACGGCGGCAACAAAA  
AGCCAACGCTTCGCGCGAGCTCGTTTCCGAGTACCGCGTGAAGAGCAGCAGCAGCTCGCGCTGAGCGTATTTGCCAGCAGCAGGACGCTGTGGGACGGCAGAACTTATACCGCGGCC  
GAAAACCGGTAAACAAACATCGCTTTTACCTGAGCCGCGTCAAACTTCACTTTACCAACGAGTTCGCGTATTTCCGCGCGCGCGCGGTACTTGCGCTCGCTTTGGGTCGGATGAAT  
TCAGTACGCTTACCCGCTGAAGAAAAACCGGAAGCAGAAATCCAAACGCTTCCAATTCCAGCTTCGGCGACGCTTC

SEQ ID 7528

SEKID 17526  
MKLQIASALNMLGISPLAFADFTIQDIRVEGLQRTEPSTVFNYLVPVKVGTDYNDTHGSATIKSLYATGFFDDVRVETADQGLLTVIERPTTIGSLNITGAKMLQDAIKKNLESFGLAQS  
QYFNQATLNQAVAGLKEEYLRGRKLNITQTEPKVTKLARNVRDIDITIDBGSAKITDIEFBGNQVYSRDKLMRQMSLTBGGIWTWLTSTRDRFORQFAQDNKXVTFDYQNNGYDFRILDT  
DIQTWEDKTRQTIKITVHEGGRFPRGKWSIEGDTNEVPKABLEKLLTMKPKGYERQOMTAVLGEIQNRMGSGAGYAYSEISVQPLPNAGTKTYDVFVLIHEPGEKTYVNEIHTYGNKNKTRDE  
VVRRELQMESAPYDTSKLQRSKERVELLYGFONVQDAVPLAGTPDKVDLNMLSLTERSTGSLDLGAGNVQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLNGSLSPFTDPYFADGVS  
LGYDIYKAFDPRKASTSVQYKQYKTTAGGVRAGGIPTVEYEDRVNFGLAAEHLVTNTPYKNAPKRYADIRKYKGTGDGADSGFKGLLYKGTVGWGRNKTDSASWPTGTYLTVGNARIALPGSK  
LQYYSATHNQYVFPPLSKTPTMLLGEVGIAGGVIKGTREKIPFLYGLKGLSGVRGYESGTLPGKPYVDYBEGEKISYGGNKAJNVSAEILLFPMPGAQDARTVRLSLFADAGSVGDWGRYTTAA  
ENGNNKSVSENAKSTPTNELRYSAGGAVTWLSPLGKMPKFSYAYPLNGKGPDEDEIRQFQFQLGTTT

## SEQ ID 7529

CGACACGAGCTGACGACAGCCATGCAGACCTGTGTACGGCTCCGGAAGGCACTCCTCCGCTCCGGAGGATTCCGCACATGTCAAACCAGGTAAAGTTCTTCGCGTGCATCGAATTA  
ATCCACATCAT

## SEQ ID 7530

RHELFTAMQHLCYGSRHSSVSGGFTTCQNVRFALHRINPHH

## SEQ ID 7531

ATGGAAGATTATACATAATACTCGCTTTGGGTTTGGTTGCGATGATCGCCGGATTATCGATCGGATTCCGGGGGGGGTGGTTTGAATACGCTGCCCTGCACCTCTTGTGGCAGGTATTC  
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TTGCTTTTATTGTTTGTCTCGGCTGCAAGCTGTGTGAACCGGATGCTTACACCAAAATGGCGAACGTTGCTTGCATCTGCTATCGGTATCTCTGCTGCAACGGTTGGAATATTT  
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GCTGTGAAATGTGTATAGACGAGAGAAATCCGCTGTATCAGATGATTGTTTCGATGTTT

## SEQ ID 7532

MEDLYIIIALGLVAMTAGFIDALAGGGLITLPAIILLAGIPVSAIATNKLQAAATFSATVSPARRGLIDWKKGLPIAAASFAGGVVGLSVSLVSKDILLAVVFLVLLIFVALYFVFSK  
LDGSKEGKARMSFPLFGITVAPLPLGYDGVFGVGSFPLIAPIVLGLCKLILNMSYTKLANVACNLGSLSVFLLEHSGIIFPIVATMAVGAFVGMILGARFAVRFGSKLIKPLLIIVISIH  
AVKLLIDERNPLVQHIVSEF

## SEQ ID 7533

TCGGTAATCTGTTTGTGTAAGAGCGTTGCGAAATATATAAGTATCCCTTCCGCTGCTAAGATATCTCTCGATATTTCGACATTCGGTGTCTATCTTTTCAGTTGCTCCGCCGCTTCG  
CGACGGCGAAGAACCGCACTATACGCCCGCAGGGGAAACAGTCAATATCTTTCAGCGGATTTTTCGGGAAATTCGTCAT

## SEQ ID 7534

SVICFVKERCBIKYFPLSKISLDSIDIPYTFQFVRRFGSGEEPNTYPAGENSQYFQDFPFGEIRH

## SEQ ID 7535

ATGCGCTCTGAAGCCCTTCAGACGGCATTTCGCGGCAACATCCGAAGGAGTTTACCATTGATCGTTTGACCCGCGGCTTTGCCGCCGCCCTGATCGGTTTATGCTGCACCAAGCGCGGC  
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AAACAGGCGCAGTTTGAAGAAGACTACAACCTCCGCCGCAACGAGATTGGCTCCCTCCAGCAAAACGCCAACCGCGTATCGTCAAAATGCCAAACAGGAAGTTTACGATGTCATTT  
TGCAGGACGTTGATTACGTCAACACCAATACGACGTTACCGACACGCTCAATAAGAAATGAACCCCGC

## SEQ ID 7536

MPSEALQTAFRGNIRRSFTMIRLTRAFAAALIGLCCTGAHADTFQKIGFINTERIYLESQARNIKQKLDGEFSARQDELQKLRBGLDLERQLAGGLKDAKKAQAEKRWGLVEAFRK  
KQAQPEEDYNLRNREEFASLQQNANRVIVKIAKQBGYDVLQDVIYVNTQYDVTDSVIREMNR

## SEQ ID 7537

AGATACTCTCGATATTTCGACATTCGGTGTCTATCTTTTCAGTTGCTCCGCCGCTTCGGCAGCGCGAAGAACCGAATATAGCCCGCAGGGGAAACAGTCAATATCTTCAGCGGA  
TTTTTTTGGGAAATTCGTATGCTGCTGTCGGATAAGTTTATATCTCCGCCAAACGCTCCGCCGCTCCAAACA

## SEQ ID 7538

RYLSIPPTPRAILFSSSAASAAAKNRTIRPQKTVNTFSGIFLGKFMVMSLSDKVFYLRQHLRLQQ

## SEQ ID 7539

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AAGAGACGCTGCGCGGTCAITTCCTGCACCTGTTCACGCGAAACGCCAAGCGAATCACACATCAAGCCATGATGTTTCACTGATTCTGTATCCGGAACAGGTTCAACGCCCTCCAC  
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## SEQ ID 7540

MTFTTQPTPKPKKSVALSGVAAGNTALCTVGRGTNDLSHRGYDILNLAQKCEFEVVAHLIHLHLPNKFELAAYKTKLKSMLRGLPIRVIKVLESPLAHTHPMDVMRTGVSMGCVHPERE  
SHPDSEARDIADKLIALSLGSIILYQYSHNGKRIEVSDEETVGGHFLHLHGKRPSESHIKAMHVSLLIYAEHEFNASTFTARVIAGTSDMSYCTGAIGALKRPGKHGGANEVAYDIQ  
KRYRNADEADIRERIGRKEIVIGFGHPVYTTISDRNVVIEKVARGLSREAGDMRLFDIAERLESVMWEKKKPNLDFSAVSQKLGVPMTAMFTPLFVISRSTGNAHVLEQRKDKGIIR  
PSANYAGPEDLAFVRIEER

## SEQ ID 7541

GTCGCAAACTGTTTCTTCATCTCTCTCGCGCTCTFTGGGCTCAACGGATAAAGTGGCTGTCGGGCGTGCCAGCAGCCGCTTCAGGCGGATAGGTTCTCCGCTATCGGCACAGAAATCCA  
TAGTCCCTTCATCAATATTGCGGATGTCGCTGTATTTTACTGAGAAGTTTTCGTTCCGATCCCGGTCAGGAGTTCCAATGCGTACTCTTCTTCTCTGTTGGCAGCTGCGGAGGAT  
CGGGGCTGATTGCTGTTTGGAGATGCCCTGTTGTAACGAGGCGTTTTCGATGAGTTCGCTTTCGATTTTACCAGCAATTCGCGGAAAAAGCAATAGGTGCTATTCATATAATC  
GCTTTCGCGCCCAATCCAATTCAAATATCTGTTCTGTCTAGCTTTACCAT

## SEQ ID 7542

VGKLFHLPLSAFLGLNG\*SGCRACQQLQADRFSRIGTESIVPFINIADGRLYTFTEKFSFPPIGTETFCVLPFLCGTVGRIGG\*FVFLMEPCNGGVDFEVLHFYQQFAEKSQHVVIHII  
VFRPNPIQNLFCQLYH

## SEQ ID 7543

ATGATTACCGCTTTTCAGACGGCTTTCAACAAATCCGCATCGACCGCTGAAAAATAAAACCCATAAAAAATACAAGGAGAAATACCATGAC

## SEQ ID 7544

MYRFQTAQQIRIDRLKNKTHKNTEKYHD

## SEQ ID 7545

TTGTTCTGTACGCTTTACCAATAATGATGCCCTCTCGGTTACCGCAAAAAAACAAGCACTACAAAGTGGCTTTATCTCTTGTATTTTATAAGGCTTATTGCC

## SEQ ID 7546

LFCQLYHNVCPLGSPQKKNALQSGFTPLIFIRLLA



## SEQ ID 7547

ATGATTCCGGCCACCTGCACCTGTGCCAAATCACCGCGCGCTCGCGCGGGAATGGCGCGCGGAGGACATTTCCGTTACCGCGGTGCGCCCGCTCGCAGACCGCGCAGGCGGAACACATCA  
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## SEQ ID 7548

MIPATCTLSQITARLGSEWRGEDI SVTAVRPLADAQAEHISFLANPKYAEVHDSSAGAIIVSAAADGFEGRNLIVADDFYLYPAKVARLPSFVVKARGGIHPTAVVEPGATVPASCEIG  
ANAYIGANTVILGEGCRILANAVVQHDCKLGDEVVLPNAVYYGCTLGRHVEIHSAGVIGADGFLAFAGDSWFKIPQTGAFTLGDVDEITGSNTNDRGMSDITVGNKTIDNQVQIGHN  
CKIGSHFVIAARTIGSSVTIGSYCIIGGVGTGHI ELADKTTIGGTSVTHSTIESGKHLAGIFPMSEHKWARNNAVYTHRLSEMNRKLTLEQQLSDSKDTQ

## SEQ ID 7549

ATGAGCTACAACTCCCATCGAAGCCAAAGACATCCAAAACATCATCCCCACCGCTACCCGTTTCTCCAGCTCGACCGCATTAACCGCTTCGAGCGGATGAAAACCCCTGACCGCATCA  
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AGCGCGCGCGAAGGAAACGAAATTTCTCTTCGCGCGCATAGACGAGCCGCTTCAAACGCGAATCATCCCGCGCAACACTCGTCTTTGAAGTCGAATCCTGACAGCGCGCGC  
GGCATCGGCAAAATCAACGCGCTTGCCAAAGTGACGAGCAAGTCGCGCTCGAAGCGGTGATTATGTCGCGCAACCGCGT

## SEQ ID 7550

MDVQLPIEAKDIQKLI PHRYPLQLDRITAFEPMKTLTAIKNVTINEPQFGHPDLFVMPGVLIIEAMAQACGLAILSEGRKENEFFPAGIDEARFKRQVIPGDQLVFEVLLTSRR  
GIGKFNAAVKVQVAVEAIVMCAKRVV

## SEQ ID 7551

ATGATGAGTCAACACTCTGCGCGGACGACGTTTCCGCCAAGCTGTGAAGAATCGAATCGCTTGCCTGCGCGGTGCGTCAATGCTTATTTCGACAGATTGGCCACCCAAAGCGGTTTCA  
AAGCCATCTATCTGTCGCGCGCGCGCGTGGCAGCTGTTCTTCGCGTATCCCTGATTGGGCAITACCAATGGAAGATGTGCTGATCGACGACGACGATTCGGACACGTCGATAC  
GCCTCTGCTGGTGACATCGATGTGGGTGGGCGGTGCAITCAATATTGCCCTGACCATTCGCAACTTGAACGCGCGGTGTCGAGCGGTCACATCGAAGATCAGGTAGCGCAAAA  
CGCTCGCGCACCGTCGGAACAAAGCCATCGTTTCCAAAGATGAATGTCGACCGCATCAAGCTGCCGTAGATGCGCGCTTGTATGAGAACTTCGATGATTCGCGCGTACCGATGCGC  
TGCGCGTAGAAGGTTTGGATGCGCTTATCGAACGCGCTCAGGCTTGTGCGAAGCGGTGCGGACATGATTTCCCTGAAGCCATGACCGGATTGAAAATGTACCGTCAATTCGAGATGC  
AGTGAAGTACAGTATTGGCCAACATTACCGAGTTTGGTGCTACACCGCTTATACGCAAGCGAGTGGCTGAAAACGCGGTGTCAGTGTGCTGTATCCGTTGTATCATTCGCGCGCA  
GCAAGCAAGCGCTTTGAAATGTTTACGAAGCGATATGCGCGATGGCACTCAGGCGCGGTGTTGGACAGTATGCAAAACCGTGCCGAGCTGTACGAGCATCGAACTATCATGCTTCC  
ATCAAAACTGGATAAATGTTTCAAAA

## SEQ ID 7552

MMQHSAGARFQAVKESNPLAVAGCVNAYFARLATQSGFKATYLSGGVAAACSCGIPDLGTTMEDVLIDARRITDNVDTPLLVDIDVWGGAFNIARTIRNFERAGVAAVHIEDQVAQK  
RCGHRNRKAIYSKDEMDVRIKAAVDARVDENFVIMARTDALAVEGLDAATERAQCEAGADMIIPFAMTDLKMYRQFADAVKVPVLANITEFGATPLTYQSELAENGVSLLVPLSSFRA  
ASKAALNVYEAIDMDGTQAADVDSMQTRAEIYELNYHAFDQKLDKLFQK

## SEQ ID 7553

GGGAATCGTCTCTTTGAGCGGGGCGGGCAACGCGTACCGGTTTTTGTAAATCACTATACCTCCGCGCGCATTTGACCGCAACAAATATCTGCAA

## SEQ ID 7554

GNRSL\*AGAGQRRGFC\*FTIPSGRHLTRNNILQ

## SEQ ID 7555

TTGCGCGATTTCGCGCGGAGGCGCGCGGGAATGTGGAGGTATGTTGTTGTCGACCGGTCAGACGCGATTATATGATGCGCGTGAAGCGGTGTCGGGTGAGGAAACG

## SEQ ID 7556

LADPAGEAAGECGGHMLSDGSDGILCMPSEAVSQER

## SEQ ID 7557

TTGATATTGCGCTTCCATTTCTGCGAACCGGCACACAGGCACAAACGCGCTCACTTATGGCTTCGGGACACGATGCGCTGGAAGGCTTCCACGCGTTCGTGGGTGTTCCCGCTTTT  
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TTAAACATCGTCGGAATGAAGCTCCGCGAGGTTGCCGAAGTTTCGACCCCAACTCTTTTCCAAACGTTTCGCGCTTTTCGCGACCAACGCTTGCCTATATGATGCGGTATCCCTCTG  
TTTGACCAATCCGCGCGCAACGCGAGCGGCATATTTCCGCGCGGAGAAATAACATTCATTTATTTCTACCTATTCAA

## SEQ ID 7558

LILPPLFLRTAHTGTNALTGFGDTPMPSEGFHGFVGCAPAF\*RYIPLKLEIPTRLLGKGNRSFKRCQTERACFCHIKPLSDGGILQCVQIQIKHSRPAADAGNAVHLRFIFQPNQTD\*F  
HDSIGNPAVCFRYFRFGIHTGYAQPDFSGCIRHNPDNAASPEVTAERTDRQSGCDKHKQCAVGADIFARGFHILRFQDKD\*NIVGKLRQGCPSFDPQLFSQTFALFRITTVGYMDAVSPL  
FDQSARNGSRHISAEKINIHYPPIQ

## SEQ ID 7559

GTGTCCTTGGGTTGAATAAAACCTAAACCGGTGGGTTTTCTTTTATAGTCTGCTGAAACTTTCAGACGACCTTTTCCGAACGCTCAAACCAACCGGTTTGGCGCACATAATCACCGCT  
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GGGCTTCGCTATGCGCGCGAAGAAGAAAATTCGTTTCTTTCGCGCGCGCTTCGCTCAAAATCGCAACGCTGCGCACGCTGCGCGCATCGCTTCGATGATGAGTACCGCGCGCATAC  
GGGCGAGTCGCGGAAATGGCTTGAATTTGGGTTTCGTTTATGTTTACGTTTTCGATGGCGGTTCAGGTTTTCATCGGCTCGAAGCGGTAATCGGTCGAGCTGGAGAAACGGGTAGCGG  
TGGGGATGAGTTTGGATGCTTTTGGCTTCGATGGGAGTTGTACGTCATGCTGTCTGCTATTCCT

## SEQ ID 7560

VSLGLNPKPVGFLFRSSETRRPFSSRSNHAFAHNHGFDDGLSVHFGNGVEFADAAPAGQEFDFKDELVAGDDLAFETGFVYAGEEEKFVFLAPAFQNRQRAARLRHFRDDEYAGHN  
GQVGEALIELGFVYGVDFDGGQGFHRLBGGNAVELEKRVAVGDEFLDVGFGDELIVHVCRIIP

## SEQ ID 7561

TTGAACGCTCAATTTAAAAATAAAGAAATCAAGGGTTAGCGTGAATATAAGGAATCTGTAGTATTTTTCTGATTTTCAAGATGGAACCGGTATAAAATGCCGTAGGAAAGACAAAGCAG  
CTGAATTTGATTTTGAATTTATCTTTATCAAGAGAACTTTTCATGTTGTTTCTATTTAGAGATCGTTTAAAGAAACAAATTTGATTTTGCCTTCGCGCAGGAGTTTAAAGACAGAAA  
CCGCTTATATGATAGCATACAACCAACCAAGAACTCTGCATTTGAAATATCAAGTTGCTTTTAAAGAAATGATACGAAAGAAATTCGCGCAATTAATCAAGTTGCAATTTATCAAAATACAA



SEQ ID 7562

LKRQPKNKESRVSVNYKECCSIPDFRMERYKNKAVRKDKAAELYLNLNLSLRELFHVVSIFETVLRNKIDICPQEQEKDRNRLYDSIQPQTPNPAKYQGCFLNNGTKESAELIKVALSKIQ  
NNSGGKFDHNLVAGLFGFGWRYLFPAGKDAQFDAAGKVLKVKFPKKPKSTPSVQYNQKWIREFLSNINPNRNRLAHHEPICPSFKGAIKDTGYARNTHQSIFELINWMDVDTASVFSHFS  
DQVIAVCDEIDKL

SEQ ID 7563  
ATGATTGGGGATCCCCGACGCGTCGGATGGCTGTGTTTGGCCGTCGGAATGTGATGGAAGCCTGTCCATACTGAAAAAAGTCTATAAAGGAGAAATA

HI GMPDASDGCVLPSECDGSL SILKVKYKGEI

SEQ ID 7565  
ATGGACAGGCTTCCATCACATTCCGGACGGCAAAACACAGCCATCCGAGCGTCGGGCATCCCAATCATTAAAAATATATGGGAAAAATTATCTTAT

MDRLPSHSDGKTQPSDASGPIIKNTWEKLSY

SEQ ID 7567

CCATCGGACGCGCTCGGACAGGCCGTTGCGCGCCCAACCCCTGCTTTTCCAAACAGTCGAAACCTTCTGTGTGAACCTCTCAACCAAGGTTTGGCGTACGCGGTACGCCAATCCAACCG  
CAGGCTTCAAACCTCCCTATTTTTCCATATAAAGTAGATTTTTGCGCGGATTCATATTCTGTTTGCCTGACGGAACGATTGCCGTCTGAAGCGGATATCTCTGATCTCTTAAAGACAGCG  
GACTCTCGCCGCAATATCCCAAAATCGATGCGCGCAGGTTTCTCGGCTTACACGAGCGGCACAGGACGAACACTCATACCACTCCGCGCAGCGCGAGCTGCAACCGTAATGCAAA  
GACCGCAGCCGTTGCGGTATATTTTATACCGGAATTTCCAT

SEQ ID 7568  
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QRSECRIFYYPNFPH

SEQ ID 7569  
ATGGGAAAAATATCTTATTGATATTTAAAAACGAATCAAAGAAAAACAGCAGACCGTTCGGAATTATGCGGCAAAACCCGAGACAAGAAGAAAAACAAGGGGATTATTTCAGAAAAGGGAAAA  
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MGKIILLIFKTNQKRTADRSELGKTADKKKTRGLFRKGNI

SEQ ID 7571

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TATCGGCAACCGGCAACACCATTCGCGGAATTACCAACCTTTAATTTAGGCACGTAACCGGCATCGGCGAAACCGGTATCGGCGACGACAACTGATTATGGGTCTGCCACCTCGCGCAC  
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TTTACCGCAGAACAGATTTCCGCGCTCAAGAGCGTATACAAACCCCTACCCATCGCGGCATTCGCTTTGAAGAAGCCCAAGCGCGCATCTTCGCGCGCGCGCAAAACCAAGCCGAGCTT  
CCGCGATTTCAGAGCTTTTCGCAACCAACGACGCGCGCATCATCGCG

SEQ ID 7572

MTLHPTAVIDPKAELDSGVKVGAYTVIGPNVRIGANTEIGPHAVINGHTTIGENNRIQFASLGEIPQDKKYRDEPTKLIIGNNTFIREPTFFNLGTTVTGIGETRIGDNNWIMAYCHLAH  
DCVVGNTPTFANNASLAGHVTVGDYVVLGGYTLVFPQFCRIGDYAMTAFAGVHKDVPPYFMASGYRAEPAGLNSEGMRNGPTAEQISAVKDVYKTYLHRCIPFEEAKADILRAETQAEI  
AYPDFFAQSTRGIIR

SEQ ID 7573  
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SEQ ID 7575

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CGCGCTCCCTGCGCGCTCGCAAGCAATTTTCGCGGATCGCGCAACCTTCACGATAACGTTCTTGCAACACCGTCAAT

SEQ ID 7576  
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 GGLQATAYGMMPRAFGDKFKFVGVLHIADVDVPHDVGQIQRLRFAVPLLNTVLARI TLSGSVNFADAV\*REGLADGNQADGRLPARLQNFQSDTVGHILTTFVLQHRH

SEQ ID 7577

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## SEQ ID 7578

MDISKQTLIDRVFNKANGTTFVTELMAGLTTFTLTCYIVIVNPLILSGTGMGAVFVATCLASIGCFVMGPIGNYPALAPMGLNAYPTFAVVGKMGVPMQVALGAVFISGLIFILF  
SPFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIVANPATLVGLDIIHQPSALLALFGFVMMVVLGYFRVQGAIIITITLITVLIASIMGLNEFHGVVEVPGIAPTFPMQMDPKGL  
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## SEQ ID 7579

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## SEQ ID 7580

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VFPAGEKEMVRSSLESITLAVISQNLKTHDGDGRVASHEILLANPAVRNLIENKITQINSVLQTRASGMQTNQSLQSLVRQGLIAPBATERRRRAQNSBSMSF

## SEQ ID 7581

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## SEQ ID 7582

MPSETPKAPQTASVFFKAVCLIDASFCTIV

## SEQ ID 7583

TTGTATAGTGGTTTAAATTTAAATCAGGACAAGCGGACGAGCGGACAGCAGTACAAGAAGTACGGCAAGGCGAGGCAACGCTGTACCGGTTTAAATTTAAACCACTA

## SEQ ID 7584

LYSGNLNLQDKATKPTQVQVRQGEATLYRFKFKPL

## SEQ ID 7585

ATGGAATTTGTTTACGACGTGGCAGAAATCGGCACTCAGCCCTGCGGTAATTAAGTAATCGGCTTGGCGCGCGCGGTTGCAATGCAATCAATAACATGTTGCCAATGTGCCAGTG  
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CCGTGCGGACGACAGGAGATCGGAGGCCATFGAAGAAGCCATTCGCGGTGCCAATATGCTGTTTATCAGCAGCGGTATGGCGCGCGGTACCGGTACCGGTTCCGCGCGGTTGTTGCT  
GAGATTGCCAAGTCTTTGGCATTCTGACCGTTGCGGTAGTTACCGTCCGTTTCTTATGAAGGCAACCGCTCCATGTGCGCAGCGAGGGTTGGAACAGTTGAAAGAAATACGTCGATT  
CGCTGATTATCATCCGAACGACAACTGATGACCGCATTTGGGTGAAGACGTAATATCGCGGAGCGCTTCGCGCGCGGCGCAATGTATGCGCGATGCGGTGCGGCGCATTTCCGAAAT  
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GGACCGGACGAGCCATTTCAGTCCGTTGCTGGACGATGTAATTTGGATGGTGACCGCGGTGTCTGGTCAATATACGACTGCTCCGGGTTGCTGAAATGTCTCGAGTTGCTGTAAG  
TCATGAAATCGTCAACCAAGCGGCATCCGATTTGGAATGCAATTCGCTGCGCGGTGAAGACGAGACCATGAGCGAAGATGCCATCCGGATTACCATTTATCGCTACCGGTCTGAAAGA  
AAAAGGACCGGTGCTATCTCTCCGCAAGGGAAGTAGAAGCGGTGCCCCGTCCAAACAGGAGCAAAAGCCCAATGTGCAAGGTATGATCCGCAACCATCGCGGTATCCGCAACCATGAAAT  
CTGACAGCAGCGGATTTGATAACAGCTCTGCTTGACGATTTTGAATTCCTGCAATTTTGGCTGTCAACACAATTCAGACAAA

## SEQ ID 7586

MEFVYDVRESAVPAVIRKIVIGLGGGCNAINNMVANNVRSVEFISANTDAQSLAKNHAARKIQLGTLNLRGLGAGANPDIGRAAAQEDREAIKEAIRGANMLFITTMGGGGTGTGSAPVVA  
EIAKSLIGLTVAVVTRPFSYEGKRHVHAQAGLEQLKEYVDSLIIIPNDKMLTALGEBVTMREAFRAADNVLRDAVAGISEVVTCPSEIINLDFADVKTVMNRIAMMGSYAGQIDRAMH  
ATDQAISSPLDDVFLDARGVLVNIITAPGLKMSLSEVMKIVNLSAHPDLBCKFGAAEDETMSRDAIRITIIATGLKEKGAVDPTPAREVEAVAPSKQEQSHNVGEMIRTNRGIRTMN  
LTAADFNDQSLVDFFPAIRLRQENSDK

## SEQ ID 7587

GTGTTGACGACGCAAAATTCAGGAATTTCAAAATCGTCAAGGACAGACTGGTTATCGAAATCCGCTGCTGTCAGATTATGTTGCGGATACCGGATTTGGTGGGATCATACCTTCGACA  
TTGTTGGCTTTGCTCTGTTTGGAGCGGGCAACCGCTTCTACTTCCCTTGCCGAGTAGGATCGACCGCTCTCTTTTCTTTTCAGACCGGTAGCGATAATGGTAATCCGGATGGCATCTTCTGC  
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ATTGACGACGACACCGCGCTGACCATCCAAAGTATACATCGTCCAGCAACGAGCTGGAATGGCCTGGTGGTCCGCTACGCGCAGCGTCGATACCTTGGGCAATAACCGCAACCATCATA  
GCGATACCGCGGTGCTCATACGGTTTTCAGCTCGGCAAGTCGAGGTTGATGATTTTCCGCTGGGCAAGTTACCACTTCGGAATGCTGCGACCGCATCGGCAATACATTTGTCGCGG  
CGCGAAGGCTTCGCGCATAGTTACGCTTTCACCAATGCGGTATCAGTTTGTGCTTTCGGGATGATAATCAGCGAATCGAGCTATTCTTTCAACTGTTCACCACTGCTGCTGCCACATG  
GACGCGTTTGCCTTCATAAGAAAACGAGCGGTAACACGCGCAACGCTCAGAAATGCCAAAGACTTGGCAATCTCAGCAACAACCGCGCGGAAACCGGTACCGGTACCGCGCCCATACCG  
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TACCAACTGGATTCTTTCGCGCATGGTTTTCGCAAGACTGCGCATCTGTAATGCGACTGATAAACTCCACACTGCGGACATTTGTTGGCAACCATGTTATTGATTGCATTGCAAC  
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## SEQ ID 7588

VLTTQNCNRNFKIVKDRLVIEIRCCQIHGADTAIGADHTFDIVALLLFRGNRFYFFCRSRIIDRSFFPQTGSDNGNPDGIFAHGLVFSGETFAPQIGMRALVDDFDHFRQLGHFQATRSSRN  
IDQHTACTIQSYIVQQRITGMGLVGRHRTVDPLGITRTHSHSDTAVAHGHGPHVKEVEVDDPARASYHFGNACDRIAQIVRRAEGFAHSYVFTQCGHQFVVRDDNQRIIDVFFQLFPCLCHM  
DAFAFIRKRTGNYGNGQNAQRLGNLSNNRGTGTGTAHTGRDKQHIGTANGFNGLPILFLCCTADIGIRTRAQTACQIRITQDLSLRNMVFCQRLRICIGTDKILHTAHIVGNEVIDCIAT  
AAAQADYFNRYNRCRCPCHVWNKFSKTPDRPVQRTV

## SEQ ID 7589

ATGGGATGTGGCGGCGGCGAGAAATCATCAATGCTGCGGACTGCCATACCTTCAAAATCTATAGTGGTTTAAATTTAAACCGGTACAGCGTTGCTCGCTTGGCTGCTTCTGTACTG  
TCTGCGGCTTCTGCGCTTGTCC

## SEQ ID 7590

MGMWRAARIINAADCHTSEIYSGNLNRYSVASPCRTSCTVCGFVALS

## SEQ ID 7591

ATGAATACCGATAACCTGCACGACATCTTGACGAAACGGTTCAAGTGATTTCTCAAAAAACAAAGCGGATCCGAAACCCGCGGCAATCGGCACACACTTCCACCGGCTGCTCGACC  
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GGAAACCGCGCATCGCGCATCGACGATGAACCGGCAACAAATCGGAAATATTCGCGGCGGACGCGGAAATCAACTACTCCGTCATTCGCGACGCGGACCGGCTACCGCGCAACGCG

TACTACAGCCCAAGCGCAGGCTTTGGTTTTCGCGCGCATCAACCAGTCATCCCGCAATGCGGGAATTTGGGCTTGCCTCGAAAACTCAAGACCTCGCGTCGACCGCGCGGCTGC  
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CAACCGCGCGCTGCATCTTTACCGAGCGGAAATCGCGCTGACACCATAACTGGCAGACGGCGGTACAAAACGCTATGCGCAATCCCCAGACGTTGGTCTGATCGCGGCAAGTCCCG  
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GCCCGCATCCAGGACTTCTATCCTGAAAGGCGACCTGATGAACATCAGTAAATCATGAAACCGCCAAAACCGGAGTGCAGACGATGACAAAACCTTTTGAACATGTACCGTCAC  
GGCATCATGATTACGAAGAAGCCCTGCGCCAGTCCGTTTCGCCCAACCTGCGATTGCACATCAACTGCACAAAGAAGGCAACACGCCGGAACCTCTTTACGACAGGGTCAACGGT  
TCAACCTCATTTCC

## SEQ ID 7592

MFTDNLHDLIDETVQVYSQKQSRSETPAEIGTHFHPILLRLCETAEQAQNASDILISKGPPSLKINSALTPOPKAL/GEETAATAASTMNAEQSEIFRRDGEINYSVQSRSGTRYRANA  
YYSQGSAGLVRRLNHVTPQMRGLPLPEKLDLAVAPRGLLIIVGPTGSGKSTMTMLHNRKNTLPGHIVTIEDPIEFYKPRRCIFTQREIGVDTINWQTAVQNAMRQSPDVVICGEVR  
SRESHEYAMQALQTHLCITFTLHANTAPQSLERILNFPYKEQHNLIDIALNLGIIQRALAKKDKTGRVAVDLINTPAIQDFILKGLMNIKIMETAKTDMQTMQNLPELIRH  
GIISYEBALRQSVSANNLRLHQLHKEGKTPPELLYDRVNLNLIS

## SEQ ID 7593

ATGGAACAGCAGAAAAGATACATCAGCGTACTGGATATCGGTACGCTAAAGTCTTCGACTGATCGGGAAGTTCAAGATGACGACAAAATCAACATCATCGGTTTGGGCGAGGCTCCTT  
CACGGGCTTTCGCGCGCGGATGTTAAACATATCGATGCCACCGTCCAGGATCAGGAGCGGTCATGATGCGGATGACGAGTACCAAAATTCACCATGTTACACAGGTAT  
CGCAGGCAACCATCCGACGCTTAATTCGCAAGGTGTGTTAAATCAAGACGGAAGTAAACACGCGACATCGACCGCGCATTGAAACGCGCAAGGCAATCAATATCCCGCC  
GATCAAAAATTTCTGATGCGGTGGTCAAGACTACATTTATCGACACCAACTTGGTGTAAAGGAGCCCATCGGTATGAGCGGTGTGCGTCTGGATACGCGGTGCACATCATTAACGGTG  
CAAGTACGCGAGTGCAGAAATGTCAAAAATGTATCGAGCTGTGCGGCTTGAAGCGCATCAGATCATGCTTCAACCGTTGGCAAGCGCGGAGCGGTGCTGACTGAAGATGAAAAGACCT  
CGCGTATGCGTCATCGACATTTGGTGGGCAACGACGATATGCGGTTTATGTAACGCGGCAATCCGCAATACGCTCCGTCATTCCGCGCGGTGTAATCTGATTACCAAGATTTGTC  
AAATCGTTGAGAACACCTCTCGATGCCGCGAGTACATTAATCCATTTATGCGCTGGCATCATGCGATACGGAAGGCTTGGGCGAGATGATTGAAGTCCGCGCGTGGGTGACCGGACAT  
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TATCGTTTCGACCGCGGTGTGTCATGATGACCGGATTTGGAATTTGCCGAAAATCTTCGATTGCGCTGTACGACCGGTGCGCCCAAGAAATGGGCGGTTTTCGACCGGTGTC  
CGCACCGCGCTTTCTACCGCTATCGGCTGCTTCATGCGATGCAAGCTGGAAGGAACTTCCGCAACCGGAAACGGTACAGTCAAGAGAGAGAAGGGGCGCGGTTTGTGTTG  
CAAGATTGAAGCGGTGATTGAAAACACCTC

## SEQ ID 7594

MEQKRYISVLIDIGTSKVLALIGEVDKINIIIGLQAPSRGLRAGMVTNIDATVQAIRQAVNDAELMADTKITHVTITGIAGNHIRSLNSQGVVKKIDGEVTDADIDRAJETAKINIPP  
DQKILDAVVDYIDITQLGVREPIGMSGVRDLTRVHIITGASTAVQNVQKCIELCLGSDQIMLQPLASQAVLFEDEKDLGVCVIDIGGTTDLAVYMNGAIRHTSVIPAGGNLITKDL  
KSLRTPLDAEYIKIHYGVASCTDEGLGEMIEVPGVDRTSRQVSSKVLAAIISARIQIFGVVLGELQKSGFPKEVLNAGIVLTGGVSMGTGIVEFAEKIFDLFVPTGAPOEMGGLSRV  
RTPRFSTAIQLHAAKLBGNLPQEPENGTVQEREKGGLLARLKRNIENL

## SEQ ID 7595

GTGTCGGGTAATTTTCAGCACAGAATATCAATAAGACAATATGTTCTTTTGAAAAATACTTTTGGTTTTTTCACCGAAGACAGGCGCGTTCAAGTCCGGAATGTTTGCATTTATTTAA  
AAGCAGAGCGGAGGTCACATGAAATGTCGAATGGGATGTGGCGGGCGCAGAAATCATCAATGCTGCCGACTGCCATATTC

## SEQ ID 7596

VSGNFSTEYSIRQVYLLKNTFFFTEDRFVQAAEIVCNYLKABAEVMTKPNFVAGGRNHQCCRLPFP

## SEQ ID 7597

TTGGGTATGCTGTTTCGCGCGCTCCATCGGACGCGAAGCGCCGTCGTCAGGTCGCGCGCGGCAATGCGGCGCTGGGGCGCTGGTGCAAAAAACACGTTTGGCGTTTAAAGGTATGC  
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CGCGCGCCCAATGGCTCGCGCACGATTCATGCTATTTGGGAGGCAATTCGCGCGGCAATTTTCACTCCCTGCTGACCATAGGTGCGGTTTGGGCGAGCATATCGCGCCATTCGCGGAC  
ATATCGCAGGTTGCAACATCATGCTCTCATCTGATGCGCGCATTTTACGCGCGCGGACACAAATCGCGGATTTACTTCCGCGCTGCTGCTATGGAANTGACCGCGCGGCAAGCGCTGC  
TGTTTTGGATGCTGATTGCTGTCATTTTCGCTCGCAGGTTTCGCGCGGTTTTCGCGCGCTCGGTTTACACGCGATCGGAATGCGCTTCCGCGCGCGGCTTCAGGAACCGCGCG  
CAAACCGGCAATGCGCCCGCAAGACCGCAAGCGCAACAGCAACAAACGGAATGCCGCTGAAAAAT

## SEQ ID 7598

LGMPLGASIGREGPSVQVGAAMGAWCKKHGLAFKGMQENDLMAAGAAGLAAAFNAPLAGVIFATELGRGIMLRWERQILLGLVLAAGFIQVAIQNNPYPYSGFNGGVLENILMWIV  
AAGLVCAAGGIFARMLYGAFAAPRKIRGFTIRNRPILLALMLGLLALLGTFYQGTGTGTGHEAQAHLHGIYAPVGLAAAKWLATVFSYWAGIPGGLFPTSLTIGAVLGEHIAATAD  
ISQGANIIVLICMAAFLAGATQSPITSAVVVMEMTGGQSLFWMILIACIFASQVSRQSPRPYPHAGSMRFRRLVQETAATGNAPARQAAANSKTMPSEN

## SEQ ID 7599

TACCTTCGCGCGGCTTTGACCGCAACATATCTGCAAGATTTATTGTGTCGCATAAATCCCGACAGCGCCTAAATAAGGTATAATCGCATCCGATTCTGTCGCGTTTCGCGCGC  
GCAGCGGATGTCGCGGTTTTCAT

## SEQ ID 7600

YPPAGI\*PATISCKIYVRINAGQPPK\*GIIASDSVPPAARRRDVGGFH

## SEQ ID 7601

ATGGGGTTTCAGATTGTTGGGCTATCAGTATTTTCTATTGGAATGCTTTTACTGATTTTGTCAAAACGCAATTTATGCCGCTGAAAAGCTTCAGACGGGATTTCGTTTGGACTCGA  
TTACTCGATATAAG

## SEQ ID 7602

WGFQIVGIIISIFYLANSFTDFVKTHLCRLKSRFRDRLDSTITRYK

## SEQ ID 7603

ATGCAAGTATTTTTCAGCAATCTCAAAGCTTTTTCGAAACCGTCAGCAGCTGGGTTTGGGATCTGTTATGTTGATGCTGCTGGTCGGCACCGGCAATGCTGACCGTTATGCTGAAAG  
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TCTGACTGCGGTTGCTTTTAGGTGTTTAAAGGCAATCGCAAGCGCTTCTTTTCACTGCTGCTGCTATGCGGCTGTTTATGTTGTTGGGCGGCTTTTCCATTTATGCTCATTAATTC  
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AGGCGGTTATGGGTTCTGCGCTATTGCGCGCGCGCGGCAACCGGACCGCGGCTGCTGAGGCTTTGGTTTCCATGACCGGCTACTTTTGGACACCAATGTTGCTGCTGCTGATTAC

CGGTATCTGTTGGTCATGGGCTCTGCTCGGCGCAGGCGGGCAGTTTTGTGAAACCTGAATTGAGCGGCGCGCTGACAAACGTCATTTTCAAAAAATGCTGCCCGGCATCGGCGGCTGG  
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ATGTTTCTTCCGTCATGCCGGGTACCGTGTGAGCCTTGATTTGSTATGGCTGGCTTCGGATACATTCAACGGCTTGATGGCATTGCCCAACCTGACTGCGCTTTTGTGTATGGCGAAAGT  
CATCGTCAATGAAACACCGGACTTCAAAACAAAAATCAACAAACGGCGAATTGCCGCAT

**SEQ ID 7604**

MQVFLDNLKAPFETVSSVWVSGVMLLLVGTGIVLTVMLKGLQFTMLGYALKQAFVPSKKYEGGAGHEGDISHPAALMTALSATIGTGNLAGVATAVVTTGGGAVFNMWMTAIPGMATKYG  
EGVLAVKYRVNNSKSGEMSGGPHYYIEKLGKNNKMAVAFALPGTFASFGIGSSVQSNSVAQVQTSFGIEPATYTGITLTVLTAVVVLGGTIGKIAKAASITVPAMAVFYVLGGLSIIVINS  
DALMPAVKLIFSDAFSAQAVAGGAIGTVIRYGVARGVPSNEAGMSGAPIAAAAKTDPVROALVNSTGTFFLDTTVVCSITGTIVLWGLLGAGGEFVKPELSGAALTVTTFQKMLPGIGW  
TVTIGLIFAYSTILGWCYGKEKCAVYVFGKFAALYRVGVYSSVMPGTVLSLWLVLASDTFNGMLALPHLTALLMLAKVIVNETRDFKQKITNGELPH

**SEQ ID 7605**

ATGTGGGATAATGCCGAAGCGATGGAACGGCTGACCGCGTGGCTGCTGTGTCATGATGGCGATGCTGCTTGTGCGCTCCGGGTGGTTTGGTPTTACAATTGCAATCACTGCCCCGTCGAAGC  
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CCGGTATCCGTGGAATTGCGTCCGCTCATGTTGCGCCCGCGTTTCCCGATACGGTTGAGGTGCTCTTCCAGCCGAGCGCAAGCCGGTTGCACGTTTGGGGCGCAACGCTCTTGGTGGACGGCGGAA  
GGCAATGTTTTTTGAAGCCCGCTTTGGACAGACCCCGGAATGCCGTTATTACAGAGGCGCGAAGCAAGCTCTCCGCGAATTGCTCCGCAAGTTTCCAGCTGTTTATGGCAAAAACGAG  
GTTTGGGCATCAAGAGAGTACCTATACCGCAGCTCTCCGGCTGGAATGCGTGTGTGGAACAACGGCTACCCCTCAGGCTCGAGCGGGAAACGAGATGAACGCCCTCCGGCTTTTATCCGA  
AGCGTGGCAGCATCTGTTGCGTAAAGAATAAAAAATCGGTTATCTCATGTGGATATGAGGTATAAGGACGGGATTTTCAGTCCGCCATGCTCCCGACGGTTTACCGGAAAAAGAAATCCGAAGA

**SEQ ID 7606**

MWDNAEAMERLITRWLLVMAMILLASGLVWFYNSNHLPVKQVSLKGNLVYSDDKALGSLAKEYTEGNILRTDINGAQEAYRRYPWIASVMVRRRFPDTFVSVVLTERKPPVARWGDHALVDGE  
GNVFEARLDPRGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKETTYTARSAMNVVLDNGITVRLGREWEMKRLRLPTEAWHLLRKNKNRLSYVDMRYKDGFSVRHAPDGLPEKESSE

**SEQ ID 7607**

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**SEQ ID 7608**

MLPRFGKKEPFAHLVFPSEPDGDAVQNDIPRRTRCIGHLFDQATLFCQNSRKFVTTAEHFGRRSFRASEYRHSGSVQAGFKNIAFAVHQGMVAPTENRLALGQDDLNRIGKTAHHDRN  
PRIPAVGFLCAIDVRPONTIMDVFFRQTAQCLLIGINQVALQRHLLDGOMIRIVKPNQGRSKOHRHHDKQPAROPFHRFGIIPHVRPSKPOYINRONRP

**SEQ ID 7609**

TTTCTGTATCCGAAAAACCAATGCGCGTCTGAAAACCGCATCCCCGTTTTAGACGGCATGATTTATCCGCCCATTCATGTGCCACACTTTATTCACCTCATAACAATAAACCGGTAA  
ACCATGAAAACCCCACTCCTCAAGCCTCTGCTCA

**SEQ ID 7610**

FPDPQNPMPSENRI PVFRRHDFIRPIHVPHFIHFITINR\*NHENPTPOASAH

**SEQ ID 7611**

ATGCCCTTCGTACTCGGCATCATCGCGGGCGCCCTGGTCGATTTGGACAACCGCTGACCGGACGGCTGAAAAACATCATCGCCACCGTGCCTCTGTTACCTCTCTCGCTACAGGGCG  
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CGCCACCTACCGACGCTTACCTACACCCCGAAACCTACTGGCTGACCAACCCCTTCATGATTTTATGCGGCACGGTACTGTACAGCAGCCGCATCATCTGTTCCAAATCATCTCGGCC  
CACCGCCACCTCCAAAGAAAGCGCCCAATGGCTTACGAACCACTCGGCGGCTACCTCTCGAAGCCAAAGCCGCACTTCTTGACCCCGATGAGGAGCCCTGGATAGGCAACCGCCACATCGAG  
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CTCCACCTTCTTCATCACCATTACGACCTTACGACGCTCTCCCTCGCAGGTTTGGACGTATACGCGCGCATGCCGCTGCGCATCATCGACACCATTATCGGGCGCATCTCTTGCTTGGGCG  
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CCGCGGACGACATAGAATACCGCATACCGCGCGCGCGCCACGAACACACGCGCGCCCTCAGCAGCAGCTTTTCGCAATGAGACGGAACCCGCAAAATTCGCGGACAGCTCTCAAC  
CGGCTTTACCTCTCAAAACCGGCTACCGCTGACCGGCTACATCTCCGCGCTCGGCGCATACCGCAGCGAATGCAACAGGAATGACGCGCCGACTTTACCGCACAGTTCCACCTTGCC  
CGGCAACACCGCTCCCATCTTTTCAACACCTCCCGGACATGGGACCGGACGACTTTTCAGACGCGATTGGATATCTGCGCGGAACTCGGCACCTTCGCAACCGCGACGCGGAAC  
AAAGCCACATCTCTCTCAACAGCTCCAACCTCATCGCCGGCACTCGAACCTTACTACCGCGCTACCGCAAAATTTCGCACAGGCGAGCCCCAAACGACGCG

**SEQ ID 7612**

MPFVLGIAGGLVLDNRILTGRLNKIATVAFTLSSSLTAQSTLTGLTLPFILAMTLTFTFGFTILGAVGLKYRTAFAGALAVATYTTITLTPPEYIMLTNFMILCGTVLYSTAIILFQIILP  
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ACRNTPAQAIRSGKDYVYSKRLGRAIEGCRQSRLRLSDGNDSPDIRHLRLSLDLNLGVSVDQPPQLRHSDSPAENDRMCDTRIAALETGSFKNWQAIRPQLNLKSCVFRHAYRLSLVVAAC  
TIVEALNINLGYWILLTALFVCPQNPYNATKSRVYQRIAGTVLGVINGSLVPPYTPSVETKMLNVIAGTLTLFFHTRYTKYSPSTFFITTIQALTSLSLAGLDVYAAMPVRIIDTYIGASLANA  
AVSYLMWDMKYLTIFERTAALAVCSSGTYSQTLQIAERLKTGETGDDIEYLRITRRRAHEHTAALSSTLSDMSSEPAKPADSLQPGFTLLKTGYALTGYISLAGLAYRSEMHEBCSPDFTAQFHILA  
AEHTAHIFQHLPEMDMGDDFOTALDTLRGELGTFLTRSSGTSQSHILIQALQLEPYRAYRQIPIPHROPONAA

SEQ ID 7613

ATGAAGTGTCTGTGTTTATGTTGCGGGTGTGCGCGTATCCCTCCGTGTGTATCTGGCAGAGGCCGGACATGAAGTAACCGTTCATCGACCGCACCAGGGGTGTGGCGATGGAAACCACTT  
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ACTGCCGAAAAACGCCGGAACCTTGGCTTTGGTCGTCAACGACTTGTTCGCCGAAGCGCGGATTTGAGCCAAGCATTGTCTGGAGCGGCTCAGGCCGATGACGCCGACAGTACG  
CCGTTAATCGGGCGCACCGCTTTGAAACCTGTTTCTGAATACCGGCGACGCTACTTTGGGCTGGAACCATGTCCCGGGTTCGGCAAAATGACGCCGATATCGTGAGCGGCAAGACA  
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## SEQ ID 7614

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FEAQTDMNFEGRRKGLQIFRQTEVEEAAKQDIAVLERYGVPPYRLKPECAEFEPALARVTAIKVIGLHLPADATGDCRLFTENLYKLCQEKGVRFYFNQTSRIDENGLRIKAVETETG  
RPETDAVVCALGCFSTVLAQLDLNLPYVKGYSITLFPVTNSDGAFTVSTVLEBSYKVAITRFDNRIRVGGHAEISGYETKLEPKRRRETLALVVNDLFPBGDLSQALSWSGLRPTPTDST  
PLIGRTFENLPLWGHGTGLGWTSPGSAKLITADIVSGKDTFIRSDDLSTLSKYKL

## SEQ ID 7615

ATGCAGAAATTTGGCAAGTGGCCGATTGATGGGTGGTTTTTCCAGCGAAGCAAGAAATCTCGCTGGACAGCGGTACCGCCATTTTGAACGCTTAAAAAGCAAGGCATAGACGCATACG  
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GCAATCGGTGCGGAAGCTGCGTTCGCGGTGATTTCCTCAAGATACCGAGCGCAACCTCTATCTGTGGAAATCAACACCTGCGCGGTATGACCGCGCATAGTTTAGTACCGAAATCCG  
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## SEQ ID 7616

MQNFQKVAVLMGGFSEREISLDSGTAILNALKSKGIDAYAFDPKETPLSELKERGFQAFNHLHGTGYEDGAVQGALELLGIPYTGSGVAASAIQMDKYRCKLIWQALGLPVPEFAVLYD  
DTPDAVEEKLGLPMFKPAABGSSVGVVVKKEGRKLSVYEELKHLQGEIIAERFPGGEYS CPVLNKGKLPGLIHIIPATEFYDYEAKNRDDTTQCPSEDLTAEBSLMLRELAVRGAQ  
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## SEQ ID 7617

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## SEQ ID 7618

MLDKYSPAELSKHYQWESQGYFAPDMDLTKPSFSIQLPPNNVTGLHMHAFNYTIMDGLTRYRMKGCNTAWIPGTHAGIATQIIVERQLAAQNVSRHDLGREKFLKXWENKEVSG  
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ELILPLTGRITPVIADIEYVEKDFGTGCVKITPAEDFNDYEVGKRHDTLRLINVDLEAKVLANAENVNPKFBAQPGFSLPEKTAGLDRFAARKQMVADLQDQGLFVEIKPHTITPKGRDTG  
SVIEPMLTQWTVMSATPNNGEPDNEFKGLSLADKAKAVDSGAVRFIPENWVNTYQNMNNTQDWCSRLWGHQIPAWYDEAGNVYVARNQBAEKQAGKTGLFREEDVLDTWFFSSA  
LVPFSTLWNPSETDELKALPLSNVLTGYELIFFVWARMIMTTHFTGKVPFAVVIHGIVRDHEGKMKSKSEGNVDPVDLIDIGLIDLKILKRTTGLRKPETAPKVEATKFLPPEGIP  
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## SEQ ID 7619

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## SEQ ID 7620

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HRMPFYKAPLVDSEHVRALLPKVSXPYATYGLDDPATIYATDIENVGAKMPTVHVQMKHGEQSGFEVVLNMPGRHNVLNLAALGVALEVGASVEAIQKGLLGFEGVRRFPQKYGDIF  
LPNGGTALLVDDYGHFPEMAATLAAAGAYPEKRLVLAFOPHRYTRTRDLFEDFTKLVNTVDALVLTETVTAAGEEPVAAADSRLARAIKVLKLEPYTCENVADLPQMLMNVLDQGDVV  
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## SEQ ID 7621

AATAATATCAAAACCAATAATCCGCCAAGAAACATFATTTCTTCAATCAGTTGCAATTTCCAAGCCCTGTTCCATTTCTCAACGTGTTTTCCCGAGTAAATGGCGCTCTCCATCGTAGGA  
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CATTAAGTTGGCTTGCTAAAATATAAACCGCAGGCTGCAT

## SEQ ID 7622

NHKKP\*IPPRHIIFFNQLQFFSPVPLQLFFPSNCLHRRMQFIPNHSNVVP\*CKSPNQLPMLVNLHQIRCNANV\*RAITLAC\*NINRRLH

## SEQ ID 7623

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## SEQ ID 7624

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## SEQ ID 7625

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## SEQ ID 7626

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## SEQ ID 7627

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## SEQ ID 7628

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FITTMVSAYRDADLVICRAGALTAELETAAGLGALLVPPHVDHQTANARFVQAEGLLLPQTQIAEKLAETLGLAREKCLKWAEARNATLALPHSADDAVBAEATACAA

## SEQ ID 7629

GGACCTGAGAAACCTTTTACCGGATAAGTTTCCGCAACGACAGACCGGATTCGCCGCTGAGCGGGAATGACGCGGAGCGGTTTCTGTTTTTTCGATAAAATCTCTAAACTCAAAAT  
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## SEQ ID 7630

GPEKPPYPIISFRTRPGFPFPERE\*RRSGFCFPR\*IPKYNPIIPKRTENQ

## SEQ ID 7631

TTCGCTGTGTCACCGTCTTAGATTCCCGCTGCGCGGGAATGACGCGTTTCATTTGCCGCCCCCTCCCGAAAAACGCAAAAAATGCCGTCGGAAGACCTTTTCGAGCGCATTTGCCGAA  
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## SEQ ID 7632

LLLSHVLDLSRLGNDAFHLPPPEKRRKMPSEDLSDGICGKTGRAGGSEEDFAPA

## SEQ ID 7633

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AAGCCAAATCAAGTACGTTGAAGTTTTCAGGACGACAGCGCGGAAACGCTGCGGCTGTAGAAAAGTCGGAGGATGCAAGACTCTTGGAAAGCATGATGTACACCGGATTTGGTCCGCGAG  
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## SEQ ID 7634

MKRFLPVLISATPAPASPIVGTWHCTGTDENIHSDTKVYKLDQGSFRGDAILKIDDDGNILAYRVVAGKMRFANNALQSQIKYGEVSRQHSPEFLAWLEKSEDA RLLESNMVTLGLAQ  
MDKPGKIDVYDLKSKGLVSEDTGTSREACTKVE

## SEQ ID 7635

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**SEQ ID 7636**

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**SEQ ID 7637**

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CAGGCAGTACGAATGTACGGAACCGGTTCCGCTGTGCTTGGCGCT

**SEQ ID 7638**

VRHVRKWSKQLYPPRRAKIPKLSSRPNTVFGIIVCGKIITHPGIRYRQFAHTRCRNGLRLFLVWRINKNQDKAAGRRQYEWYGTGSPGAMAP

**SEQ ID 7639**

TGCAACCCCTGTGTACCGAAGGTAATTTGGGTTTATAGACAACCTTCAGGGCAGCCTCTGCTGGGGCGGAAGTAGTGTGTGGCATGTGACATTTTCGTAGCTGTAGCCTACCAACCCC  
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**SEQ ID 7640**

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**SEQ ID 7641**

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**SEQ ID 7642**

LVBEIPNKRFTCRCRGSHIQIATVRLCRNVALPLPLRLNGCLPWAGAGGGRAVCYDTEVPIYKGLQPAKSTNSABSTDSRRRHSRISGNPDLRSVKRLIG

**SEQ ID 7643**

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CGTCCAGCCGCTAGCGGTGCGCCACATAGCTTTTTCGCAAGGCGCGGAGCTTTCGCGAGTGTAGAAATCGTTGCTTCAATATCTTTCGCGGATCGTCCGCGGATAGCTGAG  
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GGGGTTCCCACTATTTGCTGCGTCACATCTCTGTTAAATAAATAATCTTTTATGTGCTTTTCTTTGACTAGCTCTCGCTGCTCAAAATGAAAGACAGCGCCAAACGAGGATA  
ATCCGCAAAATTTAATAAGGGCAATTTGTCGCGCTTTTGTCTGCTATATATCCAGCTTGTTCGCTTCTTTCGCA

**SEQ ID 7644**

EEDFAPA\*AFDTAHRAGNIQAVQIVHQGAHTPSGEAPVLAGGFTTLEFCSAAACTVCRDGEIVCFVQVTHINRFVUNI SVRADGFVFPFAHYAGDLAVHFMAGLILNLRVIRHRA  
RASRSQCAAVGGIDAQNGGLCAAFVITRIAADGDKGGTYHGRFDGNALSFLQLHYPLTFARSVGLVQE\*CFILFKHLEBPASRAVLYRYLNRPLIVVKDVTNVLFPRIQYIIFQZIA  
ARTEDDDAFVQCGSNGGRGSRNLVAFENSPYRPFIRIGIAQIKAVHIAAPVAGIGDIDRAVQIFIHORGKRALAALHDFDQYITTAVPQIILYIQRGFI LAAANIFSRITGSEEGVFA  
VLGFADLRADGVA\*FHFHAI PAVIIAIFDIKQSGGWIISVDF\*IQGIRASAAKTHRTKHEMFLVLVLCNAAQDKAAVHAVAVAHIAFPKGAQLFGECEIRVAFNILARHAGDVAE  
LQIVAAPITAAVFEEDMHPVVRGGCQIPADRDNRVDDVAQIAIAVFAVSLAVFV\*FSVN\*FKSTVIGSSSTNRPRQHPPLVGPFIIDVRLNMAESA VVAGVSKSDLLIVSIQPDQ  
LYAAIQSDDCFPFHETRLFTFNI ILIQYEGIAAGFAGFSFQILKVDAAARTVGVGRNRSIHLHLAHLHRAEPQRRGQCRRRGFGIIGVRFVDAACFDLRLQA\*IDAFSPFIKRP  
IT\*KKSIQVFPSPFRQFDARFQGTQINCFALRDIPDLGFIQVQFQVQIKRGDGVFLPDIITGRIFITVACRINEVFLVFLGVPTILLRHLLVKIKYLFIVSFFD\*ALAAQIERHAQPRI  
IRQFINGRIVAAPFVVIQLVACLSLQ

**SEQ ID 7645**

ATGACTTTCCAAAACAAAAATCCTCGTCGCCGACTTGGCGGCAGGGTATTTCCATGATGCTTATCTGCGCAAAAACGGCGCGGAGGTTGCCCTTATGATGCGGAGCTGAAAGCGG  
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CGGTTGAAGATAAGGCAAAAGCGGCTTCTGATCGCGCTGATGCGCGCAATTCGCGCGGATTGGACGGCTGCGGCTTGAACCTGACCGACTGCGCTCACTTTGGAAGAGCGGCTTC

AGACGGCATACGCCAAGCGAAGCGGCGATATTGCTGCTCAGCCCCGCTGCGGAGTTTCGATATGTTTAAAGGCTACGCCACCGTTTCGGAAGTGTATTATCGAAGCGTTTAAAGC  
TTTG

## SEQ ID 7646

MTFQNKILVAGLGCTGISMAYLRNGAEVAAYDAELKAERVAQIGRMPDGLVFTYGRKLDALDNGFDILALSPGISERQPDIEAFKQNGRVLGDIELLADIVNRRGDKVIATIGSNKG  
TTVTSILVGYLCIKCGLDVTIAGNITPVLLEALQREGKADVWVLELSSPQLENTESLRPTAATVMNISEDLDRYDLDLYAHTKAELFRGDGVQVILNADDVFCRAMKRAGREVRKPSLE  
HEADFWLERGTGCLKQGNEDLISTQDIPLOGLHNAANVMAAVALCEAVGLPREALLEHVKTPOGLPHRVEKIGENGVVPIDDSKGTINVGATAAALAGLQNLPLFVILGGMGRGQDFTPLRD  
ALKDKRAGVFLIGVDAPQIRRLDGGGLN/IDCVTLEBAVQTAYAAQAEAGDIVLLSPACASFDHFKGYAHRSEVFIKFAKAL

## SEQ ID 7647

TTGTTTGTGTCGGTATCCATCGGTTTGGGATTTCGATAAATGTTTCAGATGCAATTGTATCGCAGATTTCAGCGAAACGGCAACGCCCGGGGGCGCGCGCTTGTTCGGGAGTTGT  
TCGGGGGGGGGGTTCGATGCACTGCTACGAATCGCTATCCTG

## SEQ ID 7648

LFLCGIHRVWDSDKSDCTVSQILQNGKRPGRAALFGLFGGGHQLIAIAL

## SEQ ID 7649

GTGTTTCTCTGATTTTAAATTAATTTGTATGGTAAATTTGGCGCTCCTGCTCTTTTTCGGCGCTGATGAATATGACTGCCCCACTTTTACCTCGGGCAGATTTTCGGCGTTCATCACA  
TAGCGTATTATACGTTTGGCCATCGCCCCCCCCCGCGGTATGGGAAACATCAATATGGCGCATAAAGCCGGTATGGCGAAACCTGCTTTTCAAAGTTTATTCATATTTT  
ATTCTTAAGTTTTCCTTCGCGGACGGCGCGCGCAACGCCGGGTTCGG

## SEQ ID 7650

VFLILKLFVWVNRSLFFGADEYDCPHFTSGRPCTITLAVLYCAIAPPAGMKHQYGGIKRMAENLPQSPITHILFLKFAFAGRRANAGVR

## SEQ ID 7651

TTGGAAGTTCATTTGGTTTGTCTTAAACAAATCATATTGGGAGGAGAGCTGCGCCCTTGCCTAAGCCGCTTCAGACGGCATCGCGAGCCGATTAATAACCGCTTCAGCGGTTGG  
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CTTGGCATCCCTTGTTC

## SEQ ID 7652

LESHFGVLKQIILGRRRPPLPKPLSDGLASRLITRLQALVIVAAVLVSVL/SLAKPLLSERKVLHAHAASTVIHQAIQIVLGLGILP

## SEQ ID 7653

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GATACGCGCGGTAAACGCCACCTGCCCCAAGGCATAGCGGTTTTCGACGCCGACAGGTTCGACCCGGATTTCAGCGACGCTTCGACGCAATCCGACGGGCATACCGCTACCTGCTCGAA  
TCGCGCCCCGTCCGTTCGCCCTGCTCAAAACAGGGCGGGCTGGACACACCTTCAGCTCGACATCGGACCGATGCGCGGGCTGCCGCTTATTGGTTCGGCGAACAAGACTTCTCCAGCT  
TCCGCGCGCGGGTCCAGGCAAAATCCCGCTCAAAACCATCTACCGCGCGGACCTTACCAAGCGCGGGACTCGTGGCGCTCGATTTCGACGGCAACGCTTTTTCACCAACATGCT  
ACGCAACATCATGGCGCGCTGCTTTATGTCGGCAGCGGCGAGCTCAGCGCTCGAAGGCTTCGCCGCACTGATTCAAGAACGCGCGCTCAAGGCCACCGACCTTTATGCCGCGAGCGG  
CTTTACCTGACCGCGCTCGACTATCCCGGGGCATACGGCATCGTCCGCCCAAAATCCCGAATGGCTT

## SEQ ID 7654

MDTAQKQWATILSYDSRFYQWQKQAGGVPTVQAALETALARIAGESVATTVAGRTDGVHATAQVVFHPTAAVRPAQAWIRGVNAHLPEGIAVLHARQVAPGFHARFASGRHYRYLLE  
SAPVRSPLKRNAGWTHLELDIGPMRRAALLVGEQDFSSFRAAGCQAKSPVKTITRADLTQSAGLVRLDLHGNAFLHVMVRNMGALVYVSGRLSVEGFAALIQRSLKAPPTFMPDG  
LYLTGVDPYAGYIVRPQIPEM

## SEQ ID 7655

ATGCAGAAAAAAGACATTCGCGCGACACCTTTTCATCCCCAAGTTTCCAAACACATTTCCGGCTTAAATATCCACAGCATTCOCGTCTTAAAGGCACCGGCAGCATTCGGTAAAGA  
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TCAGATGATTTTAAAAATAAAAAAGTTACCCACAGAAAAATTCCCATATCAATATAATCATCGTTTATTTATTTAAACCTTATATTTTATTAACCTTCAGGGAACCGGCACGGCA  
AAGCGTAAAGGCATCTTTTCAAAAAAT

## SEQ ID 7656

MQKRHSRRLFIPTSSKHSGLNIHSIPVLKGTGSHSVKSKMSQAQANYQNLPTKNNPQVCTKGNPPYRHPFKTAIQHLKIKKSYPOKIPHINIIVLLPKPYLFTITLQNGTA  
KRGIFSKN

## SEQ ID 7657

TTGCATTTTATCAACACTTACTCGGAGGGTATTGGAGGCAATTGCAAAACCGGGGTTATAGCGGATTAACAAAAACCGGTACGGGTTGCCCGCCCGCCAGCCAAAGGGAACGGTTCCC

## SEQ ID 7658

LHFYNTYSGGYWRLQTCGYSGLTKTGTALEPRDPKGTVP

## SEQ ID 7659

ATGAAGCGCATATTGGCGTAATCGGTTTGGCGTTATGGGGCAAAACCTGATTTTGAATATGAACGATTTCGGGATTTAAGGTTGTCGCTACAAACCGGCAATCGGTAAAGTGGACGAAT  
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## SEQ ID 7660

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FVGAGVSGGEEGARRGPSIMPGDKRAHEAVKPIFQALAAKTPOGEPCCDVGKDGAGHVFVRMHNGIEYGMQLICEAYQFMKDLGLSYDEMHRVFAENKTELDSYLIETPAALIGYK  
DEGGEPLAEKILDAGQKGTGKWTGINALDLGIPLTLEBAVFARCVSSFFKEQVQTKLFAARTATPVGEGQHEVEALRQALLASKLISYAGPHLIREAGESYWGGLDYGNTALLMREG  
CIIRSAFLNIRDATYANPDLVFLGADPYFKNLENCIPAWRKVAVAVECGIPMPCASAITFLDGYTTERLPANLLQQRDYPGAHTYERTDKPERGEFPHNWTGKGGDTASTPTDI

## SEQ ID 7661

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GCGGACGGTACAAATACGCACTTAAAGACAATTCAGGCTCAACCGGCAATCTTACACGTTGGCTTGAACCTACCAAAACAGCGGCTTCCTGCGCAATACGCGGCTTGTTCACAGATA  
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TTTCTTACGCCACCGCTTCAAAGGCACCTGTGATAGTGAACACGACCAATACTTATGACCAAGTGGTTGTGCGTGGCAATACGACTTCTCAACACGCACTTCTGCTTGGTTTCTG  
CGGCTGTTGCAAGAAGCAAGGCGCAGACAAATCGTATGACTGCCAGCGCCGTCTCTGCGCCACAAATTC

## SEQ ID 7662

MKSLIALFLAALPVAAMADVTLYGAIKAGVQTYRSEHTDGKSVKVTGSEIADFGSKIGFKQEDLNGLKAVWQLBQASVAGTNTGWNKQSFVGLKGGPOTIRAGSLNSPLKNTGA  
NVNAMESGKPTGNVLEISGMQREHRYLSVRYSPEFAGPSGVQYAPKDNSSGNESTHVLNQNQSGFFAQYAGLFQRYEGTKKIEYDQYTSIPSLFVEKLQVRLVGGYDNALYV  
SVAAQQQDAKLYGAMSGNSHNSQTEVAATAAYRFGNVTFRVSYAHGFKGTVDSANHDNTYDQVVVGAETDFSKRTSALVSAGHLQEGKADKIVSTASAVVLEHRT

## SEQ ID 7663

AACGGTGGCGCAAAAGAGACGGGCATTATCGGCGCGTATTCCTGCAAGACTTGGTCGTAAGCTGGCAAAACCGAGAAAAATCATGATGATGTTTCGCGCAGGTTTCGGTGTGACGACT  
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AACGCTCCGGAAGTCCCGGCAAT

## SEQ ID 7664

NGAAKETGIIGAYSLQDLVDKLAAPRKIMMVRAGSVVDDFVEQLPLLEEGDIIIDGNANYPTTTRRTHYLAKGILFVAGVSGGEGARRGPSIMPGGDKRAWKVPKIPQALAAKT  
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FARCVSSFPQKQVQTKLFARTATPVEGGQKQHEALRQALLASKII SYAQFGMLIREAGBSYGNWLDYGTALLWREGCIIRSAFLGNIRDAYEANPLDVLFGADPYFKNILENCLPAMR  
KVVAKAVECGILPMPMASAITFLDGYTTERLPANLLQAQRDYFAGHTYERTDKPRGEFHTNWTGKGGTASTTYDI\*FRCRNAVTRVTAFLVLEIERCSNGFPMYCGCLRRYGYGVITW  
NAPEVPRH

## SEQ ID 7665

ATGTTTTATGGCTCGCACATTTACGCAACTGGTTAACCGGTCTGAATATTTTCAATACACCACATTCGCGCGGCTTATGGCGGCTTGACCGCTTTCCTGATGTTTCGCGC  
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TCGTCGCGCAAGAAATTTGCTCTCGTCAATATGCGCGTCTGTTGTCGTAAGAACCGTGTGCGTTATGCTTACGTTGCGCTGCTGTAAGAAACCAAAACCGCATCTTCTGATGCGCGC  
GATTCATACCATTACGAACAAAGCGTGGAAAGAACCCAGTGTGCTGCTGCTTCTGATATTTACCATGCTTGGTATGATCGGTTTGGTACCTCAAAATTCGC

## SEQ ID 7666

MFLHLAHSNWLTLNLFQYTTFRVMAALTAALFSLMFPWTIRRLTALKCGQAVRTDGPQTHLVKNGPTMGSLILTAITVSTLLMGNWNPYIWLGLVLLATGALGYDDWRKVY  
KDPNGVSAKPKMNVQSSVAIVLAGLALFYLAANSANNILIVPFRQIALPLGVGVPLVLSYLTIVGTSNANVLTDGLDGLAALFVVLVAAGLAFAYVSGHYQSFYQLQPLFYVAGANEALP  
CTAMCGACILGLFNAYPAQVPHGDVGLALGAALGTVAIVRQEFVLVINGLFLVVEAVSVMQVGMVKKTKRIFLMAPIHHHYBQKWKETQVWVFWLITVLVILGLSTLRIR

## SEQ ID 7667

TTGATTCCTGTTGCCGAAATCCGCTCCGAACCGGTCGACGCAATTTGTTTTCAGGAAATAGAAAGATGTTCCAAATGGCTTTATGATGATTTGTGCTGCTTGGCGCGATATGATACGCG  
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CGCA

## SEQ ID 7668

LILPKPCRPNSRSGICFAGNRKMFQWLYDVLWLLAPIWIRRYLDKRSASAPAYRAHRDRPGKPHNPVTGAVWIHAVSVGETRAAQPLIRELRRRPPDAPLIMTQMTPTGRETAQVLFDD  
AQCRLPYDKRTVVRQFLREHRPMFGILMETEIWPNLMKECRRAGVPLFLANARLSEKSLNGLYKVRRLIRPAAASLTGCLAQTEADAARLAKLAGAASVQCGMFKYDLMPSMDMKLAGQ  
FEKRIIGRPVAVCGSTRVYRGDEAEKLLAAWQYRGDALLAVVRHPEHFTTETAKRFGFKQRSDGLPVEPDTQVWVGDSMGLYAYLLCADVAFVGGSLVSGGCGNIIEPLSCGV  
TTIFGFSTYNFSEACHALASGAAVQVESADAWREAVEKTLSEGGGMQMARVDGFIQAHRGAGARIAEAVREAVCGHRGR

## SEQ ID 7669

TTGGGAAAGTCCCTGACGCTTAATCTGCAAAAGCGTCCGAAACCTTCCCGGACAGCAAGCAAACTCAAGCGGGCGCAAGCCGATGTA



SEQ ID 7670

LGKSLHVNLOKPSETLPDSKOTSSGRKPDV

SEQ ID 7671

ATGACGCTTAAACCGAATTGCGGTACATCGTCGAAGTCGCCAAGAACGTCATTTTCGGCGGGGGCGGCGCGTGTGTTTGTGCAGCCAGCCCACTTTTGCTATTGCCAATTAAGAAATTTGGAAG  
AAGAGCTTTCGGGCTCTTTGTGTTGACCGGAGCAGCAACGATATTATTACGACCGAGGCGGGGGAACGTATCGTTGCACAGGCGCGTAAGGTATTGAAAGAGGCGGAGCTTATCAGGCATTT  
GGCAAAATGAAGAACAACAGAGCTGGAGGGTGCCTTCAAACCTCGGGCTGATTTTACGGTTGCGCCATCACTGCTGCCGAACTGATGTGTCGTTCGGCCGCTACTGCACCGGAAATATGCGT  
TTGATGTTGGAAGAGAATTACACGCATACCTTTGACCGAGTGCCTCAAACCGGGGACGTTGACGCGGATATATCGTTTGCAGCAACCGTTTCAAGAGCCGGGCATTGTTACCGAACCCCTGTATG  
ACGAACCGCTTTTTCGTGATTTGTCCGGAAGGGCATTCATTTGAGGAACCTGGATGCCGTTTTCGCCCCGGATGCTGGGTGAGGAGCAGGTTTTGCTGCTGACGGGAAGGCACCTGTATCGCGGA  
TCAGGTACTCTCAAGCTGTTCCGAAATTCGGCGGCAACACGCGCATACAGGGGCTGACCAATCATATGCAGGGCAGCTCGATCAATACAATTCGCCCATATGCGGAAAGCTTTTGGCAAGG  
AGCGTGTTCGGCGGCAACCGCTGACCGGAGAACGATCATATGCTGTTACGATTAATTCGGTTTGAAGGTACGCGCGGCAACCGCGGCGGTGATATGGCGTATCGCGGTAAATTTTGTGCGTCT  
CGAAGCGTTGTGTCGGCGGATGAAGCGCGGCGATTATCATGTCCGAGCTTCAACGGGGTAAGTTTTATCCACGAC

**SEQ ID 7672**

SEQ ID 7672

MTLTSLRYIVAVAQERHFGRAARRCFVSQPTLSIAIKKLEELAVSLFDRSSNDIITTEAGERIVAQARKVKLEAEILIRHLANEQONELBGAFKGLIITVPAYLLPKLIVSLRRITAPKMP  
LWLEENYTHITLSLEKRGDVAIDIAEFPQEGVITPELYDEPPFVITVPKGHSFEELDAVSPRMLGEBQVLLLTGECNCRDQVLSSCSELAQRIQGLTNTLQSSINTIRHVASGLAI  
SVLPATPAITFENDHPLSIIPFEGTTPPSRRRVLAYRRNFVRPKALSAMKAATMQSQLEGVSFTHD

**SEQ ID 7673**

SEQ ID 7873

TTGAGCATCGTATGAGTATTATGCGCGTCGGCCACATCATCCACCTGTATTGCGCACCGCCCTTTTGTGCGCGCGGTGTGTTTTGAAGTGCTGGTTTTGTCCGTCCTGCATACGGGAACGG  
TCTCGCGCGAGGCGCGGCGGAAGTGAAAAAGGCAATGCTCTTACCGCGCCGTCAGGGTGATGCGCTTTGCGGTCGGAGCTGCTGTTGCCAGCGGCATCGTGATGGCGGCAAAACGCTACCT  
TGCTATATCGGGCGAACCCTTTGCCACTTCCCTTCGGCACAATGCTGACGCTGAAAATCCTGTTGGCGCTTCAGCGTGTTGGCGCACTTCGCCATCGCGCTCGTCAAAATGGCGCGTTCCACG  
CTGACCGTCGGCTGGTCGAAATACATACAGCGCGCTCGCTTTTACCATATGCTGCTGATGTCCTTTTGGCAAAAGCGATGTTTTATATCAGCTGG

SEQ ID 7674

LEHRMSIYAVAH IHL YCATAPVGGVFFEVFLVLSVLHTGRVSRREARREVEKAMSYRAVRVMPFVAVGLLFASGTIVHAANRYLPISGEFPATSPFGTMLTKILLAPSVLAHFAIAVVKEARST  
LTVGSKYIHA VVPTMLLIVFLAKAMPYISW

SEQ ID 7675

SEQ ID 7675  
GTGAAATGAAAGCCGACGTTTTTTAAAGCCTATTGCGATTGCCGCGTGGTCGGCGCGTTTATGCCGGAATGCGGACGCGAGCGGTATCTTTATGAAGATTATGTTTAGACTGG  
CGCGCGGCAGAAATCCGGGGAGCTACCCGATTTCGCGATTGGGAAAGTCCTGCACGT

**SEQ ID 7676**

VFVKSRBFKALLLLAALVGAFYAGERTQAYLYEDLCCLDLGGGKNPGSTYPICVIGKVPAR

**SEQ ID 7677**

SEQ ID 7677  
ATGTCATTGATCGAACTTTTATTTCGGTAGAAAGCAGAAAAACGGCAACCGTTGCCCGCGACGCGCTTCAAATCATCATTTGCCCAAGAGCGCGCCCAAGAAGGTGAGACTCCGGATTACCTGC  
CGACTTTACGTAAGAGTTGATGGAGTCCCTGTCCTCAATATGTGAATGTTTCATTAGACAATATCCGTATTTCCCAAGAAAAGCAGGATGGTATGGATGTCCTTGAGTTGAACATTACTTT  
GCCCGAACAGAAAAAGGTA

**SEQ ID 7678**

MSI.IEL.EGRKOKTA'VARDRI.OII.IAOERAOEGOTPDYLP.TLRKELMEVLSKYVNVSLDNIRISOEKODGHDVLELNTLPEQKVV

SEQ ID 7679

SEQ ID 7679  
ATGGCTAAAAATGGGGGATTTTCTTTGTGTGCGCAAAAGAAAGAAAACGCTTTATCTTTGAAGGCAGGCATTCGCTCCGACAACTGGTCAACGGCGAAGATATCCGCGTTTACCGAAGAAG  
AGGCAACGCAAAAACCTGGCAAAAACGCGCATTCGCGCCGTTGCAGATTACCGGTGTGAAAACAAAGCTCCAAAGCGCAAAATCACACAAGAAGACATTACCGTTTTCACCGCCAGCTTTCCAC  
GATGATTAAAGCGGGCCCTGCCGTGATCGAGGCATTTGAAATCGTGGCGCGGACACGGCAACCCGCTCATGACGGAAATGCTGATGGAATTCGAGGCCAAGTGGAAACAGGCGAGCTCG  
TTGAGCCGCGCATTCCTCAAACCACCGAANAATTTTCGACCGCTTCTACTGCAACCTGGTTCGGCGGGCGAAACGGGCGGTGATTGTGAAAGCCTGCTGGACAATTTGGCAATTTACAAGG  
AAAAACCAGGCCATCCGCAAAAAGGTAAACCAGCGCTAACCTATCCGCTATCCGTCATCGCGCTCGCCATCGGTTTGGTATTCCGTGATGATGATTTTCGTACTGCCCGCTTTAAAGA  
AGTTTACGCCAATATPGGCGCGGAGCTTCCCCCACTGACCAACAAAGTGATGGATATGTCCGACTTTTCGCTCATACGGCTGGTGGTGGCTGATGCGACTGGCCCTTTGCCATACAGGC  
TTCCTTAATTTGAAGGCGGCTTCGATTAAAAATCCAACGGCGTATGGATGCCATAGCTGCGGTATGCCGATTTTCGGAGACATTGTTCGCAAGAGACGATTTGCCCTGGGGCAGCGCA  
CGGCAACGCTGTTTGGCCCGCGCGTCCCTTTGGTCGATGTTTGGACTCCACTGCGCGCGCGCGGCCCAATTTAATCATATGAAGAAGACCCCGGAAATCCGTACGCGCGCTATCCAAGG  
TCTGTCTATGACTTCGGGATCGGTGCGACGGAATGTTCCCAATATGATGTTGCGAGATGTCTCTCCATCGGCGAGGATTCGGGTTCCTTTGGACGATATGCTCAACAAAGCGCGCAATTT  
TACGAAGACGAGGTGCAATATCGGTCGGCAGGCTGTCCGTATGATGGAGCCGATTATTATTGTGATTTTGGGCTTGGTCATCGGTACGCTTCTGGTCGTATGTAATCTGCCGCTGTICA  
ACTTGGGCAACGTGGTCGCC

SEQ ID 7680

SEQ ID 7680  
MARNGGFLPAKKEKRFIFEGRHSASDKLVNGEVSAPTEEEARKKLAKRGIRLPQITVRVTSSSKKRITQEDITVTRQLSTMIKAGLPLMQAFETIVARGHGNPSMTENIMETRGRQVBOGSS  
LSRAPSNHPYKFDORFYCNLVAAGETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAPKEVYANNKGAELPPLTQTVHDMDSFFVSYGMMVLIALGFAIYG  
FLKIKARSIKIQRRHDAILLRMPIFGDIVRKGTLARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEATREIRTRVIOGLSMTSGMRATELPFMMQLQSSIGEESGSLDDMLNKAAEF  
YEDEVNAVGRSLAMMEPIIIVILGLVIGTLLVAMYLPLFNLGNVVA

**SEQ ID 7681**

SEQ ID 7681

ATGCCGCTCTCAACGACGACGAATTCGCGGTTTTCAGACGGCATTTCGCCATCCCGATATGCTCTAAACAAAACCGAAGCGTTTGCTATAATTGCACATTTTACCGCACACGACGCCCATGTTTC  
CCGATTTCTCCAAACCCCTCTCCAAAGACGCCCATTTCTGCAATCCGCTTCAAAAATCCCAACAAATACGGCGGCTTGTCCAAAATCGAAGAAAAATACCGAAAATCGCAGAAATCTT  
CTTGAACCGTTTGGCCGATTGCCCCAAACCGGAATTCGACGACACCTTGCCCGTTTCAGAAAACTCGAAGAAATCAAAAAACCGTTGCGCGAAATCAGGTAACGATTATCTCGCGCGAA  
ACCGTTGCGGCAAAACACGCGATTGCCCCAAGATTGTGTGGAACCTCGGGCGTGGGGCGGCAGGATTGATCGGGCATACCCAGCGCGCGCTTTGGCCGCGCGTTCCGTTGGCGGAGCGGA  
TTGCCGAAGAGCTGAAATCCGGAATCGGCAGCGCGTTCGGCTATAAAGTGCCTTTTACCGACACCACTCCGCGGATGCTTCGCTCAAGCTGATGACCGACGCGCATCTGTCTGGCGGAAC  
CCGACCGGATCCTTTATCTTCGCCCGCTATGACGAGCATTAATTCATTGACGAGCGCATGAAACGACCTGAAACATCGACTTCTCTTTGGGCTTACCTAAAACAACCTCTCGCCGCGCCGCCCGAT  
TTGAAAGTCACATCATCATACCTGCCACCATAGACGAGTAACGCTTCTCCGACACTTCAACGGCGCGCCCGTACTGGAAGTGAGCGGGCGACCTATCCCGTGGAAATCTCTTACCGAOCG  
TGACCGGCAAGACGAAGACGACGACGAGAAGTCTGAGCTGACGACGCGGATTGTTCGATGCGCCGACGAAATGGCAGCTTACGGCGAAGGCGGATATTTAGTATTTCTGCGCGGCGAAGCGGA  
AATCCGCGAAGCGCGCAGAAGCCCTGCGCAATTCACACTGCGCGCAATGACGAAATCTGCCCCCTGTTGACACGCTGTCGACGCGCGAACAGCACAATAATCTTCCACCTTCAGCGCGA  
AATGCGCGCATCTGCTCTGGCGACCAACGTCGCGGAAACCTCGCTCACCGTGCCTGGGCGATCAAAATACGTCATCGACACGGCTCGCGCGCTGCTCAACCGCTATTCCGCGCGCGCAAAAGTC  
AACAATCTTACGCTAGAAAAATCTTCCAAGCGCGCCGCGCAACGCTCGCGCGCTGCGGACGCGCTCTCAGCAAGCTGTGTATCCGCTTTTTCAGAGAAGATTTTAAACAGCGCTGC  
CGAATTTACCGATCCGAAATCTGTCGCGACCACTTCGCCCGCTCATCTGCGCATGACATCGCTGAACTGGGCGAGCTGACGATCATCCCGTTTTAGAAATGCGCGATTTCGCGATAT  
ATCAATGACGCTTTTCAGGTTGTGCTGGAATTTGGGGCAGTGGAGGTTGTC

SEQ ID 7682

SEQ ID 7682

MPSEQRQNAVRRHPPIPTLLKQNRVCYNCTFYTRTTPMPDFQSTLSKDRHFLQSAFKNPKHYGGLSKIEEKYRKSHEIFLKRLAALPKPEPDDTMFVHKLEIKKTVAEHQVTIICGE  
TGGSGRTPTLPKICLLEIGRGAAGLIGTQTPRRLAARSAVERIAEELKSEITGSVAGYKVRFTDHTSRDACVKLMTDGIILAEQTQDRYLAAYDTIIDEAHERSLNIDFLGLYLLKQLLRPRPD

LKVIITSATDAERFSRHFNGAPVLEVSRTYVVEILYRPLTGKDEDDAEVELTDAIVDADELARYGBEDILVFLPGEREIREAAALRKSTLRRNDEILPLPARLSHAEQHKIHPHSGA  
KCRIVLATNVAETSLTVPGIKYVIDTGLARVKYSARAKVEQLHVEKISQAAARQSRGCRVSAGVCLRFSBEDFNSRPEFTDPEIVRSNLAAVILRMASLNLGDDVAAPFPLEMPDSRY  
INDGFQVLELGAVEVV

**SEQ ID 7683**

TTGATGGGAAATGCCGCTCGAAAGGCTTCAGGCGGCATTTTGTATTGGGCATTTGGTAAATGTCTTTAGAAAAGAAATATGCAAAATTTAAAAATCCCGGTGTTCTATTCTGCTT  
TCTTACGCTATTCTTTAAAGGTGGGAATCTGGAAACCAAAAAACAACAGGAATTTATCCGAAACAACAAACCTATCCGCGTCATCCCCAGAAAGCGGGAATCTAGTTTCTGTTCAA  
A

**SEQ ID 7684**

LMGKCRLLKGFRRHFLWALGKMSLEKNIANLKNPRVLISAPLRHSPKGNLETKKQEFIRNNKTYPPSPRKRESSLLFK

**SEQ ID 7685**

GGAGATTGAACCATGACAGAATATCCCGCATCGGGTCGCGGTGTTTTACGGCGTTTTTTTTGCGCGCAGTGTGCTCATGATTGCCCTGGATATGTTTTTCGCTGAAGAAAAACGGCAGCC  
ATAAAGTCGGCATCAAGAAAACTTTGGCATGGAGCGGCTTGTGGGTTCGGGTATCTCGCTGTTTCGAGAGCTGGCTGTATTTCGAACCTCCCGGCAATCCCGCTACCGCGCGGCGAGCGC  
AAAAGAAAAATATTGGAAATCTTTACCGGCTACATTTTGGAAAAATCGTTGGCAGTCGACAAATATTTCGTGTCTCATGATATTCGGCTACTTCAAAGTCGCAACCGCAGTTTCAGCAC  
CGCGTGTCTGTACGGCGTATTGGCGCATTTGGTATTGGCAGCCGTCATGATTTTCGTGGCGCGGCACTGGTTCCGCGAGTTGAGTGGATTCTGTATCTGTTTGGCGCGTTCTGCTCT  
ATACTGGTATACATGATGAAGCCCGAAGCGGATGAGAAAGAGGATTTGGCAACAGCAGGCTGTGAATGCCGCTCAAGAAAGTCGTTCCGGTCGGCAGCGGAATTTACAGCGGAGAAAT  
TTTTACGTCGAAACCGCAAAAAATCGCCACGCGGCTGTTTTGGTGTCTGTCATGATTGAATTTAGCGGATGTCGTGTTGCTGTGGACAGTATTCGCCGCTTACCAAC  
GATCCGTTTATCGTGTGACTTCCAATATTTTCGCTATTTTGGGTTCGCGGCGATGTTATTCCTGCTGGCGGATGTGGCGGAACGCTTTATCTTCTGAAATACGGCTTGGCATTCGTGT  
TGAGTTTTATCGGTGAGAAATGCTGGTAAATGCAATTTGGTGTGAT

**SEQ ID 7686**

GD\*TYTEYPIGSPFYGVFFAAVLVMIALDMFLSKKNGSHKVGIKETLANSGLWVAVSCLFAGWLYFELAGNPGYGAAAAKEKVLFFPTGYILEKSLAVDNIPVFLMIFGYFKVAPQPH  
RVLLYGLVGLVLRVMI FVGAALVRQFEWILYLFAGFLLYTGIRHMKPBGDEKEDLANSRLNNAVKVVPVGTETPHGEKFTVENGKKIATPLFLVLVMIELSDVVFVAVDSIPAVFAVTT  
DPFIVLTSNIFAILGLRAMYFLADVAERFIFLKYGLAFVLSFIVKMLVMHNVH

**SEQ ID 7687**

GTGTTTTACACAGCAAAACAGCGGATAAAAAATCAGCCGCTACCGATGTGTCCGCGCCCGCAATATTAAAGCAAGCAATATGAAACCACTGGACCTAAATTTATCTGCGCAAGCCCTC  
AAGCTCCGATGCCGTC

**SEQ ID 7688**

VFYHSHKYGDKISRYRCVRRPNINSEKYETTGPKFHLSPQASDAV

**SEQ ID 7689**

GTGGCAAAATATTGTAGTAACCTCAGGCAAGGGCGGTGTGGTAAAAACGACTACAGTGCAAGTATTGCAACAGGTTTGGCATTTACGCGGATATAAACTCGCGTAATTGATTGATG  
TGGGTTTTCGCAACCTCGACCTCATTTAGGGTTCGAGCGTGTGTGCTTTATGACCTGATCAATGTCAATTCAGGGTGAGGCGACGCTCAACAGGCTTTGATTAAGATAAAAAATGTGA  
AAAACCTGTTTATTGTCGGGCTTCCGAGATCAGGATTAAGACGCTTTGACACCGGAGGCGGTAGAAAAAGTATGACGAGCTGTCCGCAAGAAAAATGGGCTTTAGTATATTTATTTGC  
GACTCTCTGCTGTGATTAGAGCAGGTCATTTGATGGCTTGTATTTTGTCTGATGAAGCCATTTGTAACGACCAATCTGAGGTTTCCAGTGTGCGTGACTCCGACAGGATTTTGGGAATTT  
TGCAAGCAAAATCCCGTAAGCGGAGCAAGCGGTTTCGGTTAAAGAACATCTGTTAATTACCGGCTATTCTCCCGAACCGTGTGGCAAAAGCGGAAATGCTGTCTGTACAGGATATTTCGGA  
TATCTGCGTATTCTCTTGGCTGGGTGATTCCCGAATCCCAAAACGCTTTCGAGGATCCAAATTCGGGAGAACCGGTATCCATCAGGACAGCGTAACGGCTTCCGAGGATATAAGGAC  
GTTATTGCCGCTCTTTTGGCGGAGAACCGTGAAATGCGTTTCTTGAAGCTGAGAAAAAAGCTTCTCAAACGTCGTTCGAGGA

**SEQ ID 7690**

VAKIIVTSKGGVGKTTTSASLATGLALRGYKTAVIDFDVGLRNLDLIMGCERRVVYDLINVIQGEATLQALIKDKNCENLFIIPASQTRDKDALTRGVEKVMQELSGKMGFEYIIC  
DSPAGIEQALMALYFADAEIVTNEPVSSVRDSRLILGILQSKSRKABQGSVKEHLITRYSPERVAKGEMLSVQDIDILRIPLLGVIPESONVLQASNSGEPVTHQDSVTASEAYKD  
VIARLLGENREMRFLAEKKKSFPRLLFGG

**SEQ ID 7691**

ATGACAGAATATCCCGCATCGGGTCGCGTGTGTTTTACGGCGTTTTTTTTTCGCGCAGTGTGTCATGATTGCCCTGGATATGTTTTTCGCTGAAGAAAAACGGCAGCCATAAAGTCGGCA  
TCAAGAAACCTTTGGCATGGAGCGGCTTGTGGGTTCGCCGTATCTGCTGTTTCGAGGCTGGCTGTATTTCGAACCTCGCGGCAATCCCGGTACGGCGCGGCGAGCCGCAAAAGAAAAAGT  
ATTGGAATCTTTTACCGGCTACATTTTGGAAAAATCGTTGGCAGTCGACAAATATTTCGTGTTCTGATGATATTCGGCTACTTCAAAGTCGCAACCGCAGTTTCAGCACCGCGTGTCTGT  
TACGGCTATTGGCGCATTTGGTATTGCCACCGTCATGATTTTCGTGGCGCGGCACTGGTTTCGGCAGTTTGTAGTGGATTCTGTATCTGTTTGGCGGTTCTGCTCTATACGTGTATAC  
ACATGATGAAGCCCGAAGCGGATGAGAAAGAGGATTTGGCAAAACAGCAGGCTGTGAATCCGCTCAAGAAAGTCGTTCCGGTCGGCAGCAATTTACGGCGAGAAATTTTACCGTCGA  
AAACGGCAAAAAATCGCCACGCGGCTGTTTTTGGTGTCTGTCATGATTGAATTTGAGCAGATGTCGTGTTGCTGTGACAGTATTCGCCGCTCTTTCGGCTTACCAACGATCCGTTTATC  
GTGCTGACTTCCAATATTTTCGCTATTTTGGGTTCGCGGCGATGATTTCCTGCTGGCGGATTTTCGAGAGTGGCGGAACGCTTTATCTTCTGTAATAACGCTTGGCATTTCGTGTTGAGTTTATCG  
GTGTGAAAAATGCTGGTAAATGCAATGGGTGCATATCCGATTTCCGTTCACTGTGCGTGTGTCGCGCGTGGGTGCATCGATACTGACCTCGTTAATTTATACGAAAAACAGCCTGA  
TAAA

**SEQ ID 7692**

MTEYPIGSPFYGVFFAAVLVMIALDMFLSKKNGSHKVGIKETLANSGLWVAVSCLFAGWLYFELAGNPGYGAAAAKEKVLFFPTGYILEKSLAVDNIPVFLMIFGYFKVAPQPHRVLL  
YGLVGLVLRVMI FVGAALVRQFEWILYLFAGFLLYTGIRHMKPBGDEKEDLANSRLNNAVKVVPVGTETPHGEKFTVENGKKIATPLFLVLVMIELSDVVFVAVDSIPAVFAVTTDPFI  
VLTSTNIFAILGLRAMYFLADVAERFIFLKYGLAFVLSFIVKMLVMHNVHPI SVSLSVVFGALGASILTSLIYTKKQPK

**SEQ ID 7693**

ATGCCGCTGAAACAAACCCGTGTGCGCATCGTAACCGACAGCCGCGATATTCGGGAAGCGGATGTGTTTTTCGCAATTCGCGGCGGGCGGTTTGAAGCGCATGATTTGTTGGAGGCG  
TATTGCTGCGGGCGCGCGCGGCTTGTGTTTTTCGCGCAAGATTGCGCGGCTTTGGCGGGCGGCTGAAAGTCGATGACACGCTTTCGCGGTTGCAACCTTGGCGAAGGCGTGGCGCGA  
TAATGTGAACCCGTTGTGTTCGCGATTACCGGTTTCGCGCGGCAAGACGCGGTGAAGGAGATGCTGGCTCGGATTTGCGCCCGCGTTTCGCGCATGATGCCGTTTCGCGGACGCGGCGG  
AACTTCAACAAACCATCGGATTGCGCGTACTTTATGAAATTAACGAAAAACACCGCTATGCGGTGATTGAAATGGGCATGAACCATTTTGGCGAAGTGGCGGTTTAAACGAAATCG  
CCAAACCGATGCCGCTTTGGTCAACACGCCCTGCGCGCCATGTCGGATCGGTTTCGAGAGTGGCGGATTTGCCAAAGCGGAGATTATGACGGCTTATGTCAGACGG  
CATGGCAGTATTCCTCAAGAGATGCCAATATGCTGTCCTTCAAAACGCGCAACGTTAATTTGAATACGTGCACTTTCCGGCTGATAGCGGCGATGCCGCGGAAAAATATCGTGTG  
AAACCTTTGTCGTGCGCAATTTGATTGGTGTGCGGCGAGCGCACTGCGGTGTCGCTGTTCCCGCGCCCAATGTCCACAACGCCGCGTGGCGCGCGCTGCTTTGGCTG  
CGGTTTGTGATTGAACGATGTGGCGGAAGGTTTCAAGGCTTCAGCAACATCAAGGCGCTGTAACGCTCAAGCGCGCATCAAGGCGCAACCCGATTTGACGATCTTATATATGCGAA  
TCCCGACAGTATGAAGCGCGGTTGACGTTTGGCGGCTATGCTGCGCGCGCATTTTCGTGATGGCGGATATGGCGAATTCGGCGGAGGACGAAGCGCGCGCATGACGCGCAAGTTC  
GGCGGCTACGCGCGGACCAAGGATCGAAGCGGCTTATTTGTCGCGGCAACAGCGCTGAAGCGCGGAAAAATTTGGCGCGGACGCTTGTGTTGCGCGCAAGACCGGTTGATTTC  
AAGTGTGAGCCAGATTTGCCCGAACCGGCCACCGCTGTTGGTGAAGGTTTCGCGCTTTATGCAGATGGAAGAGTGGTTCGAGGCATTGGAGGATAAG

**SEQ ID 7694**

MPSENKFSRVITVDSRDIREGTVFALAGGRFADHDFVGGVLSAGAAVVVSREDCAALGALKVDDTLAALQTLAKAWRDNVNPFPVGTGSGGKTVKEMLAALVLRFPDGDVAVSATAG  
NPNHIGLEPLTLKLNKHYAVIEMGMNHFGEALVLTQIAKPDALVNNALRAHVCGGDFGVGDIKAKSEIYAGLCSGDHALIPQEDANMAVFKTATFNLTCTGTVDSGVRAENIVL

KPLSCFDLVCCDERTAVLVPVGRHNVHNAALALALAGLSLNDVABGLQGFSSNIKGRILNVKAGIKGATLIDDTYNANPDSMTAAVDVLARMPAPRIIPVMDMDELGEDEAAAMHAEV  
GAYARDQGLEAAYTVGLDMSVEAAEKFGADGLNFAAKDPLIQVLSHDLPERATVFLVKGSRFQMKKEVVEALEDX

## SEQ ID 7695

TTGCCGCGTAAACTTACATCAITAAAAAATTCATGATGGTTTATATAATGAATGCCCTTCGATATAAAGTCGACAAAGATGGACGTATTGTCTATATCTTTGCATACATCAGACTTGTTC  
ATTTCGAAGATGTGCTGGTCAAAATTTGGCAAGAAAGTTCAAGAGTCTGGTGTTCATTTGTTCTGGATGTCAAGAATTGATTATCCCGAGTCTTTGGATCTTGTGCAATTGGTTTC  
GTTGTTTTCAGGCGATGCTATGCAAAATTTGGGTCTGAAGCATTTCAATGAACGTGGGGTCTGTGGCTATGAAGTATCATTGCTGTTTGTCTGTCTCATTCGGAAAAATGTTAAAGAA  
CTGGGTCAAGTTGAGTGCAGAAAAACGAGGATGGTCAGAAAGCAAGGAAACAGTATTGATTACATCCCTGTCCGTACCGGTACAGAGGTTTATGCCGAAGATGGCGATTGATTGTTA  
CGGGGGCGGTACAGCGAGGGCGGAATTTGATTGCAGATGGCAATATGCATATTTATGCGCGATGAGAGGGCGTGTCTTTGGCCGGGCCAAAGGTGATCTTTCGCCCGCATATTATCCA  
CTCCATGCAGGCGGAGTTGGTTCTGTCCGGGGATTTCACGTAATTTTGAACAGGATTTCGCGGACCATCTGCACAAGCAGCGGTACAGATATTGTTGCAGGATAACCGATTGGTTATC  
AGTCAATTTGGCTCAGAG

## SEQ ID 7696

LRGKL/SLKNSMMVIMNADIKSKMDVLSISLHSDLFEDLVKLKFKFQESGVVFFVLDVQEFDPYPSLDLALVSLFRRHGMQILGLKHSNERHAAMKYHLFLCLSHSENVKE  
LGQVEVQKTEDQKARKTVLITSVPTGQVVAEDGDLIVTGAVSQGAELLDGNMHIYAPMRGRALAGAKGDT SARIP IHSMQAELVSVAGTYRNFEDLDLHLKQPVQILLQDNRLVI  
SAIGSE

## SEQ ID 7697

GTCCGTAGAGCAGCGGACTTTTAATCCGTGTGGTCGAGCGTTCGAATCGCTCAGACCCACAGATAAAGCAAAAAAGCTGAGTTTCAAACTCGGCTTTTGTCTTCCGACAATCCTT  
GTTCCGAAGCGCGCATTTCCGTC

## SEQ ID 7698

VGRAADP\*SVGRAPESL/THQIKQS\*VFKTRFLSSDNPCSESAAPRQ

## SEQ ID 7699

TTGAATTTGGTGCAGAAACCGGCTGCTGAGTAATTTTATGTCATATAACGCCATCTGCCGAAAAGCAGGTGGCGTTATTTTGCATATCTGATAGATAATATGGTATTGGCTATCATGTTTA  
AAATATTAATTGAA

## SEQ ID 7700

LNWL/NRLLSNFSHITPSAEKQVALFLQYLIDNHVLAIMFKILIE

## SEQ ID 7701

AAACTCGGCTTTTGTCTTCCGACAATCCTTGTTCGAAAGCGCGCATTTCTGCAAAATCTTTGGTGGCGCTTCGGTATTTTCCGAAAAATCCCTTATAATTCGCCCTCTGCAACCT  
TCATCGGGTATGCTTTATCGGTTGCCGAGTATGAAATATTTATAGTGGATTAACAA

## SEQ ID 7702

KLGFPCLPITLVRKARHVPKFGAASVFFPKIPYNSASATFIG\*CFMRCPEY\*NIIVD\*Q

## SEQ ID 7703

ATGAACAATCCGCCGAATAAAAAATATGGATCAGACATTAATAATACATTTGGGCATTTGCGCGCTTTTAGCCTTTTGTCTTGGCGCGGCATCGCATCAGGTTATCATTTGGAATATG  
AATACGGCTACCGTTATCTGCCGTGGCGCTTTGGCTTCGGTTGTATTTTATTATATTGGCAGCGCGCTTCCCGCGGCTTCTCTAGTTTGTACTGATTTACGTCGGCACAACCGC  
CCTATATTTCGCCGTGGCTGGCTGTATGGTGGCGCTTCTTATCAGATAGTCGGTTCGATATTGGAAGCAATCTGCCGAGGCGGTAATTTGTCCGCAATCTTCCCGGCTCGCTTAT  
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TGACTTTGATTTTGTCTGCGCGGTGATGGAATAATCGCTGGCGATAAAGATTGGCGAGAACCTGATGCCCGGCTGTGTGTAATTTTTCGACCTGTATACGATTGGCTTCGCGCC  
GGCACAATATGCCCGCAAGCGCGCCACATTTTGAAGCAGCAAAAAAGCGTCAACATGGCATATCCGTCATGTTGCGCCCAAGTATAAAAAATATGTTGTGGTTATCGGTGAGAGCGCG  
CGTTCGATATATGAATGTTTACGGTTTCCCATTTGCCGATACGCTTTTGTAGTCCGACCAAGGGCTGTGATAAACGGTTACCAATTCGACCGCCACGCGCAATCTTTCGCTGC  
CGCAGACTTTGGGGCTGCCGGGAGCGCAACATAACATTTGTCAGCTTTGCGAAGCAGCGCGGTTTTCGAGCGCGTGGCTGTCTAATCAAGGAATGTTGGGCGATTTTTCGAACGAAT  
TTCCACCTATGCCCTACGAGCGATTATCCGTGGTTTACCCAAAGGGGTGATTATGGCAAAAGCGCGGGTTGAGCGACCGCTTTTGTTCGCGGCTTCAACCGGTTTTCAGAGGAAT  
GCAGGCACGAAGCTCGGCTGATTTGATGCACCTGATGGGTTCGCACAGTGATTTTTGCAACGTTTGGATAAGGATGCGCGCGGTTTCAGTATCAAACTGAAAAAATATCCTGCTATG  
TTTCCACCATCGCGCAACCGATAAATTTTGAAGATACGGTTAAGATATTGAATGAAATAAAGAAAGCTGGTCTTTGGTTTACTTTTCCGACCAGGTTTGTATGATGTGCGCAAGG  
CGGCGAGCGAAGCTTGACACAGCGGAGTGAAGCGCTCAAGCTACGCGCTGCCGTGGTTAAAAATTTGCTCCGATGACACGCGCGGCAATGATTAAAGTGAGCGCGAGCGGTTTAAAT  
TTTTTACCGCGATTCGCGAGTTGACAGGATTCGAAACCGAGTTGCGCGATGACGGCTATGATTTTGGGGGAATGTCGCCGATGTCGCGCGCAAGCAATACCTTTCCTTTATCG  
ACAGACAGTCCGACGACCCCGCGCGGTGATGCGGAAAGGCAATCGGCTAAAAATACGTTCTAAAAAA

## SEQ ID 7704

HKQSARIKMDQ/LKNTLGICALLAPCGAALASGVHLEYEYGYTRYSAVGALASVVFLLLLRGFRVSVVLLIYVGTALYLPVGMWLYGAPSYQIVGSILESNEPAAREFVGNLPGSLY  
FVQALFFIFLGLTVKVCYGVFADVKNYKRSKIMLTL/LFLSLCAVMEKLAGDKDREPDAGLLNIFDLVYDLASAPQAIAKRAHILEAAKASTWHIRHVAPKYKRYVVVIGESA  
RSDYMNVYGFPLPDPFSLRKTGLLNGYQSTAHATNLSLPQTLGLPGEFNINIVSLAKQAGFRATWLSNQMLGHFANEISTALRSYDYPWFQRGDYKGSAGLSRDLPLPAFKRVLTGN  
AGTKPRLIVMHLMGSHDFCTRLDKDARRFYQTEKISCVYSTIAQTDKFLBDFVTKLLNENKESWSLVYFSDHGLMHVKGGERTLTHGEWRQSYGVPLVLKISDDTTRREMKVRRSAFN  
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## SEQ ID 7705

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## SEQ ID 7706

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## SEQ ID 7707

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## SEQ ID 7717

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## SEQ ID 7718

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## SEQ ID 7719

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## SEQ ID 7720

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## SEQ ID 7721

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## SEQ ID 7722

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## SEQ ID 7723

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## SEQ ID 7724

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## SEQ ID 7725

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## SEQ ID 7726

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## SEQ ID 7727

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## SEQ ID 7728

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## SEQ ID 7729

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## SEQ ID 7730

IGSIRGLYSILLINIFTSRYYPDAGIRFRHTGCFYL

## SEQ ID 7731

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GCAT

## SEQ ID 7732

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## SEQ ID 7733

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## SEQ ID 7734

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## SEQ ID 7735

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ATTTACAGACATATATAAAGCAGTGCATGCTTGGGGAATATGGAATAACCAATTTTCAAGATGAGGTTGAAAATTTATTTAAAAAATTTTGTGAATAAAAAAATACGCATATAAA  
GACTACTATGATGTTGATTATAAAAAATATGCGGATATGCT

## SEQ ID 7736

MTVFRCNNWGWRLSENRIQIRLCPTTLLSLLGINTMNIKEFMSNYTNHVPVFIGTGMSLYLNDNSYTWGLLSKIAIDLPGDDREYLNISKRYCEDGRFOYEELAEELQSKFDKVL  
NDPDRFKPKINDKNSRPFENRAGNTLSRFKIYISTLLSQLNKDINSNTSELKARKKNVGSIIITNYDKLAQDIFEFNLIGNDILLSNPYGSVYKIHGCVDDPKLIIITKKDYKFKPKYK  
LIRAQLLSLFIHNPIIFLGVNDENIKELKTIPTVYEQNSPSANKIRNPLIVEYEPESNNEDIVHDIDIITGFSIRINKIKTDNFSQIKALAEILPLISAMDVRFQSIKAEITYG  
GNIKVSTFEDMDLNNNDKVAIGSTKISYNFTTSEMSNYFKIIIEBNSQLKLIDKHSIASTQYPIYGFSRICSDIHKRAVLKROQKEKLWPIIBEINRRCNNHNSIQSILDDEN  
ISDTYKNDATAWGIWNNQLSEDEVENYLNKFNVNKNTHYKRLLCMFYDKYADTV

## SEQ ID 7737

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TCAGCACCGACATCGACGTGTTAAACCAAAACATTTACAACAAAATCACCACGGTCGGCAAGAGACTTGGTGCAACGGCGAAACACCTTTCCGCCAAATACGGCGTCCGCAATTGTGAATCA  
CGCATTTCCGTACCGGATTTCCCAAAATCCGGCGGCGACAAAGCCGACAGTTATGTACAGCTGGCGCAGACTTTGGACAAAGCAGCCAAAGCCATCGGCCTGCTCTTATCGCGCGG  
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CATGATGCGCTTCCAGCGCGGTGCGCGGTGTGAGCGCGCGTTTATCCCGTTCCGAGACGAAGGTATGATTGCGCGCGCGGAGGCGAGCGGTGAGCGCTGAGCAAACTCGAAGCCATG  
ACCGCGCTGCTGCTGCTGTTGTTGACATGATTGCGGTTCGCGCGCACGCGCGCGCACCAATTTCCGCGCATCATCGCGCGAGCGCGCATCGCGCATGATCAACAGCAAAACCCG  
CCGTGCGCATTTATCCGTTAAGCGGCAAAACCGTCCGCGGACAGCGCTGAGTTCGCGCGTCTGTTGGCTACGCGCTGTAATGCCGCGCAAAAGAGGTTCGTCGGAAGTGTCTGTCACACG  
GGCGCGCAGGATCCCGCACCGGTTCAATCGATGAAAAAC

## SEQ ID 7738

LSRRNVMSIQSGEILETVKMADQNFDVRTITIGIDLHDCISTDIDLVNINYNKITTVGKDLVATAKHSKAYGVPIVNRISVTPPIAQIAAATKADSYVSVATLQDKAAKAGVSVFIGG  
FSALVQKMSPSDEVILRSVPBAMKTTDIVCSSINIGSTRAGINDAVKLAGETIKRTAEITPEPGCAKIVFVFNADVNPFMAGAFHSGGEADAVINVGVSGPVVKAALENSADVSLT  
EVAEVVKTAFAKLTIVRGELIGREASKMLNIPFGLDLSLAPTAVGDSVARILEENGLSVCGHTGTAAALALLNDVKKGGMMASAVVGLSGAFIPVSEDEBGMIAAEAGVLITLQKLEAM  
TAVCSVGLDMIAVPGDTPAHTISGIIADEBAIIGMNSKTAVRIIPVTKGTGDSVEPGGLIGYAPVMPAKESSCEVFVNRGGRIIPAPVQSMKN

## SEQ ID 7739

TTGAATATAGACGGCTTACGGGTCTTTGTTTCGCGCAAGCAAGGGCTAAGGCAGTACGGCAGCAAAATCCGCAATGTTAAAAACAGACGCG

## SEQ ID 7740

LNIDGLRVFVSRKARAKAVRQIIPQCIKTA

## SEQ ID 7741

ATGCAGAAAGTCTATGTTGTCCAGTCCGTATCAACAGGGGASTTTCTGTATCTCTCTCTGAAACGGGCGACATCGGACATACCAAATTAATTACCAATGCCGATTATTTCTACGACTTGG  
AAGAAGCGGTTAACCGCAGGTTTGGAGAAATCGGCAACCAATGCGAATTTGTCGTATTCGGATTTTGTAAAGAC

## SEQ ID 7742

MQKVVVQSVSTGDFLYLSPETGDIHTKLIITNADYDFEAVNAGLEEIGNQCEVVFVFLKD

## SEQ ID 7743

TTGGGAATGGAAACCGCTTTCCCAAAATATGGCAGGACATCAAGACGAGACGGATTTATGCATAGTTGTGCGGATTATCCGATATCAATTTGAAACGATTGGCTTTGATACCTAAAA  
ACGGAGGAAACCGTTTGGCTTTTGGCCATATCCCAATTAACAGCTGGAATGTTTATCGGAAAGACAATAGTTTAAAGACACGTTCCGTTAGGCTATGGTGGGATAAGCCCGCACCTAC  
CATAACGACCAAAATTTAGCATTTCCCAACGGGCGGTTTGGCCATCTCTGAAGAAGTAGGGCGTTATCCCTGCGAGAAGGTGCAACATTGCAATCGTTCCCTCGTAATATGCTTTTAA  
CGGGCAGTAGGACAAGATAGCCGTTTGGTGAATGCCGTTCTCCGATGTATACGAAAAAATAGGCAGGCAATTTGTGATAATATCGAATGT

## SEQ ID 7744

LGMENGFPKIMAGHODETFMHSACGLSDINLRLALIPKNGGRLFAHIPBLQLECFIKDMSFKDTFGRLLWMDKPAPTTTTKPFPSISNGRFAHPEDRALSLRREGATLQSPFNNVFK  
AGSRDKIARLIGNAVPPMYTEKIGRAIVDNIEC

## SEQ ID 7745

ATGAACAAATCGAATTTCTTTCTGCTGCTTGGGTGCGGTTCCGCTTTTTCCTGTTGTGATGCAGCAAAACAGTACAGGCTCAACTTCACAGCTTTGGACAAGCGGAAAAACAGGAA  
TCGCTTGGAGCAGGATTATGCGCAAAATGAGGCTGCAACAGGCGCGTTTGGCAATCAGCAAGCGATCAGGCGCGCGGCAAAAAACAAACCTCCATCCGCGGTTTCCGGCAATACCTT  
TATGTTGAACATCAAGA

## SEQ ID 7746

MNKSNTFLILLAVCSAFSVVMQNNYRLNFTALDKAKKQETALEQDYAQMRLQOARLANHEAIRAAEKQNLHPFVSGNTFVHEHQ

## SEQ ID 7747

ATGGCTCAACAAAAAGATTAGGTTACATTTGGTTAAAGCCTGATTGGTACAATTTGAATCTCATCGTCATGTGCACGCGGTTTAGGTTTCCGTCGTCGCGAGCATACGGTAGAGGTTT  
TAGATACCTCTGAAAACCGTGGTATGATTAAATAAATCAGCTACTTGTGTAAGTGGAGTCT

## SEQ ID 7748

MABQKKIRVTLVKSIGTIESHRACARGLGLRRREHTVEVLDTSENRMINKISYLLKVES

## SEQ ID 7749

TTTTTGGCTTTGAAGCCGAGCAGGTCCTGGGTGGTGGCAAGCCACGCGCGGAATATCCCAAGTCCGATGACGAAGCCGAACACCAAGTGCATTCTCCCGGGTAGAAGAACCCAGCCG  
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GGAATGGCGCGCGGATAAACGACCGCGCGCGCCCAAGAGTTTGGTATTTCGATTCTTCTTTTCCGCTGAGGATTTCAGTCGCGATGGTGTGTGCGCGACAGGACGAACCCATCCC  
CAGCGTCAGGGAAGAAACATAAGATTTTACGATGAATTCGTTGATTGTACAGTGTCTGATCCCATTCGATCCATGTTGGCGGATTTCGACCATAGGCAAGTTTGGTAAATGTCCCG  
TAGATTGCTGCAATTTGGCGCGCGCTGGTTGCCGCGTCCGGGTAAACGATAAAGACATCCGCGAGGGGTTACCGTCAAGCATGGAATCAGATTTTGGTCGAGATTGGACTGTAACTCTT  
CCAAACCGCTCTTCTTGGTGATAAAGCGGATGTTGTCGAGCGGTTTGTGCGCACACAGCAGGCTGCGGACGATATCGCTGTGCTTTTGTGCGCGCGCGGTTTCCATATAGACGGTGTATTG  
CGCGACTCATTTAGTTTGGCCCAACACGCTTTGCCCGCTTTGGATGCCCAAGTACATAAACAGCGGCAAGGTCATGGCGAGCGGAGCAATTATAGGGTAAGCAGTGTGCCGAAGGTTGG  
CGCAGAACTGTTGAGCGCGGTGCGCGCGGATTTCGACGTGACGAGAGGTAGTGGATGATGCTCAT

## SEQ ID 7750

PFQFEAEQVLGGGPRAEYPCQDEAEHQDFSRVEETPADIKSVGFEDGIDQGAHGREOPTAKPADGGGKDALPHGLIKEWAADKRRGRAQEFQDFDFFPSAEDLQSDGVVRDKDERHP  
QRQKIP\*DFTFDFVLVQCLYPRILHVGGFDRQFQGNVFDCLHLGGRCVRVGNKDIRQGVTVKHGNILVEIGL\*FPQTVFFADKADVVEPFVHQQAADGIAVALCGGPHIDGL  
RRLEIQAHALPALDAQVHKQGHGDEHYEGKQCAERLAQKLFERARGFDVQREVVDDAH

## SEQ ID 7751

GTGTGGCGGAGCGGACTGCCGTCGATACCGGAATAATAACAGAGAAAAACGCTGTAACGGCAATGAACAAATCGAATTTCTTCTGCTGCTTGGGTGTGCGGTTTCCGCTTTTTCGTT  
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ACGAACGATACAGGCGCGCGGAGAAAAACAAACCTCCATCCGCGGTTTCCGGCAATACCTTTATGGTGAACATCAAGATAGAAGCAGCTGTGTGCCGAATCGGATTCTTCATC  
AGGATAATAATAACGAGAAGTAAAAATGTTGAT

## SEQ ID 7752

VMSGLPVRYRNNREKRLNGNEQIEFLSAACGVFRFRFRCDAAKPVQAQLHSPFGQEKTNRLGAGLCANEAAATGAFGESRSQQGGGRKTKPPSAGFYQYLYGGTSKIEAACVPESDSCI  
RIIITRSKNVD

## SEQ ID 7753

ATGCTCGCAGTTAACCGTGAACCAAGTAGTTAAAGGTGGTCCGATATGGCTTTCTCTCGCTAACGTGTGTTGGTGATGGAGATGGTGTATGTTGGTAAAGGTAAAGTCAAAAG  
AAGTGCTGTTGACGTTCAAAAGCGGATGGATCAAGCAGCAGCTCTATGATTAAAGTACCATTAATAAATGTTAGTATCCATCATGAGGTTATTGGTCGACATGGTCTACTAAAGTATT  
TATGACGCTGCTAAAGAGGTTAGTGGCTTAAAGCGGTTGACCTATGCGTTTGGTTTGTATGCTATGGGCAATCATAATATTCCGCCAAAGTGCAGGATCTACTAACCCATATAAT  
ATCGTACGTGCAACATTAGATGGTTGTCTAAGTTGCATACCTCTCGTATATCGCAGCAACAGTGGCTTGACAGTGAAGACATTTTGGGAGTTAACCATGGC

## SEQ ID 7754

MVAVNRVTKVVKGRIDAFSALTIVVGDGGRIGMKGKSKVEVPVAVQKAMDQARRSMIKVPLKNGTIHHEVIGRHGATKVFMPAKEGSGVKAGGPMRLVFDAMGHIHNSAKVHSGSTNFPYN  
IVRATLDGLSKLHTPADLAKRGLTVEDILGVNHG

## SEQ ID 7755

TCCGAGTCGCTCTTTCGAGAGCGCAGGATCGCGTGTCCGTAGTCCGCCATCAGGGTTTCGTCATGTGCGGCGAGATGACGGTTGTTCCCGCTTCGTGGAAGGTTTGAACAAATCCATA  
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CGGATCGTCCATTTCTCGTCTTTTCAGGCGGACTTTTTCGATGGCGATGCGGGCAGCTCTTCGCTTTTTCGCGCGGATAGCCGATAATCCGAAGCGGAGGATGACGTTTTCGAGGAC  
GTTGCGGTCGTAGAGGATTTTGTGCTTTTGAACACGATGCCGATGTTTGGCGCATAAAGCCGATTTGGTTGTCGGAATATGTCGCGAGATCTGCGCGTTAAACAGGATTTTGGCCCTG  
CTCGGCTTGTGATGCGCGAATTCAGCTTGAGGACGGTGGATTTCGCCGAACCGGAGTGTCCCGGATAAATATCAATTTTCGCTTTTGTGATTGGAAGCTGACGTTTTCAGGCGTTCAA  
AACCGCGGAGTAGGTTTGTGAACTTGTTCGAACCGGATCATAGGAGTCTGTAAAGAAAGGCGGCATATCGTTTCGGCGGTTGCGTCCGAGGATATGCGCTGTAACAA

## SEQ ID 7756

CESSFRQAQDAVSVRHQGFVMCGDDGCSRFEQFENIERVGAVEVGGGFVGNQAGLVNDGAGDAQALLFTAGEGYIVQFSSQADFFDAGTLFGFARRIADNPKRQDDVLQD  
VAVVEDFVLEHDAVDLVAHKADLVVGGQCAELFVRQDFAPARLDARNQLEDGGFARTGVSRRDKYHAFVLEADVQGFRTAGIGFNLFTEDHRRSCKEGRHIVSGGCVRRMDPSEQ

## SEQ ID 7757

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GTGCTGAAGGTGATAAAGTATTGGCTCAAGCTCTACATTGGAAGCTGAGGTGCGCGTAGTCTGAAATCTGGAAGCAATGTTGAAGCAGCTGCAATAGTTGTAAGCTATTGCTGAGAA  
GGCTAAAGCAGCAGGTGTAGAAAGGTTGCTTTTGTATGTTACAGTTTCCAAATATCAGCGTGTGTGAAGGCTTTGGCTGAAGCTGCTGCTGAAATGTTTAAAGCTCT

## SEQ ID 7758

MDKHPTLRRLRRARRIADLKMVRLCVFRSNNHIYAQVISAEGDKVLAQASTLEAEVRGSLKSGSNVEAAIIVGKRIAEKAKAAGVEKVPFDRSGFYHGRVKALAEARENGLSF

## SEQ ID 7759

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GGCTGATTTTGTGCGGTTTGGGCGATGCGGGCGGTTGATTGTTTTCGACAAAGACCCGACGGCGATTGCTGTGGCAGAGAGCTGGCGGTTTCGGAACAAAGGGTCCGTGCTGCAATG  
CGGTTTTCGTTTCGTTTCAGACGGCATTTGACGGTTTGGGTATCGGCAAGGTGGACGGTGGCTGTTTGTATTTGGGGATTTCGCTCCGCAAAATCGATGACGGCAGCGCGGTTTCAGCTTC  
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TCCTGCGACGCGCACTTCCAGGCAATCCGATCTTTTAAACCGGAGCTTGAAGAAGTAGGGCGGTTTGGCGCAGGTCATGTCGCTGCTGAAAGAGGGCGGGGCTTTGGCGGTCAAT  
GCTTTCCATTCGTTGGAAGACCGCATTTGTGAAGCAGTTTGTCAAAAAATATTTCGCAACACGAGCCCTGCGGAGCTGGGCGGCGGTGAGAGAACGGGATTTCGCCGATCCGCCCTGAAAA  
TCGTGGGCGAGGCATTAAGCGCGGTGAAGCGGAATTCGCCCAACCCGAGGCGGAGGAGCGAGTTTTCGCTGTGCGGAGCGGACTGCGCGTCCGATACCGGAA

## SEQ ID 7760

VSGAESYKHITVLINAEVDALAVREDGVYVDGTFGRGGHSLILSRLGDAGRLLIVFDKDPQAIIVAEELASDKRVGVVHGGFASFQALDGLIGKVDGALFDLGLSSPDIDGSRGFSF  
RFDAPLDMRMDTTRGMSAAEWIAVASEQDLHEVIKNYGEERFSRQIVRAIIVQRAESPIDTRKLAQIVQNVTRERQDPATRTQPAIRIFINRELEEVGAVLPQVMCRLEKGGRLAVI  
AFHSLDRIKQPVKKYQHEPLPSMAAVREADLPDPPLKIVGRALKPGEAEIAANPRARSALVLRVAERTAGPIE

## SEQ ID 7761

ATGTCACGTGTGCAAAAAACCCAGTGACGGTTCCCGCTGCTAGAGTAAAAATTGGAACAGAGGCATTGGTTATTAAGGGTAAGAACGGTGAATGTCTTTTCCCTTTGCAATTCGTATG  
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AGGTTTTCAGAGAAATTAATGATGGCGGTGGGTATCGTGTCTAAGCACAAAGTAAATCTTGAATCTGCTTTGGGTTTTCCTCATCCGATCGTATATGAAATGCTGAAGGTGTC  
TCCGTTCAAACTCTAGCCAAACAGAGATTGTTTAACTGGCTCGGATAAACAAAGTTGTTGTGCTCAAGTTGCTTCTGAGATTGTCGCTCCGCTGCTGAGCCTTATAAAGGTAAGGTG  
TTCGCTATGTAGCGAAGTAGTGGTAATGAAGAAGCCCAAGAAAAA

## SEQ ID 7762

MSRVAKNPVTVPAGVEKFTGTEALVIKNGKLSPLHSDVAIEFNDGKLTFFVANNSSKQANAMSGTARALVSNMVKVSEGFEEKLQLMGVGYRAQAQKILNLSLGFSPHPIVYEMPEGV  
SVQTPSQTEIVLGSQVVGQVASEIRAPPEPYKKGVRVYVGVVMKEAKKK

## SEQ ID 7763

TTGGGCGATGTCATGTTGCGCGCGGCACACGAATTAAGCATCGACAGTAAGGGCGGTTGGCTGTTCTCGCCAAATTCGCGCAGATTCGTGCGCGCTCTATACGCTGCCGTAGTGCCAA  
CGCTCGAGTCGAACATAAGCTGTTGATGTACCTGTTCCGGAGTGGGAAAGGTTGCGCGCAACTTTTAACTTAAAGTGGCGGATAACCTGTTTTCGCGCGGTTTCAAAATCTTTT  
CTGCGATAACCGCGAAATTTTGAATGGGACAGCGCGCGAGGTTGCTGGTTCTCGCGGACTGAGGAAAGGGTGGATTTCGACCGTGAAGTTGTTTGGTGGCGCGTCCCAACCGTTG  
GAGCTTTGGGTCGCGAGCAGTGGGAGGCTGAGATGTTTCAAGCTTTGGATGAGCATCTGACGAACCTGCTTCCAGTTGAGTCAGACGGATTTCGCAATTG

## SEQ ID 7764

LGHVMPGGAHLSIDSKRLAVPAKFRDILSRLVTPAVVATLESKHKLIMYPVAEWKVAQLNLKLVADNPVLRFPQNLILLHNAETLEWDSAGRVLPAGLRKRVDVDFREVVLVGRANRL  
ELWGRBQWEAMVQALDDDPDELAFQLSQTDLQL

## SEQ ID 7765

ATGAGTATGCAATGCTATTTCCGATATGTTGACTCGTATCCGCAATGCGCAACGTGCTAATAAGCAGCAGTTGCAATGCTCTTCTCAAAATTAAGTGTGCTATGCAAGGTATTGA  
AAGAAGAGGATATATTGAGGACTTCGAGTTTCACTGACGTAAAGCTATATTTGGAATTTCAATTTAAATACTATGCAAGGTGCTGCTGTAATGCAACAAATCAAGCGTGTATCTCGCCC  
CGGTTTGGTATTTATAAAGCGTCTAGTGAGATTCCAAGTGTATGAATGGCTTGGGTATTGCTATGTTAGTACTTCTAAAGGTGTAATGACTGATGTAAGCAGCTTCTCAAGGTGTT  
GGTGGTGAAGTTGTTATGCAATGTTAGCC

## SEQ ID 7766

MSMHPISIMLTPRIRNAQRANKAAVAMPSSKLKCAIAKVLKEGYIEDFAVSSDVKSILEILQKYIAGRPIVBIQIKRVSRPGLRIYKASSEIPVMNGLGIAIVSTSGKVMTRKARSQGV  
GGEILCTVA

## SEQ ID 7767

ATGGCTAAGAAAGCACTTATTAATCGTGATCTGAAACGTCAAGCTTTGGCTAAAAATATGCGGCTAAACGCGCGGCAATTAAAGCGGTAATCAATGATTCGAATGCAACTGAGGAAGGC  
GTTTTCGAGGCTCGTTTGAAGTTTCAATCCATCTCTGTAATGCGGCACTGTGCGTCAACGCTGCTGTTGCTGTTTACAGAGTTCGCGCTCGTGGTACTTTCCGTAATTTGGTTTGGGTCG  
TATTAATAATCCGTGAATTCGCCATCGCTGGCGAAATTCGCGGTGTTGTTAAAGCCAGCTGG

## SEQ ID 7768

MAKKALINRDLKQALAKKYAAKRAAIKAVINDSNATEERFEARLRFQSI PRNAPFVRQRRRCALTRFRGTFRKFLGRIRKIRIAMRGEIPGVVKASW

## SEQ ID 7769

TTGTTTATTTGGTTCGCTCACTGCTACTGCAACCGCGCTGCGGTTGTCGTCATTTTATCTTATTGTTTAAACAGATAAAAAATTCAGATATGTTAATGAGTTTTCATGCCCTGATT  
TGACCGAGTGTAAAAATTTCTTATAGTGTGATTTGGTGGGAATTTGGGGCAAGGTGCTCTCTTTTACCCCTTG

## SEQ ID 7770

LFIGSVTLCTRRRAVVIFYLIVFKQNKNFVRYNEFSCPDLTECLKFLIVSIGGELNGKVSLLPL

## SEQ ID 7771

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CCGATGAGGAAGCGAAAGCTTTATTGTGCTATTGTTAAATTTCCGTTCAAGAGA

## SEQ ID 7772

MARLEFYKFTVPELVKQPGYKSVMEVPRIEKITLNMVGVEAVADKVMHEAVSDLERIAGRPVVTVARKSIAFGKIRDNPVGCKVTLRRDQMFELDLRLITIALPRVRDFRGVSGKS  
FDGRGNMVRBQILFPEIEYDKIDALRGLNITITTAKTDEEAKALLSLKPFPPFG

## SEQ ID 7773

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CGGGGATTTTATTACCGCACCGACCCCTCACCCCTGTTTTCACAGACACTGGCAGCCAACTTCAAGAACTCTGCGCCCAACCGCGGGCAATATCTATGAATTCGCGCGGGAACCGGA  
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CATCTCAAAAGTTGTCACCTTGACCGCACTTCCGGAAGCGTTTTCGCGCATCATCTCGGCAACGAATTAATCGATGCCATACCTGTCGAAATTCGCTCGGTAATTAAGGAGGATTACT  
CGAGCACATCGGCTTTCACGGATAACGGCGGTTTCGCTATTTCTGCAAGACCTTGCACGACCGGTCGCTTTCACCTCGGCTTCCTCTATTTTCTCAACAGATTATCCCTATACC  
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ATCAAGGCACATTGATCGGACACTACCGACACCACGTTATCCACAATCCTTTCGACTTCATCGGGTGGCAGATCTGACCGCCACGTCACCTTTACCGACATTGCCCAAGCCGGTACGGA  
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GCTGTTCAAAAACGATTGACAGCATGAAATGGCGCACTGTTTAAAGTCATCGCATTCGGAATAATCGGCATCGACTGGGCAGGATTCCGCTTCGGCGACATCTGCCACAACTCC  
AACCTCGTCCGCTGTAATCCGCTTCAGACGCA

## SEQ ID 7774

MTAPVPTCNMGNPILNHLITFIMLPSPEARQSSNLQTLIAERIGKHGNIWPFPSRMELVLYAPQYGYTGGSHKIGNTGDFITAPTLPLFAQTLARQLQELLPQTAGNIYEPGAGTG  
QLAADLLGSVSDSINCYIIEISPELAARQKNLIQARAPRASQKVHLTALPEAFDGIIGNELLDAIPEIVRKNEGGLLEHIGVCTDNGRFAYSARPLHDPSSLTSASLYFPQTDYPT  
SELHPQYAFIRTLASRLRGGMIPIDYGFDAQYYPQNRQGTLIHGYRHVHINPFDIFGLADLTAHVNFPTDIAQAGTDAGLDLTGYLPQSHFLNLGITELLAQTGRTDSAAIYIREAA  
AVQKLIQHEMAGELFKVIAFGKNIGIDWAGFRPGDICHKLQPSCLRNPLQTA

## SEQ ID 7775

ATGCGTGGCATTAAAGGCGGTATTATTACTAAAGAAATGCCTTTGGATATTCTTAATATCGCAATCTGAATCCGGAACATAATAAGCGGACCGTGTGGTATTAGCTGATTGAAATG  
AAGGCAAGTTAAACGCGTTCGTTCTTCAAATCAAATGGCTCTATCATTTGAGCA

## SEQ ID 7776

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## SEQ ID 7777

TTGATGGCGTTTACACATTAAGCGCCCTCAACAACAACCTTTACCAACCAACACTCGAATCTACTGACCTGCTTACCTTTATCTTACCAGCAATTACTACAACCTATCGCCCTTTAATG  
ATTTTATTCATCGTCTATTCTTATAATCTTCAGGTGCCAATGAACAGATTTCATAAATCGCTCAGTACGCAATTCACGGGTACCGGACCAAGATACGAGTACCCAAAGGTTCAAG  
TTTATTATTCAGCAACACGCGGCGATTGTATCGAATTAATTAACGCACCATCAGGACGACGACACCTTTAGCAGTACGAACAATACCGCATTTATATACATCGCCCTTTTTCAGACGG  
CCACGCGGAACGCGATCTTTACTGCGACTTAAATATATCGCCAAACAGAAAGC

## SEQ ID 7778

LMAFYNINALNNPFTQHSNYLTLITFILTSNYNPIAFNDPIHRAIPYNTSGANETIFINRSVRNSRVTPKIRVPKSSLLFSNTAALLSNLINAPSGRRTPPLAVRTTALYTSPLIR  
PRGTASLTATLIIISPTFA

## SEQ ID 7779

TTGCTGTTTTGAAGCAGTGGTTTTATCTTTATTTTCCGGCAATCAGGCAATAAAAAAGCACATACCTTTTACGGTCTGTGCTTTTTTATCTGGTGGAGGTAAGCGGGATCGAACCCCTG  
ACCTCTGCGATGCCATGCAAGCGCTCTACCACTGAGCTATACCCCCGAAATCTGGTAGCGAATCAGGACTCGAACCCCGACACAGGATTA

## SEQ ID 7780

LPVLKAVVYSLFSNQAIKKHIPFTVCAPLSGGKRDRTADLLHAMQALYQLSYTPENLVANQGLEPRTGL

## SEQ ID 7781

ATGATTCAAATGCAGACCATCTTAGATGTGGCTGATAACTCTGGTGGCGCTCGCGTAATGTGTATCAAGGTATTGGCGGATCTAAGCGTGCCTACCGTTCTGTTGGCGATATTATTAAAG  
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CAATGCCCGCGTGTCTGGAATAATAAATCGAACCTTTGGGTACTCGTATCTTTGGTCCGTAACCGGTGAATTCGCTACTGAGCGATTATGAAATCGTTTCATTTGGCACCTGGAAGTA  
TTA

## SEQ ID 7782

MIQMPTIILDVADNSGARRVMCIKVLGSKRYASVGDIIKVAKVDAVPRGRVKGDVYNAVVRRTAKGVRRPDGALIKFDNNAVLLNNKLEPLGTRIFGPVTRRLRTERFKIVSLAPEV  
L

## SEQ ID 7783

ATGCTGATTTGCTGATTTGCTGCGCTTTGCGCGTTCGCGTTCGCGAGCAGTTTGGGGCTGCTGGTGGCGAGCTTCCTGAATGTGCTCATTTACCGCGTACCGGTATGATGGAACGCGGCT  
GGACGGTATTTGCCAAAGAACATTTAAACCTGCCGCTGACCGACGATGAAAGCCGTACCTTCAACCTGATGAAGCCGGATTCCTGCTGTCCCAATAGCGGTATACCGCGCTGGCA  
GAACATCCCGATTGTCAGTTACCTGCTCTGCGCGGCAATGCGCTTCCCTGCCAAACCAAAATCAGCATACGTTATCCCTTAATCGAGCTGCTGACCGCGCTATTGTTCCGGCTGGTGGCC  
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ATCGTTATGCGGCTGCCAAGGGCGGCATTTTGCCTTCGGCCCCGCACTGACAGTTTTCGGCTGGATAATTTTACGGCAACAGATTCCGTATGGCGGCGGTCACTGGTGGCTGACCC  
ATCCGCTGAGA

## SEQ ID 7784

MSDLSVLSFFAVPLAALVGLLVGSFLNVVIYRVPMERGWTVFAKEHLNPLTDDSRFTNLAKPDSCCPKRVPIRAWQNIPIVSYLLLRGKASCQTKISIRYPLIELLTGVLFGIVA  
WQYGSWITLGLLITAFILSLTIDADTQYLPDSMTLPLIWLGLIFNLDDGFPVLPQSAVLGAVAGYSSLNLLCAVYKLLTCKTGMNGDFKLIALGAWLGSALPLVLFVSSLIGLVA  
IVMRVAKGRHFAFGPALTVSGWLIPTANDSVNRVNWNLTHPVR

## SEQ ID 7785

ATGCAAAACATAAAATCAAGCAGCAGCTCAGGCATTCATGCCAACACAATCCGACAAATGACAAACCACTTCAGACAACTCGTTTTT

## SEQ ID 7786

MQNTKNQARSSGIIHAQHNPTNDKPLSDNLVF

## SEQ ID 7787

GTGAACAATTCAGTATCACCGTCATCGGTAAAGACCGCGTCCGGCATCGTGTACGATGTTTCCAAATTTTGGCGGAAAACCGAATCAACATCTCTAATATCAGCCAACAGCTGATGGACG  
ATTTTTTACTATGATTATCTTGGTGGATACCTCGAAATGCCCTAAATCGCGCGAGAGATTTTGGATTGTTTGGCGAAGAGAGCAAAAACTCGCGCTTGACATCCGTATGCAAAACGA  
AGAAATCTTCAAGCGATGACCGCAT

## SEQ ID 7788

VNNSVITVIGKDRGVIVYDVSKILAENRINILNISQQLMDDFFTHIILVDTSKCPKSRQELDLFARESKLLALDIRMQNEBIFQAMHRI

## SEQ ID 7789

ATGAGCGAAATATAAATGTTCTGACTTTGCAAGGCAAGTAGTAAGCGACAAATAGGATAAAACCGTAACAGTATTGGTTGAGCGTAAAGTAAACATTCGCTGTATGGTAAGATTATTC  
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TGAGAAAGCACGTTCTATT

## SEQ ID 7790

MSETKNVRLQSKVSDKMDKTVTVLVERKVKHSYLGKIIRLSTKIHADENNQYIGIDVVVISESRPLSKTKSNVVSSELVEKARS

## SEQ ID 7791

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TTATGATGCTCCTGAAACATTACCGATTTTTCACCTGCGATGATGTCGGTTGATTTGATAGGCTTTATTTGCCGCTTTTGTTCGGGTTTGGTAGCGGTAAAGCAGCTGCTGAAGTTGT  
TCCAAGAAAAATATATCCCGTTTGCTTATACCGCATTTGTTTCGGCATTTGTCATCAATAATTTGTTGTTGTCGGCTGGATAAGTTGGAA

**SEQ ID 7792**

MDPLIVLKMMLVVEGTFEFLPISSTGHLIVGNLIGFHSNHKVFETAIQLGAVLAVVFEYRQFQSNVLHGVGDKRKNRVLNLAIAPIPAVMGLLPDKQIKEYLFNPLSVAVMLVIG  
GPTILWVEKQSRABPKIADVDALRPIDALMIGVAQVPALVPGTSRSGSTVMGMLNGIERKTATFSPFLAVPMVAATAYDVLKHYRFTLHDVGLIILGFLAFAVSLVAVKALKFV  
SKNVIPPAYIRIVFGIVIIILWLSGWLISWE

**SEQ ID 7793**

ATGAAAGCAAATGAATTGAAAGACAAATCCGTTGAGCAGTTGAATGCAGATTTGTTGACTTGTGAAAGCTCAGTTTGGCTTACGTATGCAAAACGCTACCGGTCAATTAGGCAAAACCA  
GTGAATTGAAACGCTACGTGCGCATATTGCTCGTATTAACCGCTTTAACTGAAAAAGGTGCTAAG

**SEQ ID 7794**

MKANELKDKSVBQIWDLLDLKQFGLRMQNTATGQLGKPSSELKRVRRDIARIKTVLTKGAK

**SEQ ID 7795**

ATGAAGTTTAAACATCTGTTGCCGCTGCTGCTGTCGGCAGTGTGTCGGCGCAGGCATATGCCCTGACGGAAGGGAAGACTATCTGTGTTGGATAAACCCATTCTCTAAGAACACCGG  
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GGTCTGGCGGCTGAAATGCTCGGTCTGGCAAGATGGCTGCTGCGGTCAAGCTGTCGGGTTTGAATATCAGGCAAACTCTGCTGTGTGTTTAAAGCAGTTTACGAACAAAAATCCGTTT  
GAAACACAGGCTGTTGCCGGGAAATGGGCTTTATCTCAAAAAGGTTTTCAGGCAAAACTGATGCGCGCTATGATTTCCCGGAGAGCTGCGCGCTGCGCATTAATAATCGAAGACTGA  
CGGAACAATACGTTATGACAGCAGCGCGACCGTTATTTGTCGGCGGAAATACCGCTTATCTCAATAATGGCTTTGATGGCGGCTTCATACGATTAAAGAATTGGTTGCCAAAGTCAG  
GGAGAAGCGCAAGCGTCAGACCCCTGCTGTACAGAAA

**SEQ ID 7796**

MKFKHLPLLLSAVLSAQAYALTGEGDYLVLDKPIPOEQPGKIEVLEFFGYFCVHHFDPILLKLGKALPSDTYLRTEHVVRPEMLGLARMAAAVKLSGLKYQANSVFKAVYEQKIRL  
ENRAVAGKWLSQLGFDGKLLRAYDSPEAAVALKMKQLTBYQIDSTPTTVIVGGKYRVLINNGFDGCVHTIKELVAKVREERKQTPAVQK

**SEQ ID 7797**

ATGCTGCAGCAACTAGACTGAAATACCGTAAGCAACAAAGGTCGCAATACCGGCATCGCTACTCGCGTAATAAGGTAAGTTTCGGTGAGTTGCGCTGAAAGCCGTAGGTCGTGGTC  
GTTTGAAGTCCCGTCAAAATCGAAGCTGCTCGTCGCAATGACCCGTCACATCAACGTTGGTGGTTCGTTATTTGGATTTCGTGATTCCTCTGACAAACCGATTACTGAAAAGCCTATTCAAGT  
TCGTATGGTGGCGGTAAGGTAACGTGGAATATTACATTTGCCAAATTAACCAAGGTAAGTGTGTATGAAATGGATGGCGTTCCAGAGGAAGTGGCTCGTGAAGCATTGAGTTGGCT  
GCTGCCAAATTCCTTATCTACAACCTTTGTAGTAAGACAGGTGGGTCAA

**SEQ ID 7798**

MLQPTLKYRQKGRNTGIATRGNKVSFGEFLKAVGRGLTARQIEAARRAMTRHKKRGRIRIWRVFPDKPIITEKPIQVRMGGGKGNVEYYIARIKPGKLYEMDGVPEELAREAFELA  
AAKLPIPTTFVVRVQVQ

**SEQ ID 7799**

ATGGGCAAAAGATTAAACCTTACAGGCTTTCCGCTGGCGGTAACCTAAAGACTGGGCTTCAAAATGGTTTGTCTAAAAGTACCGACTTTTCTACTGTTTGAAGCAGGATATCGATGTTCCGA  
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CAGCAGTTGGAAAAACGCGTTCAATTCCGTCGTCTATGAAACGAGCAATGCAAAATGCAATGCGTTCTGGTCTAAAGGCATTAAGATTATGACTTCAGGCGCTGAAATGGTGGCGGATA  
TTGCCCTAGCGAATGATCTGTAAGGTGCGTGCCACTGCATATTTACGTGCAAAATGTAGATTATGCAACAGCGAAGCGCACACCATATGTTGTTATGGGTCTGAAAGTTTGGGT  
TTATACGGAAGCAATATTAATCTTCCAAACCTGAACATGAGAGTAACAAAGAAAGGCAAGGTAGACGTAATGCTGCAGCCAAAC

**SEQ ID 7800**

MGQKINPTGFRILATFKDASKWFAKSTDFSTVLKQDIDVRNLYRQLANASVGRVILIERPAKSARITHSARPGVVIGKKGEDIEVLKRDQLVLMGVPVHVNIEIRREPELDAQIADGIA  
QOLEKRVQFRAMKRAMQNAMRSGAKGKIMTSGRLNGADIAREWYREGRVPLHLTLRANVDYATSEAHITYGVGLGLKVVYVTEGNIKSSKEPHESQRKAGRRNAAAN

**SEQ ID 7801**

ATGTTTATGAACAAATTTCCCAATCCGGAAGAGTCTGTCGGGTTCTCTTCGGTTTGATAGTGGCAACGGTCATTATTCGGGTATTTTGTCTTATCTGAACAGGCGGTCAAAATG  
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TGTTCGGAAGAGGACAGCAGTCGATCGGAAAGAGCTGCGCAACGAGCCGCTGCGGCAAGAGCCGACGAGTTGAAGAAAAGCGGCGGAGACGGAAGAGCGGAGAGCGGAGCA  
CAGCAGTTCGCGAAGAACGACTGACGGAAGAGCGTGAACAAACCGTCAGGGAAGAAAGCGCAGAGAAGAGATGCCGAAACGGTTAAAAAACAGCGGTAAACCCGCTTAAAGAACAGAGA  
AAAAAGCTTCAAAAGAGAGAAAAAGGCGGCAAGGAAAAAGTTGCACCAAAACCGACCCCGGAACAAATCTCAACAGCGGACGATCGAAAAAGCGCGAGTGGCGTCCCAAGAGT  
GCAGAAATGAAACGTTTGGCAAGCGGAGCAACGCAATTATCTGCAATGGCGCGGTATGCCGACCGCGGAGCGGAGGCGAGCGTGCCTCAAACTGGCAATCTTGGGCATATCTCC  
GAAGTGTGCGGTATCAGGCGGACATAAACCGCTTTACCGCTGCAAGCGGCAATATGTCGCCGATGCGGTGAAAAAATGCAGGACGAGTTGAAAAAGCATGGGTTGCCAGCGCTGA  
TCCGTGCGATTGAAGGCAAA

**SEQ ID 7802**

MFNKNFSQSGKLSGFFPGLILATVIIAGILLYLNQGGQNAFKIPAPSKQPAETELKLNQPKEDIQEPADQNALSEPQVAKEAQSDAEKAADKQPVADRADEVEEKAGEPEREEDPG  
QAVRKALTEERETPVREKAQKDAETVKQAVKPSKETEKASKEKKAKEKVAKPPTPEQILNSGSIKARSAAAEVQKMTFGKAEATHYLQAGAYADRRSAEQRAKLAIIIGISS  
EUVGYQAGHKTLYRVQSGNMSADAVKMKQDELKKGHVASLIRATEGR

**SEQ ID 7803**

ATGAGAGTAAATGCACACATAAAAAATGCCGTTATCTGCTCAAAAGGCTCGTTTGGTAGCTGATTTGATTTCGTGGTAAAGACGTTGCCCAAGCTTTGAATATTTGGCTTTCAGCCCTA  
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CTTGAAACGTTTCAAGCTCGCGCAAGGTGCGGTAACCGCATCGAAAAACAACTTGTCTATCAATGTTGACAGTGGGTAAC

**SEQ ID 7804**

MRVNAQHKVARIASQKARLVADLIRGKDVAQALNLAIFSPKKGAELIKVLESAIANAEHNNADIDELKVVTTIFVDKGPSLKRFPQARAKRGNRIEKQTCCHINVTGVN

**SEQ ID 7805**

ATGGCTCGTTTATGAAAAAGGCCCATATGTAGACCTGCATTGCTGAAAAAGTAGATGCTGTCGCGCAAGCAACGACAAACGCCCGATTAAACCTGGTCTCGTCTTACCATTC  
TGCTGATTTTATCGGTCTGACCATTTGCCGTGACCAACGGTCGCCACCATGTCCTGTGTTATCAGCGACAATATGGTGGTCAATAATAGCGGAATCTCATTGACCCGTACCTTTAA  
AGGCCACCTGGCGGATAAAAAGGCTAAAAAGAAA

**SEQ ID 7806**

MARSLKGPYVDLHLKKVDVAVRASNDKRPKITSRRSTILPFIGLTIAVHNGRTHVPVPSIDNVGHKLGEPSLRTTFKGLHLDKAKKK



## SEQ ID 7807

ATGGCAATCGTTAAATGAAGCCGACCTCTGCAGGCCGTCGCGCATGGTTCGGTGGTAACAGAAGGTTTGCACAAAGGTGCACCTTATGCACCTTCTGCTGAAAAGAAAAATCTACTG  
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CGAATACGATCTTAACCGTACTGCTTCATCGCATGTTGTGCTATGCAGACGGCGAGCGCTGTACATCATCGCTCTCCGCGTATTCAGCCGGTGTGTAATGGTTTCCGGTGTCTGAA  
GCTGCCATCAAAAGTAGGCAACACCTGCGCATCCCAACATCCCGTTGGTACGACTATCCACTGTATCGAAATGAAACCCGGTAAAGGTGCTCAAAATCCGACGTTCTGCGCGGTGCTCTG  
CGGTATGTTGGCTAAAGAGGTGCTACGCTCAAGTCCGTCTGCGCTGCGCGAAGTTCGTAATAATCAACGTAGATTGCGGTGCGACCATCGGTGAAGTCGGTAACGAAGAGCAAGCCCT  
GAAAAAATCGGTAAAGCCGGTGTAAACCGTTGGCGCGGTATTCGTCGACCGTACGCGGTGTGTGTCATGAATCCCGTGCATACCCGCGATGGTGGTGGTGAAGCCGTACCGCGCAAGCC  
CGCAACCGGTTAGTCCATGGGGTACTCTGCTAAAGGCTACCGCATCGTAATAACAAACGACCGGATAATATGTTGTTCTGCGCGTACTCAATAAAGGT

## SEQ ID 7808

MAIVKMKPTSAARRGNRVVTEGLHKGAFYAPLLEKKNSTAGRNNNGHITTRHKGKGKHHRVVDPRKNDGISAKVERIEYDPRNPTAFIALLCYADGERRYIIAPRGIQAGVVLVSGAE  
AAIKVGNFLPIRINIPVGTTHICIEMKPGKGAQIARSAGASAVLLAKEGAYAVRLRSGEVRLINVDCRATIGEVGNEBQLKKIKGAGANRWGIRPTVRGVVNMVVDHPHGGGEGRTGEA  
REPVSFWGTPAKGYTRNNKRTDMIVRRRYSNG

## SEQ ID 7809

ATGTCGCTTGGCTTGGTTACAGCCGCGCTTGAGCGGTATGAATGCGCGTGGTTCGAAGTGAAGCCACCTTGCACACGGCTGCGCATTTCAACATCGTCCGACTGCCGATACCG  
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GACGAATTTGGTAGAAGTTGGGCATTTGGCTCTGCTCTGCCCAACCAACCAACCACTCGACAGCAACCGTCTTTCCGAGTTCGCGCATACGGCGCAGCGCGGCTATGGTGGCG  
CGGCTCGGATCCGCGTTCGGCGGAGATTTCAATGGCGCATACGGCGTTTATTTTGGACGAATTCGCCGAGTTCGACCGCAAGGTTTGGAGGTTTTCGCGGAACCGTTGGAAGAACG  
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## SEQ ID 7810

MSLALVYSRALSGMNAFLVEVAHLNGLPHFNIVGLPDTEVKESRDRVRAATIQSGFEPAKKITVNLAPADLPKESGRFDLPPIAIGILASSQVAPEKLAEYEFAGELALSGLLRPVRG  
ALAMAWQGMQAKRAFLVPEENAGQAAMVRGITVYGARISGEVAHLNGIEPLAQTECSVPQMPSEHGGQPDLCVKGQHSARLALEIAAAGHSLIMMGPPTGKMSLSQRLPGILPLAE  
DELVEWALRSLLPNHQQLDSNRPRSPPHGASAAAMVGGSDPRPGEISLAHGVLFDELPEFDRKVLVLEPLRENGEIHISRAARQAVYPAKFQVLAAMNPPCYGLHPVKPCRC  
TPESVARYRSKISGFLDRIDLITIEVPSLSAAELMQEAGESSASVLERVIAARGKQYARQGVNAALSVSELDQACIQKEAQALGSLEKLSLSARSFHRIMRVARTLADLAGDEBVG  
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## SEQ ID 7811

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TTGTCGTATTTTGGGTGCGCGCAGCGATGTTAAAAAGCTTATGTAAGCTTGGTTCAGCGTCAAGAGTTGGATTTCGAAGCCGCTGCTCAGCTGCAGATAAGGAA

## SEQ ID 7812

MTFKVLNATKPEIKAAVELLFGVQVASVTTVTTKGTRKFRGRLGRRSDVKAYVSLVDGQELDLAAAAADKE

## SEQ ID 7813

TTGGATCTCATCATCTCCCGACTCAAATCGCGTCATCGCTTGAAGATTCTTCGTTTTCGATACGGATGTCAGCGCGAGTTTTCGCTCTTCGCGCAACAAATCCAAATCT  
CTGCGCGCGATTATAGGCGATTTCGAGGTATCCACCAAGATAATCATAGTAAAAAATCGTCCATCAGCTGTGCGTGATATTGAGGATGTTGATTCGGTTTTCGCGCAAAATTTTGAAGAC  
ATCGTACAGATGCGCGCGCGTCTTTACCGATGACCGTGATGACTGAATTTGTCACAGGCTTACTCTCTGCGATATCCGT

## SEQ ID 7814

LDTHIIPPTQMRICIAWKISSFCIRMSSASFLLSANKSKISCRDLGHFEVSTKIIIVKSSISWLLRLMRFSARILETSYTMPPRSLPMTVMTLFTGLLLADIR

## SEQ ID 7815

TTGGGGCTCGGCAACGGTATCTTTCAGCAGCTATCTGTTTACAGATTGTTTTTCAAAAAACGAGGTGTCTGAAAGTGGTTTGTCAATTGTCGAGTGTGTTGGGCGATGAATGCTGAGCT  
CGGTGCTGATTTT

## SEQ ID 7816

LGLNGILQQLSVYRLFKKRGCLKVCHLSDCVGECLSCVLF

## SEQ ID 7817

ATGAAATATATGAAATGTAAATATCCGTTTCAGCATAAACCAATTTCTGTTTTCGAAAGCACTTAAATGGCTTAAAAAGCCGAGTTTGAACGATGCGCATCGGAAAAATCATTTA  
AAACAGCATATGTTTGTAGTGTCTTGAATGTAATCGGGCGTTCGCGGAATATGAAATCCGTTTTCAGGCGCGAGGTGTCGAAAGTGAATTTTACCAACCGCAAGGGGCGCGGT  
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GTCGCTCGAAATCAGCGAAACCATCGCCAACAGCCCTGCCAAGATGTGGAAGAAATATTAAGGCGATGCTGGCGCGCGCTTCAACCGTATGAGTTTGGTTACGCGCGAAGATTTCG  
ACATCCAGCAGCAGGTTTGTATTAACCCGTACCAAACTGCGCGCTTTGGAAGCAGCTGTCGGCGAACTCGAAGCGCGCAAAATCCCAACCGCGCAGATTGGAAGCGGCTGAAGCGCG  
TGCCGAAGAGCGCTGCGCGAAATCAGGCGCAACCGAAGCGCGGAA

## SEQ ID 7818

NKLYEIVNPFQHNPLSVVCKALKWLKPKSLKRCASEKSFRTAYCFVVSNCVIGRCAEYETIRFQAAGVSKCNFSNRKGGAVCFDDYPPVPPFRHPSLYNSRLNLI CSGRMQIMFGKQLFEE  
VGSKISSETIANSAPKDVEKNIKAMLGAFNRNDLVTRREEFDIQQVLIKTRTKLAALERLAKLEAQNPRQAALAEAAAEAEVAETIRQTEAGE

## SEQ ID 7819

TTGAAGATAATTTATCCGAATCCCTTTTCGGGTATCCGATTTTCCGTTGACTTTTTCATTAGAAAAACATTTTCAGGCGCAAGTGTCTGCAATTTCAAAGCCTGTAAATCTGAAGTTTATG  
ACGAGGAA

## SEQ ID 7820

LKIITPNPLSGIRIFRCTPIRKTFQAQVACNFKACNSEVLDEE

## SEQ ID 7821

ATGGAATGAAGTAATTCAGCGCTAAAGGACAAGTTTCAGGCGAGCTGTCTGTTTCTGATGCTTTGTTTCGCGCGCAATACAAATGAAGCGTGTGTTACCAAGCTGGTAAATGCCCTACTTGG  
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GTGCGCTAAAGCGCGTTCGCGGTTCGCCAACAACCCGACGAAAACTTCACTCAAAAAGTAAACCGTAAATGTACCGTCCGCGTATGCGACTATCTGTCCCAATTCGCGCGGTGACGAG  
CGTTTGTGATTGAGCGTTGACTGCCGAACCTCCCAAAACCAAGTTTTCGCCAACAAGTAAAAAATTTGGCTCTGAGCAAGTCTGTTTGTAAACCAACCGCTGACGAGAAATG

TTTACTTGGCTTACGCAACTTGCACAACTATTGGTTTGGAGCTCAACAAGTTGATCCTTACAGCTTGCCTGCTATATAAAAAAGTAATCATCACTAAAGATGCGGTTGCACAATTAGA  
CGAGCAATGGTA

**SEQ ID 7822**

MELKVIDAKQVSGSLSVSDALFAREYNEALVHQLVNAVLANARSGNRAQKTRAEVKHSKKPWRQKGTGRASGMTSSPLWRKGRAPFNKPDENFTQKVNRMKMYRAGMATILSQLARDE  
RLFVIEALTAETFPKTKVFAEQVKNLALQVLFVTKRLDENVYLASRNLPNVVLLEAQVDPYSLLRYKKVLIITKDAVAQLEEQMV

**SEQ ID 7823**

ATGACTTTAGGCTGGTTGGACGCAAAAGTTGGTATGACCCGCGTGTTCGACGAGCAGGGTGTTCCTGTTCCGGTAACCGTTTGGATATGTCTGCCAACCGGTTACACAAGTAAATCCA  
AAGATACTGACGGCTATACCGCGCTTCAAGTTACCTTTGGTCAGAAAAAGCCAATCGTGTCAACAAGCCGAGCCGACACTTTGCAAAAGCAGGTGTGAAGCCGGTCCGCGTTTGAT  
TGAGTTGCTTTGACTGAAGAAAACTGGCTGAATGAAAGCCGGTGACGAAATCACCGCTTCTATGTTTGAAGTCGGTCAACTGGTTCGATGTAACCGGTACCTCTAAAGGTAAAGGTTTC  
TCCGGCAGGATCAAAAGCTCAATCTTCGGTGCACCACTACTTCCACGGTAACCTCCGCTTCTCACCGCGTTCAGGCTCTATCGGTATGGCGCAAGACCCGGTCCGCTGTTCGCCGTA  
AGCCGCTGCGCCGCAATACGGCAACCAAGCACTGTTCAAAAATTTGGAAGTTGTCGGTGTGATGTCAGAACCCCACTGCTGTGGTTAAGGGTCTGTTCGGGGTGGCGTCAACAG  
CGATGTTGATGTTCTCCGCGGTGAAAGTAGTGCG

**SEQ ID 7824**

MTLGLVGRKVGMTVPFDEQVSVVPVTVLDSANRVTQVKSQDVGTVAVQVTFGQKKNRNVKAEAGHPAKAGVEAGRGLIEFALTEEKLAELKAGDEITVSMFEVQQLVDVTGTSKGGF  
SGTIKRNFQAQRTSHGNSRSHRVPGSIGMAQDPGRVFPGRNAGQVGNKATVQKLEVVVRDAERQLLLVKGAVPGAVNSDVVVRPSVKVGA

**SEQ ID 7825**

ATGAATCCCATGTACATCACTTTTGCAATCTATTGGTTGACGCTCTCTCATCGGCTTGCCTTATTTTCCACGCGCAATTCGATGATTATATTTTGGCGGGCCGACCGCTGGGCC  
CGTTTGTACCGCGATGTTCGGCAGGCGCGTCCGATATGTCCGGTGGCTTTTGTATGGTCTGCGGGCGCGGATTATTTTGAAGCGGTTGAATGAGGCTTGGATTGCCATCGGCTCTGGT  
CGGCGGCTATTTCAACTGGCTCTTGGTGGCGGGCGCTGCGCGTGCATACCGAATATGCCAACAATCGCGTGACGCTGCCGATTATTTCTTCCACCGCTTCGGCGGGCGGACACTTG  
ATGAAAGTGGTTCCGCACTGATTATCTGTTTCTTTCACGATTTATTCGCGCTCGGGCATTTGCGCGGGCGCAACCTGTTCAAAGCCTGTTTGAAGGTATGACTTACATCAGGCAA  
TGTGCTGCGGCGGGCGGCGGACCATCGCTATACCTTCTTGGCGGCTTCTTGGCGGTGAGTGGAGCGGATACGCTGCGGCTCTTGTGATGATTTCGCGCTGATTATTAACCGCGGTGAT  
GGTCTATCTGGGCTTGGCGGGCGGCGAAGATGTCTGCCGCGATTCAAAGCGTCCGCGCAGGCGCGGCAAGAAATACGGCAGCTGTTTCCCGGTACGACCGTCACTCGGCATCATTTCC  
ACCGCGCGCTGGGCTTGGGCTATTTCGGACAGCGGCACATTTCGGCGCGCTTATGCGCGCGCGGAAAGCGCGAAATCGCTGGTATCCGACGCGCGCATCGGATGACTTGGATGGCGTTGT  
CGCTTTCGGCGCGCGGTAGCGGTGCGTTATTTCGGCATTCGCTATTTCGGTCAAAACCCGACAAAGTTTCTTCTATGAGCGGCAACCGCAAGCGCATCTTCATCGCGCTTCCACCGCTGCT  
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CTTACCGGTGGCGAGGTTTCGGTGGCGCATTCGCGCGGATTGATGATTCTGTCGCTATTGTGAAACCGCATCACTGCTACGCGCGGTGTGTCAGGATGTTGCGAGTCAACCGTTGT  
TGTGTGGCGGAATGGTAAACCAACCGCTTCGAGCGCGAGCGAAGCGGCTTGTGACGATGTACGAAATCGTCCCGGCTTATGTTGCTGTGATGTTGCGGTGTTGGTTTCCGCT  
TTCAACAAAGAACTTCGCGCGAAATCCAAGACGCTTTGAAAAAGCCGACGAGATTACCGCGCGCGCGCA

**SEQ ID 7826**

MNPHYITPAIYLAVALLIGLAAYPSTRNFDYILGGRSLGPFVTAMASAGSDMSGMLMGLPGAIIYLSGLNEAWIAIGLLVGAIFYNMLLVAGRLVHTVEYANNALTLPTDFPHRFAGGHL  
MKVVSALILFFPTTYCASGIVAGATLPSLFEGMTYNQAMWLGAAGATIAITFLGGFLAVSWITDLQASLMIFALILTFVMVYLGLGAEQMSAAIQSVAAGTKEYGSLFAGTTVIGLIS  
TAAMGLGYFGQPHILARFMAESAASLSVARRIGMTWMALCLAGAVAVGYGFIAYFANPDKVSSMSGNHERIFIALSTLLFNPWLAGIILSAILAAMVMSYLCQLLVCSSAITEDFYKGF  
LRKNAQSELVWVGRLMVLAIIVISILIASDPNSKVLGLVSYAWAGFGAAGPFIIVLSVLKRIITAYGALSGNVAGASTVVVWAENVKPARAAGESGLLWYIEIVPGFIVCLIVAVLWSL  
FNKPSREIQERFEKADADYRAAR

**SEQ ID 7827**

TTGGCTGCTCTTCAGACAAAGTTAAACTTGGCAAAATGTACCAAGCTTGACATTATATCTCGACAAGTCAAAGAAATATCAACAGAAATATCAGAAATATCTTCAATATGCCGCTCTGAAG  
CGTTT

**SEQ ID 7828**

LACLSDKVILKKNVPSLTLYPTSQRNINRNIRNIFNMPSEAF

**SEQ ID 7829**

TTGTGTTTACCCTTTCATTTTCAAGAAACGGAAGCACCAGTCTGCCCGCATTTGAAGCTTGTATTTTCATCTGCGGATTATTACGATATTACCGTATTACAGCCGACCGGATGCGG  
TC

**SEQ ID 7830**

LCFTFRIFKETEAPILPAFBAALYFICGFTITLPSYDRTDAV

**SEQ ID 7831**

TTGCCCTGCCCTTCCGCTACTATTGTACTGTCTCGGCTTCGCTGCTTGTCTGATTAAATTTAATCCACTATATTTAAACAACAAAGAAATTGAATTTGGAAGAACGGCATGATTGG  
AGCGGGCGGTAAAGTCTTCAGGACACGACGTCATCCCGTTTGTGCGAGAAAGATGCATAAGCCG

**SEQ ID 7832**

LPRLAVLPLVLSAASSILCPDLNLHLYILNNKELNLEERHDLERAVKILQDTHVIPVCRKRMHTP

**SEQ ID 7833**

TTGAAAAAGCCGACGAGATTACCGCGCGCGCGGATAAACCCCTTTCAGACGCGACGGCATCCCGGTTCGTGCGCTGGAACCGCTTCCGGGCAACACAAATAAACCTTGCCTGCATA  
CAGGCTTATTGTGTTTACCCGTTTCATTTTCAAGAAACGGAAGCACCAGTCTGCCCGCATTTGAAGCTTGTATTTTCATCTGCGGATTATTACGATATTACCGTATTACAGCCG  
ACCGATGCCGCTGGAACCCCGGAAAAAATTTGGAGGATCAAAAAATGTTTCATTTTGCATTTCCGGCACAAACTGCCCTGCGCCAGCGATAACCGATGCTTACCGCGG

**SEQ ID 7834**

LKKPTQITAPPDKPLSDGTASRFVPSEPASGPNINPKCLHTGLICVLVPSFSKKRKHFPCLHKPCISSADLLRYRIQTAPMPSEPEKLTLEDPKNVSFICISGFWCPAPSDNRCLPP

**SEQ ID 7835**

TTGTGCTCAAGAAATTTTCAGACGGCATTTTGTAGTGAACAAAACAGGATATTTTATCCATAACTTTCCTAAGGCTTGCCTCCCGGAAAAAGGTAGAATCGGGCTTGGTTTGGCGAGAA  
GCATCCATCTGATCTAAGGATGGATGATGTTTATTCTCAAGTAA

**SEQ ID 7836**

LCLKNFQTAFFSEQNRIFFIHNFPKACPPKGRIGLGLGRSIHLILRMDVLFSSK

**SEQ ID 7837**

ATGGATGCTTCTGCCAAACCAAGCCGATTTCTACCTTTTTTTCGGGGGGCAAGCCTTAGGAAAGTTATGGATAAAAAATATCTGTTTTGTTCCTAATAAAATGCCGCTGAAAAATCTTG  
AGGCACAAAAAAGCCGATTTTCACCGACCGCACTGTTTTTGTGATTTTGTGTTTGTGCTT

**SEQ ID 7838**

MDASATKPDSTFFRGASLRKVMKKYPVLPFKKRLKILEAQNKPSPTALFFDFVVL

## SEQ ID 7839

TTGGCGCAGGCGAGTTTGTGCCGGAATGCAAAATGAAACATTTTGTGATCCTCCAAAGTTTTCGGGGGGTTCAGACGCATCGGTGCGGTCTGAATACGGTAATATCGTAATAAATC  
CGCAGATGAAATACAGGCTTCAATGCGGCGAGAATCGGTGCTTCGGTTCTTTGAAATGAAACGGGTAAACACAAA

## SEQ ID 7840

LAQGSILCRKCKMHFLDPKPFPRGVQTSVRSEYGNIVINPMKYKASNAGRIGASVSLMKRVKHX

## SEQ ID 7841

ATGTTGCAACGTGCACAGATGAGTGACGAAGAGCGCAACGCCGCTCCGAGCTTGCCTCCGCTTTGGTTACCAAGTCCGCGCGCGCCACCAAGCGCGCGGTGGATGCGGTGATGC  
ACGAGTTTCTACTCTCCAGCAAGAAGGCATCGCGCTGATGTGTCTGGCAGAAGCCCTGCTGCTATCCCGCAACGCCACGCGCGACCGCTGATGCGGACAGATTTTCAGACGGCAA  
CTGGAAGAGCCATTTGAACAACAGCCCTTCCCTCTTCGTCAATGCTGCGGCTGGGGTCTGCTGATTACCGCAAGCTGACCGCCCAACAAACGACAAACAAATGAGTTCCGCACTCGCGCG  
CTGATCGGCAAGGCGCGCACCGCTCATCCGCCAAGCGCTAAATACGCCATCGCGCTTCTGGGCAACAGTTCGTCAACGGACAGACCAATTGAAGAAGCCCTGCAAAACGGCAAGAAC  
GCGAAAAATGGGCTACCGCTTCTCTTCGATATGTTGGGCGAAGCGCTACACCAAGCGATGCGGACCGCTACTACCGGACTATGTGGAAGCATCCACGCCATCGGCAAGATGC  
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TTGTTCTCTTTGGGTAAATAACGATATCGGTATCAACATCGATGCCGAAGAAGCAACCGCTTGGAGTGTCTTTGATTTGATGGAGGCACTGTTTCCGACCCCGATTGGCGCGCT  
ACAAAGGCATCGGTTTCTGTTCAAGCCTACCAAAAACGCTGCCGCTTCGTCTGACTATCTGATTGACCTGGCGCGCGCAACCAACAAACATGATGATCGGCTCTGTAAGGCGC  
GTATTGGGACAGCAAAATCAATGGGCGCAAGTGGACCGCTTGAACGGCTATCCGACCTACACCGCAAGTGCATACCGACATCTCTACCTCGCTGCGCGTGCAGAACTGCTTTCCGCG  
CAAGACCGGTATTTCCCGCAATTCGCCACCCACACCGCTACACCTTGGGCGCAATCTACCAATGGGCAAGGCAAGATTTTGAACCAATGCTGCAACGGTATGGGCGAAACCTTGT  
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GTCTTTCTGCAACCAATCTTGTGATGAAACATCAGCATCGACCGCTGATTAAAGACCGCTTTCGACACCAATCGCGGAACAAGGCATCCACTGCAACACCGCTGCGCGGTGCGCGGT  
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TCAACGCGCAAGCGCGGTGTCGCGCAAGCGCAACCGATTAAAAACCTGCGGACCAAGCGGATGTTGTCGTTACGGTACGCTTTGCGGATGCGCGCTTGGCCAAAGAGCGGTGGTGC  
AGCGGTGCGCGCTTCCCGCAATGGAGTGGACACCTGCGCGGCAACGCGCGCTGCTGCGCGGTTTTCGCGGACCTGCTGCAACAGCACACCGCGCGCTGATGATGCTTCCGCGTGC  
GAAGCGGCAAAACGCTGAACAACGCGATTTGCCAAGTGGCGAAGCGGTGATTCTGCGGCTACTACGCAACGAAGCGCAACACCGCTGCTCAAGACGCAAAAGCGCTGCGCGCA  
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TTATGCGCTTTCCCTCATGCAAGCGGCGCATCCGCACTTCCGCTGCAACTCATCTCGCGCGGCGACACGCGGTGCGGCACTTGACCAACGATGCGGCGGTGATTGTTTC  
ACAGGCTCGACCGAAGTGGCGCGCTGATCAACAAGCCCTTGCACAAACGCGCGCAACCTCGCTGATTGCGGAAACGCGCGCAACAAACGCGCATGATTGTCGATTTCCACCGCACTTG  
CCGAACAAGTGTGCGCGGATTTGAACCTCGCGCTTCGACAGCGCGGCAACCGCTGCTGCGCGTTCGCTATCTTATGCGTCAAGAAGAGCTTGGCGACGCTGATGCTGACATGATCAA  
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CGCGCGCAACCGCTTTGATGATACAGCGCGGCAACGCTTCAAGCGCTTTCGCGCACTGACCGGACTTTCGCGCTTCCGCGTACAGGCGAGTGTGCAACCGGACAGCGCGCTGCGCTTCTAC  
ACCGCGAGTGTGAAGGTCTGCTGCTGCTCAACGGCAACCGCGCAACCGCGGTATCAGCGAGCTTTCGCGCTTACAGCGCGGCAACAGCAACTTTCGCGCGCATGAGCG  
GCGCACTCATCGCGCTTCCCTTCCGAAAAACGCACTCGACATCTCGAAGTGTGGAAGAAATTTCTTGACGATCAACACCCACGCGCGCGCGCAACCGCGCGCTGATGCGCGTTC  
CGAC

## SEQ ID 7842

MLQRAQMSDEERNAASELARLVTVQVRAGRTKAGVDALMHFSLSSEEGIALMCLAEALLRI PDNATRDRLIADKISDGNWKSLLNNSPLFVNAAWGLITGKLTATNDKQMSALGR  
LIGKGGAPLIRQGVNYAMRLGKQFVGTQIEALQNGKERKMGYRFSFDMLEAAYTQADRYRYDYVEAIAHIGKDAAGQGVYENGISVKLSAHPYRSRAQHRVYAGELPLRLKE  
LFLGLKGYDIGINIDAEENRLESLDLMALVSDPLAGYKIGFVQVQYKRCPPVIDYLDLRLARNQKLMIRLVKAYWDSKIKWQVDLNGYPTTTRKVVHTDISYLACATKLLISA  
QDAVFPQFATHNATFLGATYQMGKDFEHQCLHMGGETLYDQVVGPNLGRVYAPVGTTHETLLAYLVRLLENGANSFVNQIVDENISIDRLIKSPDFTIABQGIHLHNAFLPLPRD  
LYGKRLNSQGVLSNENVLQQLQEQMNAQAQDFHAASIVNGKARDVGEAQIPKNADHGVVGTVPFADALAQAQVGAAVAAPFWSATPAERAACLRFPADLLEQHTPALMHLAVR  
EAGKTLNNAIAEVREAVDFCRYANEAEHTLPQDAKAVGAIVAISPWNFLAIFGTGEVVSALAAGNTVIAKPABQTSLSIAGYAVSIAMHEAGIPTSLALQILGAGDTGAALTNDASTGGVIF  
TGSTVEARLINKALAKRGDNPVLAETGGQNAMIVDSALABQVCADVLNSAFDSAGQRCALRILCQVEDVADRMILDHIGAMDELVVGKPIQITDVGPIVDAEQAQNLNHNKMGV  
AKSYHEVKAADVDSEKSTFVRPILFELNNLQREVFPGVLHVVRVYRADELDSVIDQINSKYALTHGVHSRIEGTVRHRSRIEAGNVYVNRNIVGAVGVQFPGHGLSGTGPKAGG  
SFYLLQLTRIPENWAPTLQIGQADEAALKRLEALIHKLPPNAEKKAAALGHARILTRAEFTVLTGPTGERNSISWHPKRVIHGGSTVQAFAALTGLAASGVQAVVEPDSPLASY  
TADLEGLLVNGKFPETAGISHVAALSPLDSARKJELAAHDGALIRVLPSENGLDILQVFEISCSINTTAAAGNAGIMAVAD

## SEQ ID 7843

ATGCGCGCGGTCAACTGCTGCTGACCATCCGCTGAGATGACGATGCGTTCGAGTACCGCGGAAATCGGCGAGCGGCAATCGCGAGCGCGCAATTTTTCGCGATTTGGCGGTGC  
CGCGCATGATGCGGACGCGCGCGGCACTCTGCTGACGCGCTTCAGACGCGCATCGCCCTGCGGAAATCAGCGCGCTGTTTCGCGGACACCGCTTTTCGACACACAGGCTTTGTCGCGCGCA  
CATTTGCGGTAAAGAAATCTTTGCTCCCATCGCGCAAGCGCTTCTCGAATCCGCTGATGTTGCGCGTGAATTTCTCAGAAATCAAAAAACAGCAAGAACTTTACGATGCGGTLLAC  
GGCATTTGCGAAATTCGCTGCTGACGGAAGCGCTCAATTTATCAGCGCTGATACGCGGTGCTGCTGACCATAGCGCACTTTGGAAGAAAGTATCGCGAGGATGGACGCGCGG  
TGACGCGCGCGGAGTTCGCGGCGGATCATCAGCCATCAGGATCCGAATCCGAACGCGCTGCTGCTTCAGACGATGATGCTCAATGACGCGGCGCTCAAGCGCTACGTTGAGAAACAAAT  
GCTCTGACGCGCTTTTATTCAGGATTTTCGCTCAAAACCAACACAGGAAACACAAATGC

## SEQ ID 7844

MAGGQLVADPSGENTAWVLGFGIGSGKSAQAQYFADLGVPRIDADAHAHSLTASDGIALPEIRRLFGDTVFDQGLLRDILRKEIFASPSRKALLESVMLPLIFSEIKKQETFTDAVY  
GIVEIPLITEKRQFISLIRRVLTISAPLEKRIGRVMARSLTRGEVADIISHQASESERLLADVDLLNDGSLKSLREKTMILHAFYSGIFASKPTQKING

## SEQ ID 7845

ATGCGGAAACGTTTCGCTGACATTTATGATTGCTGCGCTGATCTGTTTCGCGCTTATAAGGCTTCGCGGCTGCTGATGCGGTGTTTTTCGCGTTACGATGATGCCAACAAATGTGC  
ATTACGCGGTTTATCAAGCTGGATGACGGGTATTAACATTTGCTGATGCTGAAAGAGGTTACCGAAGTTCGCGAGCGCGCGCGCTGATGTTGGAATAGTTGCGCTGCTGCTTTGTTG  
GGGCGTGGCGAAGTCACTGTTGTTTCGAGCTTGCAGGTTCCGCGTAAGACGCAATTTTCTGCGGATATCTGTTGCTCTTCTTAATGCTGATGATTTTCGTCGCTGCTGCTGCAACAG  
AAACAAGAGCAGCGTATTTTCGCGCAACCGGATACAGCGCATCAAAGCAATTTTTCAGCTTCGCTTATTTTCGCGCGCGGTGTTGCGGTATCAGTTGTTGATTTAAGCAAGATCC  
CTGTGTTCAACAGCGCTGCTCCAAGCAAAATCGGCAAGGCAATTTCAAAATATCGCTGATTTATGGGCGAAGCGAAGCGCGCGCATTTGAAATGTTTGGTTACGGGCGCGAAG  
TTCGCGCTTTTAAACCGCGCTGTGCAAGCGGATTTTAAAGCGGATTTGAAACAAAGTATTTTCGCGGATTTATGACGCGGAGTATCTGATGCGCGGCTTCTTAAAGTCAATACGCAACGCG  
AACGCGCTGCGAACAATTCAGCGCGCGGATACCAATATGTTCCGCTCGCAAGAGGATGAGGCTTATGAAACGATTTTTCAGTGCAGGCTGAAAACCAATGGCAATTTTGAACCTTAA  
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GCATTTTATGCTGTTGCAACCAACGCGTTCGCAACGCGCATGTTGCGCGCTCAAGTAAAGTATTCGCGCAAGCGGATTTGTTGATAGTACGCAACACCATTCACAAA  
ACCGACCAATGATTAACCGTATTCGAGCAGTGCAGAAAGCGCTGACGCGCACTGCTGTTGCTCTATACCTCGATCATGGCGATGTTGCGCAAGATATCTACAAATCAAGGCA

CGGTGCAGCCCGACAGCTATATTGTCCTCTGCTTTTGTACAGCCCGGATAAGGCCGTGCAACAGGCTGCCAACAGGCTTTTGGCCTTGGAGATTGCTTCCATCAGCAGCTTTCAC  
GTTCTTGATTCACAGCTGGGCTACGATATGCCGTTTTCAGGTTGTCCGAGGCTCGGTACAGGCAACCTGATTACGGGCGATGCAGCAGCTTGAACATTCCGCAACGGCAAGCGGAA  
TATGTTTATCCGCAA

**SEQ ID 7846**

MAETFAUTFMIAALYLFARYKASRLLIIVFPAPSMIANNVHYAVYQSWMTGINYWMLKEVTEVGSAGASMLDKLWLPALMGVAEVMILFCSLAKFRKTHFSADILFAPLMIMIFVRSFDT  
KQEHGISPKPTYSRIKANYFSFGYFVGRVLPYQLFDLSKIPVFKQAPSKIGQSGIQNTIVLIMGESAAHLKLFYGRGTSFPLTRLSQADFKEPIVKQSYSAQPMATVSLPSFFNVIPHA  
NGLEQISGDTNMFRLAKEQGYETYPYSAQAEQMAILNLIGKKWIDHLIQTQLGYNGDNMPDEKLLPLFDKINLQQGRHFIVLHQRGSHAPYQALLQPDQKVFGEADIVDKYDNTLHK  
TDQMTQTVFELQKQPDGNWLFAYTSDHGQYVRQDIYNQGTVPQDSYIIVPLVLYSPDKAVQQAANQAPAPCELAHFHQQLSTPLIHTLGYDMPVSGCREGSVTGNLITGDAGSLNIRNGKAE  
YVYFQ

**SEQ ID 7847**

TTGGTTGGAACACGCGGGGCGAGCGTTTGTGTTTCTCTTACGCGCGAGCAGTTATTTGGCGAAGAGTGAGTTGGAGGAAATGCCGCTCTGAAGACGATTGTTTTCAGACGGCATT  
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CGTACTGTTGGGTTTTCGCGCGCTTTCGCGCGCAGACCTATTCTGTTTATTTAATCAGAACGGGAACTGACGGCGAGCATGCTTCTGCGCTTATATCAGGCAATATAGTGTGGCG  
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AAGACGGAATGTTTATGTTCAACGATGAGCTGCCAAATTTCTGACTTGGGATGAAAGCGCGGCTTACTTTTCGGAACGTCTATCCGCCACCATAAACGCAACGGGTTGTTGAGT  
GGTATGAAGATGTTCTAAAAGAGCGAGGCTGTTTATCAGGATGACAAGTTGGTCAGGAAACCCCAATGGGATAAGGATGGTTATTTAATCGAAACCC

**SEQ ID 7848**

LVGNRGRFRCTPLDARAVIGRRVSWREMPSEDDLSGDIPTIHCFFPDWLRNPFYHIVYKLIIVFYIAIMKKLSRIVFSIVLLGFSALPAQTYSVVFNQNGKITATMSSAAYIRQYSVA  
AGTAAHQDFYYPMSKKYSEPIVASTQIKSFVPTLQNGMLILWHFNGQKQKMAAGFSKPKPDGEWVWVYFNGKKSAMVMPYKNGLSEGTGYRYYRNGKRESEIQPKQNKANGVWKQWYADGSI  
KTEMVHVNDPAKILTWDESGRLLSELIRHKKRNGVVLEWYEDGSKKSEAVYQDDKLVRKQTMKDGYLIEP

**SEQ ID 7849**

ATGGCAAAACCAAAAAATCCGTATCCGCTGAAAGCTTATGATTACGCCCTGATTGACCGTTCTGCAACAAGAAATCGTTGAAACTGCAAAACGTACCGGTGCTGTTGAAAGGCCCGGATTC  
CTTTCGCCACCAAAATCGAGCGTTTCAACATTTTTCGCTTCTCCGACGTGAACAAAACTTCCCGTGAACAATGGAATCCGCACCCATTTCGCCCTGATGGACATCGTGGATTGGACCGA  
TAAACTACCGATCGCTGATGAAGCTGGATTTCGCCGCGGTGTTGATGTAGAAATTAAGTCCAA

**SEQ ID 7850**

MANQKIRIRLKAYDYALIDRSAQEIVETAKRTGAVVKGPIPLPTKIERFNILRSPHVNKTREBLEIRTHLRMDIVDWTDTTDLMLKLDLPAGVDVEIKVQ

**SEQ ID 7851**

TGGACTTTAATTTCTACATCAACACCGGCGGCAAAATCCAGCTTCATCAGCGCATCGGTAGTTTATCGGTTCCAATCCACGATGTCCATCAGCGCAAAATGGGTGCGGATTTCGAATTT  
TCACGGGAAGTTTGTTCACGTGCGGAGAACGCAAAATGTTGAAACGCTCGATTGTTGTCGCAAGGAATCGGGCTTTTACAACAGCACCGGTACGTTTTCGACTTTCAACGATTTCCT  
GTGCAGACCGTCAATCAGGCGTAAATCAAGCTTTTCAGCGGATACGATTTTTGTTGCTTCAATATCAATATCTTCAAT

**SEQ ID 7852**

LDFNFYINTGRQIQLHQRIGSFIPGIDHVDQAQMGADFQLFTGSFVHVRRITONVETLDFGRQRNRAFYNSTGTFCSFNDFLCRTVNGVVISFQADTDFLVCHLSISFN

**SEQ ID 7853**

GTGTCGGTCCGCTACGATTTCGCGAGCTGAGGATAGCGCGAGATTATGCCGCTTACAGAAAGTGAACAACAGTAAATATTCGTTCAACATAAAAAGGGTGAAGAAAAAATGGCAGCG  
GGAAAAAAGTACGCAAGACCTGAAGACGGAATCAGGAAAAAGTACGTTCCACCGCTTCTTCTCTCGGCTTGTCCGCGTTTACGATTTCGATACCGGTTCCCGCTTCAACCCCTA  
TGCAAGCGTGTGCGGTACGATACGACACGTCAGACACAGCATCGATTGCAACAAAAAACAACAGATGTATTACCGCCCCCCCCACTACTCTGACGAGCAGCTACAACATTATAATGCT  
AATCCACAGACGCAAAACCTTTATCACCAGCAGACGATCCGCGCGTGGGCTCGGGTTCATCGCGCGGTGCGGTTTCGACATCAGCGCCCAAGCTGACCTGGACACCGGCTACCGCT  
ACCACACTGGGAGCGCTGGAAGAACCCCGCTTCAAAACCAAGAGCTCATTTGGGATCGGCTACCGCTTC

**SEQ ID 7854**

VSVGYDFGSWRIADYARYRKWNNSKYSVNIRKVENKNGSGKKLQDLKTNQENGTFPHAVSSILGSAYVDFDTGSRPKPYAGVRVSYGHRVHSIDSKTKTDTVITAPPTSDGAPPTTNA  
NPQTQNPYHQSDSIRRVGLGVAGVGFDTIPNLTLDTGYRYHNWGRLENTRFKTHEASLGMRYF

**SEQ ID 7855**

TGCGATTATCAATATCCTTCAATTAAGCGATAACAGAGAAACACGCGCGCACCCAGGTACGGCGCGCTTCGGAATCGCAAGCGCAGACCTTCTTCCATAGCGATAGGCGCAATC  
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ACGGGATATGCGCGCGCGCTCTTCTTGTCTAATACGTACACTTCTGCTTTGAACCTTGGTGTGAGGAGTATAGTACCGGTTTGGCCAATACCTGACCGGTTCTACGTTCTCACGTTT  
GGTACCGCGCAGCAATACGCTTACGTTGTGCGCGCGCTGACCTTCTGTCAGCAGTGTGCGGAACATTTCAACGCGGTACAGGTGGTTTTTGGGTTTCTTTCAGACCGACGATTTCAATC  
TCGTCACCAACGTGGATGATACCTGCTTACACGCGCGGTACTACGTTACGCGCGCGGAAATGAGAACACGCTCTCGA

**SEQ ID 7856**

LPFINILQLSDNRNHAHTGTAAPANRKAQTFPHSDRRNQFYSNGYVLTTRHYHFHTPFQSNRAGTVSGTEVELGTVVGEKRGMAAALFPAQYVHPCFELGVRSDSTRFGQYLTAIFYVFTF  
GTAQQYAYVVARL/FVQQAEBFNAGTGGLGFFQTDFFNLVTNVDDTSLYTAGDYGTAAQKWRTELK

**SEQ ID 7857**

ATGTTCCGATTATACGTGTCAGTTATGCCGTTGAAAAATGCCGTTTGCCTTAAAAATGCCGTTGAAAGTTACAGCGGCATCGGTATCGGGAAATCAGAACGGTAGCGC  
ATGCCAA

**SEQ ID 7858**

MFLYQQLCRLKMPFARSCALKMPSESDGIGIGSEAVAHQ

**SEQ ID 7859**

ATGTTCCGCAAACTGCTGGACGAAGGTACGCGCGGACAACTAGGCGTATTGCTGCGCGGTACCAAACTGGAAGACGTAGAAGCGGTCAGTATTGGCCAAACCGGGTACTATCACTC  
CTCACACCAAGTTCAAAGCAGAAGTGTACGATTGAGCAAGAAGAGGGCGCGCATACCCGTTTTTCGCCAACTACCGTCCCAATCTACTTCCGTACCACTGACGTAAACCGGCGC  
GGTACTTTGGAAGAGGTGTGAAATGTAATGCCGGGTGAGAACGTAACCATTTACTGTAGAAGTATTGCGCTATCGCTATGGAAGAAGGCTCTGCGCTTTCGATTTCGGAAGCGCGC  
CGTACCGTGGTGGCGCGGTGTTCTTCTGTTATCGCT

**SEQ ID 7860**

MFRKLDGQAGDNVGLLRGTKREDVERGQVLAKPGTITPHTKFAEVVLSKEEGRHTPPFANYRPQFYFRTTDTVTGAVTLEKGVEMVMPGENVTITVELIAPIAMEEGLRFAIREGG  
RTVAGVSSVIA



## SEQ ID 7861

GTGCGGCGGATTCGGCTTACGCCCTACGAGCATCATCCCGCGATTATCCCGAAGCAACCGGTGCAAAAAAGGCACAACAATAAGCACGGTAAGCGATTATTTCAAAACATCCGCCCC  
GCTCCGCTCCACCCCGGACCTCGCCCTCGGCTTACGATTTCGGCGGCTGGCGGCTTTTCGCCGCCCGCGCTGCGCGCGGCTCCACCAATCCCTTCAATATTACCGATCCGCCCATTCGCC  
CCGATTCCGTCAAATCCATCAATCCCGCGAATCAAGCTTATCCCAAAAAACCT

## SEQ ID 7862

VQADLAYAYEHITRDYPEATGAKKGTITISTVSDYFKNIRTSVHPRALGDFGWRVFSAPAVAAGLHQSLOYYRSRHCRRFRQIHQFRITPIPOKP

## SEQ ID 7863

GTGGTTTTTGGGTTCTTTACAGCCGACGATTCAATCTCGTCACCAACCTGGATGATACCTCGCTCTACACGGCCGGTACTACGTTACCGCGCCGGAAAAATGGAGAACAGCTCTCG  
ATAGCCAGCAGGAATGGTTTGTCCACCGCACCGCTCGGAGTCGGGATGTAGCTGTCCAATGCGGTAGCCAGTTTCGAAGATTTTTCTTCGTAAGCGGCATCGCCTTCAAGGCTTTCAGTG  
CGGAACCTTGTACGATCGGCGAGTCGTGCGCGGGAAGTCGTAGCTGGACAGCAGGTTCGGGATTTCCATTTCACACAGTTCCACAGCTCGGCATCGTACCAATGTCCGATTGTTCAT  
GAACACGATGATGAAGTACGCTACTTGACGGCCAGCAGGATGTGTTCGGGCTTTCGGCATAGGGCCGTGCGCAGCAGAACATACAGGATTGCACCGTCAATTTGTGGCGCGCG  
GTAATCATGTTTTTAAGCTAGTCGGCGTGACCGGACAGTCTACGTGTGCTAGTGGCGGCTTTCGGTTTCGTAATCTACGTCGAGGTGTAAATGGTAATACCGCGTCTTTTCTTCGG  
GTGCGTTGCGATTGTGTCGTAAGCTTTTCGAGCGCCGCGAATTTTTAGC

## SEQ ID 7864

VVFWVSFRPTISISSPTWMPRSTRPVTTVPRENGEHPDRQEWVHGTGSRDVAQVCGSQFEDFFVSGIAPQGFQCGTLYDRAVVAGEVVGQVADPHFNQFQQLGTVHVAFVH  
EHDVRYAYLTGQQDVGAVLRHRAVGSRTYQDCTVHLCGAGNHVFNVVGRTVTVVVCVAGPGFVTVVRVNGNTACFFPGCVVDLVVSPCSAAEFFS

## SEQ ID 7865

TTGCCGCGGCTCCACCAATCCCTTCAATATTACCGATCCCGCCATTGCGCGGATTCCGTCAAATCCATCAATTCGCCCGAATACGCCCTATTCCCAAAAAACCTTGATGCGCGCGG

## SEQ ID 7866

LPPASTNPFNITDPAADSVKSINSAESRLFPKNDLAAG

## SEQ ID 7867

ATGGCTAAGGAAAAATTCGAACGTAGCAAAACCGCACGTAAACGTTGGCACCATCGGTCACTGACCTGGTAAACACCCCTGACTGCTGCTTTGACTACTATTTAGCTAAAAAATTCG  
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CTGTCGGGTCACGCGGACTACGTTAAACATGATTACCGCGCGGCACAAATGACGCGTGCATTCCTGGTATGTTCTGCTGCGCAGCGCCCTATGCCGAAACCCGCAACACATCTCTG  
CTGGCCGCTCAAGTAGGCGTACCTTACATCATGTTTCATGAACAAATGCGCATGTTGACGATGCGCGAGCTGTTGGAACCTGGTAAATGGAAATCCGCGACCTGCTGTCAGCTAGC  
ACTTCCCGCGGACGACTGCCGATGCTACAGGTTCCGCACTGAAGGCTTGAAGGCGATGCGCGTTACGAAGAAAAATCTTCGAACCTGGCTACCGCATGGACAGCTACATCCCGAC  
TCCCGAGCGTCCCGTGGACAAACATTCCTGCTGCTATCGAAGACGTGTTCTCCATTTCCTCGCGCGCGGTACCGTAGTCACCGCGCGGTGTAGAGCGAGGTATCATCCACGTTGG

## SEQ ID 7868

MAKEKFKSPKPHVNGTIGHVDHKTTLTAALITILAKKPGGAAYDQIDNAPEEKARGITINTSHVEYFTETRYAHVDCPHADYVKNMGTAAQMDGAILVCSAADGPHQPTREHL  
LARQGVPIYIIVFMKNCMDVDDAELELVEHEIRDLLSSYDFPGDDCPVQGSALKALEGDAAYEERIKFELATALDSYIPTPERAVDKPFLLEIEDVFSIFRPRYRSHRPRARYHPRH

## SEQ ID 7869

TTGCAGGCGGCGCTTACGCGCGCGCATCAAGGTTTTTGGGGAATAGCGGTGATTGCGCGGAATGTAGTGAATTGACGGAATCGCGGCAATGGCGGGATCGGTAATATTGAAGGATTGG  
TGGAGGCGCGCGCAACGCGCGGGCGGAAAGACGCGCGCGCGCAAAATCTAGCGAGGCGGAGTGGCGGGTGGACGAGCGGCTCGCGATGTTTTGAAATAATCGCTTACCGTGC  
TTATTGTTGTCCTTTTTTTCACCGGTTGCTTCGGGATAATCGCGGTTGATGCTCGTAGCGGTAGCCAGATCCGCTGCACATACGCGCGCGCCCATGCTTACCGCGCGCGCTG  
CCAAGCATAGGCGGAGCAGGAGGCGTTGTATTGATGTTTGGCTTTCGGAATAATCGGA

## SEQ ID 7870

LQGLQPAASRFLGNRRDSAEMLDLTESAAMAGSVILKGLVEAGNGGGKDPAAETVAEGESGVDGAGADVFEIAYRAYCAFFCTGCPGIIAGDVLVGVSQLRLHIRAAAMPVTRRL  
PSIRASRRGLYCNVRLSEKIG

## SEQ ID 7871

ATGGCTCGTAAGACCCCGATCAGCCTGTACCGCAACATCGGTATTTCCGCCATATCGATGCGGGTAAACACGACGACAGAACGATTCTTCTTATACCGGTTTGACCCACAAGCTGG  
GCGAAGTCATGACGCGTCCGCTACTACCGACTACATGGAACAAGAGCAGGCGGATTAACCATTAACCTCCGCTGCCGTACTTCTACTGCTCCGGTATGGCGAAACAAATCCCGGA  
GCACCGCTTCAACATCATCGACACCCCGGGGACGTTGACTTTACCGTAGAGGTAGAGCGTCTATGCGTGTATTGGAAGCGCGGTAATGGTTTACTGTGCGGTGGCGGTTTCAACCG  
CAATCTGAACCGTATGCGCGCAAGCCAAACAAATACCAAGTTCCGCGCTTGGCGTTTGTCAATAAATGGAACCGCAACTTCTTCGCGGTTTCGCGCAAAATGGAACCCCGTT  
TGCAGCGCAAAACCGTACTTCTGCTCATTTCCGCTAGCGCGGGAAGACAGTTTACCGCGTGTGTCGATTTCGTAATAATGAAATCTATCATCTGGAATGAAGCGGATAAAGGTACAACCTT  
TACCTATGCGGATATTCTTCGCGAATTTGCTGCAAACTGCGGAAGATGCGCTCAAAATATGATTGAAGCGCAGCGAAGCCAGCAAGAACTGATGGAACAAATACTTGGCGGTGAAGAT  
CTGGCGAAGAAGAAATCGTAGGCGGCTGCGTCAACGTTACTTTGGCAGCGGAAATTCAGCCTATGCTGTCGCGTTCTGCAATTTAAACAAAGGTTTCAACGATATGTTGACGCGATG  
TAGAATGCTGCCAGCTCTACCGATATTCCTCGGTTCAAGGTGTTAATCTCAACTGAAGAAGCGCAGCGCTCAAGCCAGCGATGAAGAGAAATCTCTGCAATTTGCAATTTCAAAAT  
GTTGAACGCAAAATACGTCGCTGCTGCTTATTCGCGTTTACTCAGCGCTAGTAAATCCCGCGATACCGTGAATTTCTGTAAGGCACTCGCGAAGCTATCGCTGCTTTGGTG  
CAATGACTGCCGAGCCGACTGAAATCGAAGAACTACCGCTGCGGACATCGCAGCGCTATCGCTGTAAGACGCTTACTACCGCTGAAACCTTGTGTGGCAAGCGCGCGGATTA  
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CCGCGTTCTACAGCAAGAAATCCGCTCAACCAATTTTCCGCTATGGGTGAGCTGCACTTGGAAATTTTGTGACCGTATGAAACCGCAATTCGCTGGAAGCAAAATATCGGTGCA  
CCTCAAGTGGCTTACCGTGAAACTATCCGCAAGCGGTTAAAGCTGAATACAAATGCAAAACCAATCCGCTGGTAAAGGTAATACCGTCAAGCTTGTGATTGAAATGGAACCTATGGAAC  
CGGCTGTTGAAGTTACGAGTTTATCGATGAAATTAAGGTGTTGATTCCTCGCGAATTTTATTCGCTGTCGATAAAGGTATCCGCGATAGCTTGCCTAACGGTATCGTTGCGCGCTA  
TCCTGATGTTGACGTAGCTATCCGCTGCTGTTTACCATGATGTCGACTTCTCCCAATTTGCAATTTGAATTTGGCTGCTTCTCAAGCGTTTAAAGAGGATATGCTGCAAGCACT  
CTGCGCTGCTTGAAGCGGATTTATGCGAGTTGAAGTGAAGAACTCCGGAAGAAATACATGGCGGACGTAATGGGCGACTTGAACCGCGCTGCGGCTGTTGATTGGGTATGGATGATGAGGTA  
TCGCGCGTGAAGAAAGTCCGCGGAGTACCTTGGCAGAAATGTCGCTTACTCGACCGACCTGCGTTCTGCAACCAAGCGCGCTACTTACTCTATGAGGTTCAAGAAATATCTGTA  
AGCTCCGCGCCACATAGCTGCTGCTGTAAGTGAAGCCGTAAGC

## SEQ ID 7872

MARTPISLYRNI GISAHIDAGKTTTTERILPYTGLTHKLGVEHDAATTDYMEQEQERGITITSAAVTSYWSGMAKQFPEHRFNIIDTPGHVDFTEVERSHRVLGDGVNVYCAVGGVQP  
QSETVWRQANKYQVPLAFVNMDRQGANFRVVEQMKTRLRANVPVPIVUGAEDSPTGVVDLLMKSIWNADKGTFTFYGDI PARLVETAEEWRQNNIEAAEASEELMDKYLGGED  
LAEEIIVGALRQRTLAGETQPHLCGSAFKNKGVRMLDAVVELLPAPDIPVQGVNTEADSRQADEERFSAFALFKMLNDKYVGLTFIRVYSGVVKSGDVLNSVKGTRERIRLV  
QMTAARDTEIEVRAGDIAAATGLKDVTTGETLCAESAPIILERMEFPEPVHIAVEPKTKAQKMGILALNRKAKEDPSFRVTRDEESQPTISGMGLHLEIIVDRMKREFGVEANIGA  
PQVAYRETIRKAVRAEYKHAKQSGKGQYGHVVIEMEPMEPGGEGYEFIDEIKGVIPREFIPSVDKIRDTLPXGIVAGYPPVDVIRLRFVSGYHVDSSQLAFELAAASQAPKEGHRQAS  
PALLEPHAVEVETPEEYMGDMGLNRRGVVLGMDDDIGGKVAEVPVLAEMFYSTDLSATQGRATYSMEFKYSEAPAHILAAAVTEARKG

## SEQ ID 7873

TTGATCGCGCGGCTGAAGCCCGGCTGCAACCTCTCTATGCAACCCCTTTCGAGCGCGGACACTACGCAACATCTTGAGAACCCATCCTGTCAAGAAATACCGCAACCGTCCCGGATACAC  
GTAATCTCAAAACCGCTCATTCGCGCTGCAATGGGACATCGCGCGCAGCGGCGGCTTTCCCTTCGCTCGCACTGTTCTGCTCTGTTCTCATCATAGGTATGACAAACACCGGAGGA  
CGCTTCGCGCGCGGTGCAATCCGTTGACGCAATGCGCGGACGCGGACGCGGACGCGGATGGGATCGAAATCCCGCGCGTGGCTACTATAGTGGAT



## SEQ ID 7874

LMRRAEARPATLSMHPASPTLRNLI LRTHPVKNTRTPV IHRNPKTRHSRAAMGHRROQGGFPFARTVSALFPHRYAQHGDDASAGRCNPFDAHGPARQPTWASKSRACRTIVD

## SEQ ID 7875

ATGCCAAGACGTAGAGAAGTCCCAAGCGCGAGCTACTGCCAGATCCTAAATTCGGTAGCGTCGAGTTGACCAAAATTCATGAACGTATTGATGATTGACGGTAAAAATCCGTGCCGAGC  
GTATCGTTTACCGTGCCTTGGAACAGATTGAGAAAAAACCGGCAAGCAGCAATCAAGATTATTAAAGCAAGCCATTGCAAACTCCAAACCTATCGTGGAGTGAAAAAGCCCGCTGTAGG  
TGGTGCAAACTACCAAGTTCCTGTTGAAGTTCGTCCTTACACGCGCTGCGCTTGGCAATCGCTTGGGTTCGCGACGCGCGCCGCAACCGTGGTGAGAAATCCATGGATTCGCGTTGGCA  
GCGAGTTGATTGATGCGTCCGAAGGCGGTGCGGTGCGTTGAAAAACGTGAAGAGTACACCGTATGGCTGAAGCCACAAGCATCTCTCACTCCGTTTC

## SEQ ID 7876

MPRRREVPKRDVLPDPKPGSVELTKFMNVLMDGKKSVAERIVYGALEQIEKKTGKAAIEVFNEAIANSKPIVEVKSRRVGGANYQVPVEVRPSRLALAMRWVRDAARKRGEKSMDLRLA  
GELIDASBGRGALKKREEVHRMARANKAFSHFRF

## SEQ ID 7877

ATGGTGTCCGATTTTATGGCAGCCCCAGCGCGAGCATGCCGCCGAGCAGCCATATTTTCGGTTTGTGCGAGCTGTACGTGCGGACGGCGCGGATGGTGGGTTAGGAATA

## SEQ ID 7878

MVSDPMAAPRADDAAEQPYFRFVDVYVRQARMVGLGI

## SEQ ID 7879

TGCGGACATGGTGTGCGCAAAATATTAACTCAACAGGACGAGAAAAATATGCCAATATCAACCAATTGGTACGCAAGGCGGTCAAAAGCCCGTGTACGTAAACAAAGTCCCGCACTGG  
AAGCCTGCCCGCAAAAACGCGCGGTGTGACCCGTGTATACAGACTACCCCTAGAAAACTAACTGTGCAATTGCGTAAAGTATGTAAGTCCGCGTACCAACGGTTTGAAGTCATTTC  
ATATATCGCGGTGAAGGCCACAACCTGCAAGAGCAGCGTGTACTGATTGCGCGCGCGGTGTAAAGACTTCCGCGGTGTACGTTACACACTGTACGCGGTCTTTGGTACTGCA  
GGTGTAAAGACCGCAACAGCCGTTCTAAATACGGTGCTAAGCGTCTTAA

## SEQ ID 7880

LPTWCRQIFNSTGRENMTINQLVRKGRQKPVYVNVKPALEACPQKRGVCTRVYTTTPRKPNALRKVKVRLTWGFEVLSYIGGBEHNQEHSSVVLIRGGVRKDLPGVRYHTVRGSLDTA  
GVKDRKQARSKYGAARPK

## SEQ ID 7881

ATGGCTGAATCGCGCAACACGCCCTTCAAGTCAAAATGTCGACCTGTCAACCGGCACTAGTATGGAACCGGAAACCGCATTCGCGCGGTCTGTTCGCAACGCTGCAAACTGATCGACT  
TGGGCGGATGGGACAGCGGAAATATACGGTTTCCGGTCAACCGGAAAGTTTCCCGGAAATATCCGAACCGGACGGGCGCATACCG

## SEQ ID 7882

MAESRQTRLQVKPTCTQAVVWKPENAFRPFCSQRCKLIDLGGWADGKTYTSGQTESLPEISEPDGAYR

## SEQ ID 7883

ATGCCCGATTTCACCGCAATACACCTTTAGGATTCAGAAACTTTGCCGCAATCAGAAGAATCTGCCGTGGTGGCATCCAAACCGTCCGCGCGCGTCCCAACGCCAATTCGGTTTCGTGC  
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CTTCCAGACCATTAATCTTCAATATTGATCCCTGCAACTTCCAAAGCATCCAAACTCACATCAACCCGATCAATTTGGGCATCAGGATAATGGTCCGCCATCTGAATGGCAAGGCAACCGCT  
TCCGGTGCAAGATCCAAAGCATATGCACAGCTCATCTGATTCTATCCAAAGTCCGATCCCGCAATTCATAAATAAAGAGCGCGGTACAATCAGCGTTTATCTACATAA  
AAATCAAACTCCCGCTGCCAGGCTGGTGTGTAATAAGCGGCAAGATGTGTCGACAGCAGCGCTCAATAACCGCGACACTTCTCTTTTCAGCTTCCAAAGAGTTTTCGATCAA  
GATATGGGGCAAGCATATCCAAAGCAAAATTCAAAGTATGCGAATCAATAAACCGCTTCAATCATGCGCATTATCTGTTCCATGACCAAAAAGAGCCCTGCTCATTAACCGGCTGAC  
TGCAAAACG

## SEQ ID 7884

MPDFHQQYTFRIQKLCRIQKNLPGGIQVPRPAAQRQFRFVQIFLRQSPNRLCIHRIIRGNQIISAFQSLQIGMKNLMTLFQTIIFNIDPNCFQSIQTHINRLNIRIMVRHLNGKATA  
SGAKIQSIMHQLIVFYPRSKSVTQDFINKRARNHAFYIKIKLPLPLVLCQISGRNVFDSITLNRQHFLFFSFQEPCKIKIWGKHQRIQIQSMQNIINRPMRIICSMTKKEPCLIKTAD  
CKT

## SEQ ID 7885

TTGCCGATACCGGGTGCAGGCTCGGTGCGCTACGATGTGAAGGTACGTTTTTTTGGGATGTGGCTGCGGTTTCGGCGCAAAATCAGGATAAACCCGCGTGTTCGGGAAAAATCGGGTAA  
TTTCAGGT

## SEQ ID 7886

LPPIGAGSVGYDVKVRFPADVAASQAQITINPRCFGKNRVISG

## SEQ ID 7887

TTGCCGACCATGTGCGCAAGAGCGGAATTATATTTTATTGCAAGCAGACAGTCAAGCATAACGACAAGAAAAAGATGATTTTCTGTGTTGCCGATAAATATTTACCGACATCCCTCA  
CAATCAGTCCGACGCGTGGAGAAATACGTGTCAATACGTTTTTTTCCATAC

## SEQ ID 7888

LPPTCRQERNYIFIASRQSSITTRKKMIFLADKYLPTSLTISRAGENTVNTFFPY

## SEQ ID 7889

TTGCTTATAGTTGTACGGTTTGACATATGCACGGAAGGAAACGCCATGACTTTCTTCAAAACCTCTACCGTCTGTGACCGCATCCGCACTCGCGTTTCGCGCTGCGTTGCGGACCCG  
TAACCGGACAGCAGTCCCAACAAATCCGCCATGTACGGTTTGGTGGCGCGGAGTGTGCGGCATCGTGGCGCACTGACCCACAGCGGCAAGGCGGACGCAATTCGCGCTTGCCCTG  
CGGCGCAATCGCGGACGCGTGGCGGCTATATGGACTACCAAGAGCAGCGTTTGGCCAAAACCTTGGCGGCACGCAAAATCGAAATCCAAACGCAAGGCAACCAATCAGGCTGTGATG  
CCGGAAGCGTTACCTTCGCGACCGGCGGCGGCTGGCGGCGAGTGCAGCAATACGCCCTGAACACTGCGGCACAGACGCTGTGCGAGTATCCGACACGAGCTGACCATCAACGGGC  
ACACCGACAACAGGTTCCGATGCACTCAACATCCGCTTTGCAACACCGCGCCCAAGCGGTTGCCACTATCTGACAGCGCGCGCTGGCGGCTTCGCGCTGACGTTTACGGCTA  
CGGTTCCGATATGCGGCTGCGCTCAACGCTACGTTGAAGGCGCGGCGCAAAACCGCGCGTGAATCTCATCAACCCGACCAACGCGCGTCAACGCGGACGCGCATG

## SEQ ID 7890

LLIVVRFDICTEGNAMTFKPFSTVVLTAALALSGCVADPVTGQSPNKSAMYGLEAAVCGIVGAL/THSGKGARNALACGAIGAGVGGYMDYQERLRQNLQAGTQIETQROGNQIRLVH  
PESVTFATGSAALGSAQYALNTAAQTIVQYPTTLTINHTDNTGSDAVNNPLSQHRAQAVAYYLQTRGVAASRLTVYGYGSHMPVASNATVBGRQNRREVELINPDQRAVNAAREH

## SEQ ID 7891

ATGGTTTGTCAATGGAAGAAACGTATTGACAGTATTTCTCCAGCGCTCCGACTGATTGTGAGGATGTGGTAAATATTATTCGGCAACAGAAATCATCTTTTTTCTGCTGCTTA  
TGCTTGACTGTCTGCTGCAATAAAAAATA

## SEQ ID 7892

MVCQYGRNVLTFPSPAVRLIVRDVGKYLANKKIIFLVVMLDCLLATKI

## SEQ ID 7893

TTGGCGTTCGACGGCGCGTTACATGTGCCGTGCGCGTTGACGGCGCGTGGTTCGGGTTGATGAGGATTTGACGCGCGGTTTTCGCGCGCGCTTCAACCGTAGCGTTGACGCGGAC  
GCGATATGCGAACCGTAGCGTTAAACCGTCAAGCGGCAAGCGGCCACGCCGCGCTGTCAGATAGTAGGCAACCGCTTGGCGCGGTTGCGGAAGCGGATTTGACTGCATCGGAAC  
CTGTGTGTCGGTGTGCCGTGTATGGTACGCTGCTGCGGATATGCAACGAGCTGCTGTCGGCAGTGTTCAGGCGGTATTCGCGACTGCGGCCCAACGCGCGCTGCGGTTGCGGAA

GGTAACGCTTTTCGGGCATCACCAGCCTGATTGGTTGCTTGGCGTTGGATTTCGATTTCGCTGCCGCAAGGTTTTCGGCAGAAACGCTGCTCTGGTAGTCCATATAGCCGCCACGCT  
GCGCGGATTTCGCGCGCAGGCAAGCGCGGAATTGCGTGCCTTTGCGCTGTGGGTTCAGTGCAGCGCAGGATGCCGCACTGCCGCGCCACCAACCGTACATGGCGGATTGTTTGGGG  
ACTGCTGTCCGGTTACGGGGTTCGGCAACGACCGCGGAAGCGGAGTGCAGTTCGCTGAGCAGCGTAGAGGTTTGAAGAAAGTATGGCGTTTCTTCCGTGCATATGTCAAAACCG  
TACAACATATAAGCAATCATGCCGTCTGAAAAAGTCAAT

## SEQ ID 7894

LALQGAHVPCGVDGALVGVDEDFDAVLAAPNRSVGRDRHMTVAVNRQARSRAARLQIVGNRLGAVLRKRIVDCIGTCVVGVPVVGQRRVGLHQRICGVSQVLRATAQRRAAGGE  
GNAFGHHQPDILVALDFDLRAGKVLQTLILLVHLAAHACADCAAGKRGIAACFAAVGQCADDAACRATQTVHGGFWGLLSGTGVGNAAGKRECCGQHDGRGFRESHGVSFRAYVKP  
YNTKQSCRLLKKN

## SEQ ID 7895

ATGGATAACGCTTCGCGCTTTGCGCGGAAACCGCAGATTGCAGCGCGTGGCGTCAAGTGGGCCCAACCTTCGACAGCTTACCGCCATACCGGATACCCCTGTAACTCATCGTTTAAAC  
AGATATTCAATCAAAATGCCGTC

## SEQ ID 7896

MDNVSEFFAGKQILAAGGVQVGPQLQTLPPYRDTPTVSSPKQIFNQNAV

## SEQ ID 7897

ATGAGCGCGCTTTATGGCATAAAAACTGCTGGAAAGGATTACACCCCAATAAATTCCTGTACAACAAGAACACAGCAATATGCCCGCTTTTATTCGCACAGCGGCAAGGGAT  
GTTTGTGAGTATGAAAAACGTAT

## SEQ ID 7898

MSAALWHKRLSNKGFPTQINFRYKNNNSNMPAFYSHSGKGFVSHKTY

## SEQ ID 7899

ATGTTTCGAGCGCGCGATCTATACCGTGAAGTGTGTTCGGAAGACCGGATCTTGTTCATCCCGCTTTGATTTCGGCGTGAAGTGTGTTCGGAAGACCAATATCGTGAAGCATTCGTTTC  
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AGATAATGTAAACATCGCTCCCTTTTCACGGGACATCGTCATCAACGCGCGGAANTGGATAAAATCGGAAGACAGCTGCCAAACGCGCCACCGGATAGGATACGAACTGGCGTTGAT  
CGGATGTTTAAATATGCGAGCAATCACTTTGCGCGCTTAGGCATCAGCGGTTCGCGGTGTGCTATTATTGGAATGCCCGGATTTTACGGAACAGGCGTTTCATGCCGAAGTAGGCTACCGTT  
ATCGGAATAGCGCTTAGAGTGGGATTCGCGCTTGTCTAAACAAACCGCGTGGGCAATACCGTTTATACGGCAATACGGGTATTGTGTGATACAGCGCGCTCTGAATGAAAA  
ATGCGCGCAGCACCCTTTTCCAGTATGCGCGCAACCAATACCATGACGAATATTTGGCAAAACGTTTACACAGTAAACGATTTCGGTGAGCGGTACGTTTACGCTATTACGCTATGTCG  
GCTTGCAGTGTACGCGGTATTAGCGGTATGTTGATAATCTGTGGAGAAAGAGCAGGCTTCACGCGCTTATGTTGTAAGTTTGGGTACGCTGAAATATTAGACGCGCGCTCTGGAC  
TGAAGTTGGGTGCGGTTACACGAAACGGATATTAAAGCCCTGCAACATTAATTTACAATTTTACTCGCGGTGATGAT

## SEQ ID 7900

MFEAADLYRELLSERPDLVYPRFDLGVMLFEDKQYREALVQLHRAEEVLPDMRQLAREYIRQAEAVQAMHPSFNMNYEQTDNVNNAISLRDIVINGRKNIKSEDSLPRKANGIRYELGVD  
RHFIMAGNHFARLGISGSGVHYWNARDFSEQAFHAEVGYRYRNSRLEWGFPRPVKQNLGNRYTANTGIVLDYSRRLNEKNRSTQSFQYGRKQYHDEYLAKRYSKTLISVSGTFSYAHNS  
ANQLYGGISGMPDNTVKEQASRRYGVSLGTVKILDLGLGLKLAGYTKRIFKAPATLIYNPTRRDD

## SEQ ID 7901

ATGAAAATCACCCTTGGAACTCAATTCGCTCAATGTGCGGCTGCGCAGGTGCAAAACCTGCTTGTGCAATCCGCGCGATATTTTGGTTTTCAGGAACTCAAACCTGCATCAGGACA  
AATTTCCGCGCGCGCTTGCAGATGATGGCTGCGCTGTGTTTGGAGCGCGGAGAAACCTACACGCGCTGGCAATCGTCAGCGCGCTGCGCGAGGAGCTGCATTTTCGTTTTCGCT  
TTCCTGCGGATGACCGCAACGCGCGGTGATTCGCGCGCAGCGTTCGCGCGCTGCATCAATGTCTATTGCGTCAACGCGGAGCGCTTCGACAGCGCCCAATCAATATAAGGAA  
CAATGTTTTCGCGCTGACGAGTGTTCGCGGATGAAATGTCCCGCCAGCGCAACTGGTGTCTGCTGGCGGATTTCAATATCGCGCTGCGGATGCGGAGCTGTTACGACCTGAAATAT  
GGTATGAAAAATCCTCTGCTCGTCCGTCGAACGCGCAGTGGTTTCAAAACCTGCTGATTTGGGATTGACCGCAGCGCTGCGCAAGTCCATCCGAGGCGCGCTCTATACCTGCTTGA  
CTATCGCGCGCGATGTTTCAACGCAAACTGGGCTGCGTATCGACCATATATTTGTTACATCCGAAATGGCGCGCTTTTGAAGGATGTCGCGATCGATTTCGAGACGCGCGCGCTGGAG  
CGTCCGACGACACCGCGCGCTGGCGCGAGAAATTTGATTG

## SEQ ID 7902

MKITTNNVNSLAVRLPQVQNLVDPDILVLQELKLDQDKPAAALQMMHNCVWSGQKTYNGVAIVSRSPQDVHFLPSLPDDPQRRVIAATVGGVRVINVYCVNGEALDSPKFKYKE  
QWFAALTEFVRDEMSRHGLVLLGDFNIAPADACDYPEKWKYKHCSSVERQWQNLIDLGLTSLRQVHPEGAPYTFWYRGAHPQRLGLRIHLIIVTSEHAVALKDVRIIDLETRALE  
RPSDHAPVAABFDL

## SEQ ID 7903

ATGGCGTGTGCTGGGCTTTTATTGAATTTGTTATGAAATGATGAAATCTAAAAATATCTTTTATGGGATACCTAATCGCTTCGGCGAGCTTTGCCGAGGATATCGCGCTGCTGTG  
AACCGATTACCTGCTGGTAGTTCGCTGCGCTGAGCGCTGAGGGGAAAGCCTCGCCCTCTCTCGCTTTCAGAGGATGTCGCGCGGCTTCGCGATGCAATGCCGTCTGAAGTCTCTAAAG  
CGCGCGAGCGCGGATGTTTCGAGGCGCGGATCTATACCG

## SEQ ID 7904

HALLGILFEFVMKLNKSNIFFGYLIASATFAEDIGVPEPFINVGSRAAMPSEGESLALLPFAEDVPPVRDAMPSEVPKSAAGGDVRRGRSIP

## SEQ ID 7905

GTGGTTCGCTCGGACGCTCCAGCGCGCGCTCTCAAAATCGATCGGACATCTTCAAAACGCGCCCATTTTCGGATGTAACCAATATATGTCGATACGACGCGCGAGTTTTCGCTTGGAAC  
ATCGCGCGCGGATAGTTCGAACCAAGGTATAGAACGCGCCTTCGGGATGGACTTCGCGCAGGCTGTGCGTCAATCCAAATCCAGCAGGTTTGAACCACTGCGCTTCGACGAGCAACAGT  
GGATTTCATACCATTTTTCAGGTCGTAAACAGTCCGATCGGACGCGGATATTGAAATCGCCAGCAGCAGGTTTTCGCTGCGCGGACATTTTCATCGCGGACAACTCCGTCAG  
TGGCGCAACCATTTGCTCTTATATTGAATTTGGGCTGTCGAGGCTTCGCGCTTACGCAATAGACATTTGATGACGCGCGCGCGGACGCTGCGCGCAATCAGCGCGGCTTCGCGG  
TCATCCGCGAGGAGGCAACGAAATGACGCTCTGCGGACGCTGCGGCTGACGATTTGCCACGCGCTTGTAGGTTTTCGCGCGCTCCAAACAGTGCAGCGCCATCATCTGCAAGG  
CGCGCGCGGAAATTTGCTGATCGAGTTTGAAGTCTCTGCAAAACCAAAATATCGCGCGGATTTTCGACAGCAGGTTTTCACCTGCGCGAGCGCACATTTAGCGGAATGACGTTTCA  
AGTGTGATTTTCATAACATTTCCGAAAAATGCGCTCGAACGTTTCAGCGCGCAAAAGAAAGGATT

## SEQ ID 7906

VVARTLQARLQIDADILQNRHFGCNQYVMDTQAQFALEHRAAIVPEPIERAFGMDLAQAVQSQIQVVKLPDPDGRVDFPIFFRVVTVRIGRRDIEIAQQHQFVAVAGHFIADKLRQ  
CGKPLFLIFEAGVGFPAVDAIDIDDAHADGRNHAALRVIRQGRQTEHVLRAAADCHAVVGFLPAWNTVPAHLQGGGRKFLIEFEFLQNIQRIIVDRQVHLRQPHIERIDVP  
SGDFHNISEKRLKRSDEKRGF

## SEQ ID 7907

ATGCCAGCAACGCCATTTTCTTTTCGATTGCGCGGCCATTTATGTTTCAAGAAATCAACTGTTTAAAGAAATATTGCTGTTTTCAGGATTGCAATGCCGCTTGGCAGTATTGCG  
ATTTGGCGGATGTTTTCGAGAAATGCCGCTGAAACTTCAGACGCGATCTTGCCCGGACAAACGCGCACTAAATAGAAATAGTGTCTTCTTCTTCTGCGCGCGGAAACCGA

## SEQ ID 7908

MPSNAIFLFLVPLPGHLCVSRINCFKRYNCCFEVLHCLRAVFDLADCFLLKMPSETSDGILPQTLNRNSAFSISRRRNR

## SEQ ID 7909

ATGAACACAATACCGCTCCACACCTACTCAAACTTATGGCGCATCCGAAACGTATGGCGATATGATCCAACTGTTGGACAGCGAACGCAATATCGTGAACATGGCAAAATCCTTATCCC  
TGACGGGACCCGCGGTTTCTGTCAATTTGAACCGCTGAGGGCGGGCGGTCTGGTGGACTTTACGGTTACACCGCATATCGAATACCGCTGTTTCCGAAGACGCGCAACGATTC  
GCGGACAATCCGCGATTTGAAAAACAAACGCGCGCA

## SEQ ID 7910

MNTIPLHPTILKLMHAHPERMAILIQLLDSEKNIVELAKSLSLTATAVSCHLNRLRAGGLVDPTRYHRIIEYRLVSEDAATILRTIRDLNKRRA

## SEQ ID 7911

ATGTCGGTTCACCAAGCGTTTCGGAACAACGAAAGACAATGCAATGTTGATGCGAAGATGAAAAGTTATTGAATATCTGAAGAAATCATATTAAAGATGTACCAAAAGAAATTGC  
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TAGTAAGGAACAATTCAGAGATGGATGTATATGTTAATGGTAAAAAATACGAAAGTATGAGGGGGGGAACATAGATGTTCTCCCAAGGTTTGAAGTACGAAAGATTGAGTTTAC  
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GACAAAATCTGAAGAGATCTTTTGTATCTGGGCGACATTAGAGCGGTGGCAACAGATGAAGACAAATTACCAAGGCTGGGAGCTTTCAATATGAAGGTGGGCAATTTGGCGG  
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## SEQ ID 7912

MSVQPSVSEQLKDNANVDKDEKVIHYLKKSSLDVFKELQAKVLKVGDEYTVGRKQYAGKLKGSVSKAMFLDGEFFSKBQLKMDVYVNGKKEGSGKGLDVLPLKLSBQKIEFY  
GADKEQNYALLKLTWVYEPYSVVRGTPYGRKDNPIEGDQNPKEIPFDLYLDIRGVATDEKLPKAGSPQYEGRAFNGMVLKESLDNHNHGVFRYITDFDRRKSGSGIEBMEQYQKI  
KLEEAATIERIPYRESGSLGLKDRVSYPGVNVEGAMLEKDNIEKKYHLGIFGEAAAEVAGAVSQEKKHQAIVIGFGEKK

## SEQ ID 7913

ATGCATAATTTGACGCGACGAAGATATGGGACACTTATCGGGCTTATATCCACAGCCCTCAAAATGACGAAAACGCTTGTGTTTTCCTTAAATCGGACAAAGAAAACCGCAAGCTCAAGGC  
TTGCGGTTTTTTAT

## SEQ ID 7914

MHNLFARRYGTLLGLISTRILKMTKTLVFPALIGQRKTASSRLAVFY

## SEQ ID 7915

ATGCAAAATATGAAAAACCAAGTACCGGATCAGGCGATGGATGCCGATCCAAACCGGCCAATGTTTCAGACGGCTGCAAAACAGTTCGGGCGCATATCGGTACCAACACGCGCTACCGCC  
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CGGAGCGCGACAAAGGTTTGTCCAACAGCAGTTGGTGCAATGGTGGCGTCAATATTTCTGTCGACCTGAGGATGCGCGAGTGGCGGAGCTGCACCAACAGCTTGGCCAAACCGCGA  
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GCAAGCGCATATCAAGAGCTGGAACAAATGTCGAGGAAAAACCTGACGCTTGGCGAAGCAAGGACAGCCGCTTTCAGACGCGCTCGCGCGCTTAAATGATGATTGAAGAAATTGAG  
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## SEQ ID 7916

MQNMKNQVRSGMDARSNPANVSDGLQNSSGHIGTNTYRL/TKLGEQMARLPIDPKIARILIAAKKHDCAEILVIALSALSIQDPRERPLEARDAAKAHERPTDKQSDFLTYLNIWDSFQ  
RERDRGLSNKQLVQWCRQYFLSHLRMRWRELHQLAQTAIENGLITKEAARFRPPEVKOLTSSENAGDQDLSARLKQKQKQHRTOIRATKEAGYEQIHRALLTGLIANVGMKSPDSN  
DYTGARGSRPHLPFASALFKAKPKWMAELVETTRLYARDVAVIQPEWIEQEAHLVRYHYFEPHWEQKRGVAVASERVTFYGLTVLPRRPYSYKVAPEAREIFRSALVAQBYDLKA  
DPFVHNKLIKETILEHKSRRQDVLVDDEALFAYHERLPDFYMDASVSEGLCPANPQQTTPSPVKGWEGGKTVAQNTFSATAANPLFNPPLQEREQSASVSTVSGSLKTMSCEARLN  
PCEAKTKTSSLSHSQRLSENITPPSDGLRNPANPQQTTPSPVGBWEGGKTVAQNTFSATAANPLQEREQSASALTVSDDPKPKQPSAQGRKLPLPLADIRTFEAMLIKTAERDNPRL  
LPLSRDDLQHAHAHITEEQPKHMTADGKFLSYRFEHPHLDGVTLTLPVLNRISPAELWLVPMIREKIQIQLKALPKQIRRICVVPVEFTQPLQNPDRNAPILPQLAQALIA  
KTAGDIRILBQINQDEWAPRLPEHCYFNLRIIDDEGEQELAMGRDLIQIQQQLKAATTTFRDNTQEFERDNTVAMDIGILPESTKFPARGQQLTGYLGLQKKKGRILRLPDSAAAGH  
AHLGVIEMKLQKBEQVKLDNGIQGPTQAMLLKHINADTLRDDLTQAVCDRAPIGEDKLPNEKAPKEQIKRARSRLPAVKEALSRYLQETAAYAEINLKLKHLPLTHLLRLQLTL  
LAPGFATRTFWAQWRLPIYLKAMFLRLKESNNPADAAREADIQLEQMWQKTDGLAKQGPVSDGLAAPKMWIEELRVSLPAQELKTPYPSVKRLKLMWELL

## SEQ ID 7917

ATGGTTCATATTTATTTAATCAGGCGCACAAAGATTGACGACTATCCGCTGATGTTTTACGTTTTCGAGTACAGCGTTTAAATGAGGCGAGGCTCTTTTTTGGTCATGGAACAGATAATG  
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GCGTCGTCGTCGACACATCTCTGCCGCTTATTGACACACCGAGCGTGGGAGGGGAGTTTGAATTTTATGATGATGAACGCGTATGTTACCGCGCTCTTTATTTATGAATTTGCTG  
GGTACGAGCTTCGACCTTGGATAGAATACGATGAGCTGGTCAATGCTTTGGATCTTTGCAACCGGAAGCGGTTGCCCTGCCATTCAGATGGCGCAACCAATCTCTGATGCCCAATG  
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TGATTGTGTTTCCAAATCCGCTTATGTGGATGCAGATCGGTTGGGGCTTTGCTTGAGGANTATTTGCACGAACCGGAATGGCGTTGGGCAGCGGGGACGGGTGGATGCCACC  
AGGCAGATTCTTCTGAATCGCGCAAGTTTCTGAATCTTAAAGGTATTTGCTGGTGGAAATCGGCATACACGGGATGTAATTGAAGCAGCGTATCCGAGTTGCCCTTTACTTGGTTGG  
AAACACGCGGGGGGACGGTTTGTTCCTCTTGACCGCGAGCAGTTATTTGGCGAAGAG

## SEQ ID 7918

MVHIMFQAAQELTTIRDLRFAVSRFNEAGLFFGHGTDNAHDRAVYLILHLNPLDMLAPYLDKILLEAKKEBVLAVIERRAVEHIPAAYLTHQWQGEFDYVDERVI VPRSFYIELL  
GDGLRPMIYEDLVEHNLALDCTGSGCLAIQMAHYPDAQIDAVDVSLDALEFVAGINIEBYGLEERIQLIHLTDLFBGLEGTVDLIVSNPPYVDAESVGLPBEVLEHEPRLALGSGADGLDAP  
RQILLNAARFLNPKGVLLVEIGHNRVLEAAYPELPTWLETSGGDFVFLITREQLLGE

## SEQ ID 7919

ATGATTCGCTTCGGCAACAGGGTCAGGCAGGGTAGGGCGGCAGTTTATGCGCTGTGAAAGCCGTCTTTACGCTTGTTCGAAATAAGTGGGAAAAGAACATACAATCCTGTACAA

## SEQ ID 7920

HIPFGNRVRQGRGSGFMPSESLSLRLFAKIVGKGYNPFVQ

## SEQ ID 7921

ATGGAAGAAAGATTTTATGCCATCAAAATCGGTATTCCTCTCCGAAACCATCCGCTCATGGTCTTATGGCAAGTTAAAAACCTGAAACCATCACTACCGTAGCTCAAAACCCGAGC  
GCGACGGCTTGTCTCGCCAAAATCTTTGGCCCGGTCAAAGACTACGAATGCTTGTGCGGAAAATACAAACGATTGAAATTTAAAGCGTAACCTGTGAAAATGTGGCGTAGAAGTTAC  
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GATATCGAACCGCATTTGTACTTTGAAGCATTCGTGGTGACCGATCCCGCATGATCCGTGTCAACGTCGTCAATTTGCTGACTGAAGACGATTACTACAACAACTGGACGAATACGGCG  
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CGCGTAAGGTTTGGCGGATACCGCTTGAACAAACCGCACTCCGCTTACCTGACCGCTGCTGCTGTTGATGTAACCTAAGACTTGTGCTGTTGTAAGACGATTGCGGCTATTTACAGCGG  
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GCCGCTACGTTGTTGACTGAAAACTGGTGGATATGATTGACCAATCCGCTGCTGATGAAGTCAAGTCCGCTACCTCCGATTCTGTAACAAACCGCCACCGCTGTGCGCGCACTGTTACG  
GCCGCGATTTGGCGCGCGCAACCTGCTCAATGCCGCGGAGGCGAGTGGCGGTGATTGCGGCTCAGTCTATTTGGTGAACCGGCTACCGAGTTGACCATCGTACGTTCCACATCGGTTGCG  
GGCATCCCGTGGCGGACGAGCAGCGCAAGTCCGAAGCAATCCAAAGCTGACCGGCTTTCAGCAGCCAAATCGGTTATGTTGCCAACAACAAAGGCGAGTTGGTTGTCATCGGCGCTCT  
TGCAGAGTCTGATTACGATGACATCGGCGTGAACGCGAACCCACAAAGTACCTTACCGTGCCATCTGCTGTTACAGAGCGTATGGCCATTAAGCGCGTCAAACTTGGCACTT  
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CGGTTGCCGAGCTGTTTGAACACCGCTGCCGAAGATGCGGATGCTGCGGAAATACCGGTACCGGTACCGTTCTTCTCGGTAAGGAGACCAAGGCAACACGCTGATTATCACTGAGCT  
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CGTCTCAAGGTATCGAAGCACTGCGACGCTACATTTGCCAAGAGGTGCAAGAGTTTACCGCTGCAAGGTGTAAGATTTCGATTAACACATCGAAGTCAATCCGCTCAAAATGTTGC  
GCCGTGTGAACATTTGGCGATGCGCGGAAACCGGCTTTATTTACCGGAGAGCAGGTGCAACCGCGGATGATGATGGCGGCAATGAAAAGCTTTGGAAGAGGCAAGAGCGCGACGTTA  
CGAAAACATATTTGCTGGGTATTACCAAGGCTCCCTGTCCACCGACAGCTTCAATTTCTGCGCATCGTTTCAAGAAACACCGCTGTTGACCGAAGCTGCCATCATGGGCAACAGAG  
GAACGCGCGTCTGAAGAGAAATGTCATGCTGCGTCCGCTGATTTCTGCGGTACCGGTTGACTTATCACCGCAGCGCTCATCAGCAATGCAAGGGTAGACAGGAGACTGCTGAAA  
CCCAAGTAACGGATGAA

## SEQ ID 7922

MEEFDAIKIGIASPETIRSWSYGEVKKPETINYRTYKPERDGLFCAKIFGPKVDYELCGKYKRLFKGVTCEKCGVEVTLTKVRRERMGHIELAAPVAHIFLKLSPSLGMLNHTLR  
DIERVLVFEAFVVTDPGMPPLQRRQLLTEDDYINKLDEYDDFDKMGAEIGIRELLRLDVLAGEIEILRQLESTGSDTKIKKIAKRLKVLFAFHRSGMKLEWMIMDLVLPPLDLPLVLP  
LDGGRFATSDLDLYRRVINRNRRLKRLLEHAPDIIVRNEKRLQEAQVDSLLDNGRRGKAMTGANKRPLKSLADMKKGKGRFRQNLILKRVDSYSGRSVITVGPYLRHLQCGLPKHALE  
LFPKPIPHKLEKQGLASTVKAAKLVEQEVFEVDILBEVIREHPINLARAPTLHRLGIQAFEPILIEGKAIQLHPLVCAAFNADFDGDMVHVLPLSLAQMEARTLMLASNNVLSPANG  
EPIIVPSQDIVLGLYMYTRDRINAKGEGSLFADVKEVHRAYHTKQVELGKTIVRLREWVKNRAGEFEFVVRNYETTVGRALLSELPLKGLPFYFNKALKKKIKSLINASFRLCGLRDT  
VIFADHLMYTGFGPAAGGSLIAVDMEIPKEKAALLAEANAEEVKEITEDQYRQGLVTNGERYNKVVDIWRAGDKIAKAMMDNLSKQKVIDRDNBEVDQESFNSIYMMADSGARGSAQIK  
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AGTLLTEKLVDIMDQSGVDVVKVTPITCKTRHGLCAHYCGRDLARGKLVNAGVAVGLAAQSTIGEPGTQLMTRFTFHIGGAASRAAASQVEAKSNGTARFSSQHRVYANNKGLVWIGRS  
CEVVHDDICRERERHVKVPYGAILLVQDMAIKAGQFLATWDPHTRPMTTEHAGVKFENMEEGVTVAQTDVDTGLSTLVLVDGKRSSASKLRLPVLKLLDENGVEICIPGTSTPVS  
APFVGAVITVREGQIEKGVDLARIPOASSKTRDTTGLPRVAELFEARVPKADGLABITGTVSFGKETKQKQRLIITDVGVAYEYELISKQQLIHDVQGVNVRGETIVDGAVDPHDL  
RLQGTIEALARYIVQEVQEVYRLQGVKISDKHIEVIRQLRRVNIADAGETGFTTGEQVERGDVMAANEKALEEGKEPARYEMILGITYKASLSTDSFISAASFQETTRVLTEAAIHEKQD  
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## SEQ ID 7923

TTGTGTCATCCGTTATTCCTAAACCTTTTCCGCGCGCAAGCGGATTGACGGCGCGCAGATATGGATGATTTTGAATATCTTTATAAATTTTATATAAATCAATGTTTATTTCTCATT  
GTACAGGATTTGATGTTCTTTTCCCACTATTTTTCGAAACAGCGCTAAAGACAGGCTTTCAGACGGCATAAATCGCCGCCCTACCTGCCCTACCGTGTGCCAACCGGAATCATCCG  
TATTTT

## SEQ ID 7924

LCSSVFLKPPFAKRIDGRQIMILIFINFIINQLFISHCGLYVPPFTTIFANKRRDRLSDGILPPLPCLTLLPNGIIRIF



**SEQ ID 7925**

ATGGATATTTTCCTGTAATCAAGGCCGCTTCTGCGCAGCAGCGTGTC AACGCCAACATCCGGTTCGGCATTTTCATCATTCGCCGCCGACGATACGGGCAAGACCGCATTCGGTCGTGCTTCC  
TAACGATGCAACCGCATCCTCGACAAGGAAAACCAGATACATACCGATATGGCTTTAGCGTTGCCGGCGGTAGTGAAAGACGCGAGTGGCGATATGGGCAGATATGGATACATTTGGATAGGTG  
TTCGGC

**SEQ ID 7926**

MDIFRESRPFCATGCPTPTSGSAFHRRRRYGQDRIGRAFLTHRILDKENQIHTDMALALPAVVKDAVAIWADMDTLDRCSG

**SEQ ID 7927**

ATGCCATAATCGCGCCTGCCTGAAATGCTGTTTTTCTAAAGCATCAGACCTTCACGAAAATGCCGCTCTGAAGAAATATTCAGACGGCATTCCCTCCCTGAGGCCAA

**SEQ ID 7928**

MPKSRLPEMLFFLKHHDLHEKCRLKNISDGIPSLRQ

**SEQ ID 7929**

[illegible]

SEQ ID 7930

[illegible]

SEQ ID 7931

ATGTCAGGTAAAGGAAACCGCTTAAACCGTAATCCGGTTATTGCCTCAGGGAGGGAAATCCGCTCTGAAATATTCTTCAGACGGCATTTTTCGTGAAGGTGTGATGCTTTAGAAAAACAGCAT  
TTCAGGCAGGCGCGAATT

SEQ ID 7932

MSGKPIINRNPVLA SGRECR LKYS SDGIFREGRDALEKTAFOAGAI

SEQ ID 7933

TTCTTTACATTATATTTGCATAGTTTTTATCAAATCATTTGCAAAATAAATGTAAATATCAGATTGATGCGTACCGTTGTTTTTCAGACGGCCTATTATTGAAAATTACTTTTCGGAGTGTGTGA

SEQ ID 7934

SEQ ID 7994  
LFTFICIVFIKSLQINVNIRLMRTVVFRPIIENYPSECV



SEQ ID 7936

SEQ ID 7937

**SEQ ID 7938**

**SEQ ID 7939**

**SEQ ID 7940**

**SEQ ID 7941**

SEQ ID 7942.

SEQ ID 7943

SEQ ID 7944

**SEQ ID 7945**

SEQ ID 7946

SEQ ID 7947

SEQ ID 7947

ATGGCTAAAGTATCTAAACGCTTGAAAGTCTCTGCGCTCTCTGTTGAAGCTAACAACTGTACGCAATCGACGAAGCAATGGCTTGGTTAAAAAAGCTGCTACCGCTAAATTTGACGAAT  
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CGTATCGTGGTCAATTGGGTACCAATCTGGGTCTCGTGGTCTGATGCCAAACCCATAAATAGGTACGGTTACCCCTAATGTGGCCGAACCGGTAAAAAATGCAAAAGCAGGTCAAGTGC

AGTACCGTACCGACAGGCAAGGATTTGTTTCATGCAACGATTGGTCGTCTTCATTCGCTGAAGCTGATTTGAAAGAGAACTTTGATGCGTTGCTGGACGCTATCGTTAAAGCCAAACCTGC  
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**SEQ ID 7948**

MAKVSRLKVLRSVSEANKLYAIDEALIVKKAATKAFDESVDVSNLGVDSRKSQVIRGSVVLFGKGTGKTRVAVFTQGVNAAEAKAGADVGFEDLAARIKAGNLNFDVVIASPDAM  
RIVGQLGTILGPRGLMNPRTGTTVNVAAEAVKNAGQVQYRTDKAGIVHATIGRASFAEDLKENFDALLDAIVKAKPAAKQYLLKVVAVSSMTGLGVVDTSSVNN

**SEQ ID 7949**

ATGGGCAACCTGATAGGCTGGGAAGGAACGGGGCTGGTTGCCGGCAAGCAGTGGATAACCGCAAAAGACGACAAGGTGTCGATGTCGCAATGCCAACGGCGGGATGGGGTAATCGGTT  
TGCACGAGCCTTTTCGCCACGCTGCGTTGACGATACCGGAGCATCCAAATGGCAGGTGCGCGGTGTTCCCGTTGTCGGGCGGACAGGCAAGCTGGCGAAAGGCAGCGCGCGATGGAAAC  
GGGCGATGGACGGCAGGTGAGTGTGTTCCGATATCGGGCGGCAATGGGGGAATTTGCTGAAACAAGGAGCTTCGTAAAGCGGCTATGCAAGTATGCGCGTGATAACTTTGTCGGCAAAA  
GCTATGTCAATGAAAGCAGCGGGCATGAAC

**SEQ ID 7950**

MGNLIQWEGTGLVAGKQWITAKDDKVDVNCANGMGVIGLHEPFSHGALTIPHEPNRCVAVPVVGRGTGKLAKGSRAMETGDRQVRLFPYRAANWGNLLKQSFVKRLCSMRVITLSAK  
AMSKAAGNN

**SEQ ID 7951**

ATGTTTCCTTTGAGTCTGGTTTTCAGACGGCATGAAGTTTCCCGCTCTGTTTTCAACTGTTTTCATTATGCTCAACTTGAGTATAATATGCAAGGTGCTGTAAACAGGTTTTCGAT  
ACCGCAAAACCGACCGCTTCGTTCCGACAAACCGCTTTGGTTTACAATAAAGCCTTTCACCCCGCAGAAAGCCGAGCATGGACGCTACCCCGAAGCCGAGCTCCGCTGCAAGCATC  
GTCGAGCTGGTTCCCGTAT

**SEQ ID 7952**

MFPCSWFSDGMKVCRLPFKFLHYAQLEYNQRLKTLRLYRKTDPLRSDKPLWFTIKFPFPAESRAWTPTPKPKLRCKASSWFPY

**SEQ ID 7953**

ATGCAAAACCGCCGCCCGCTCGTTTCGATTACGATATGCCCTCATCCAAACCGCGACTTCCGCTGCCAAATCCGTCAGGCGTGGGCGAAGGTTGCCGACACGCCGACCAAGAGACGG  
CAGGTCGTCTGAAAGACGAAATCAAGGTCTTCTGCTGAAGCGGAAAAACCGGCTTGGTGGCGCATATTACGTCGATCCGCTGATTCAGGATTTGGCTTTGGAGACGGCGGATGCGTGG  
CGATTTCGTGAAATGGCGCGCTTCGGCGCGGAACACGAAGCGGTACGCTGGTGGCGGGCGTGGCTTCATGGCGCAGAGCGGAAATCCTCTGCCCTGAAAAACCGGTCTGTATG  
CTGATTTGGAGCGGAATGTTCTTTGGATTGGGTTGTTCCCGAAGAACGCTTTTCAGCGTTTTCGACCAACACCCCGACCGCAGCGTGGCGGTGTACGCCAATFCTTCGCGAGCGTGA  
AAGCGCGTCCGACTGGTGGTAACGCTTTCGCTGGCGTTGGAAATCGTGTCTATCTGAAATCCGCGCGGAGAACTGATTTGGGACCCGACCGCCACCTTCGCGACTACATCCCGCG  
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CAAAACAGCGCTGACAGCGGACGCAACGAAATCCTGTTGACAGAAAGCTGGCGGAAGCCGCAAACTGCTTTGACGCGTATGCTCGACTTCGCGCGAGGACTCAAAACGGGGATGTG  
TTCAACGGCATGGGCGCGC

**SEQ ID 7954**

MQTAARRSFYDMLPIQTPTSACQIRQAWAKVADTDPHETAGRLKDEIKVLLKRNVLVHAYTVDFLIQDLALETGGCVGDSLEHARFGAEHAGTLVVAGVRFMGESAKILCPKFTVLM  
PDLEAECSDLQCPPEAFSAFCQDHPDRTVAIVANTSAAVKARADVVVTSVALEIVSVLKSRLGKLIWGPDRHLGDYIRRETGADMLLNQGSICVHNEFKQELAAALAEHPDAVVLVHP  
ESPQSVIALGDDVVGSTSKLLKAAVSRPEKKFIVATDLGLLHEMQKQAPDKFIAAPTAGNNGSCKSCAPCPWMAMNSLGGIKHALTGGRNEILLDRKLGEAAKPLQRLMDFAGLKRGDV  
FNGMGPA

**SEQ ID 7955**

GTGGCAAGAAATATCGGCTATATTAACTGCAAAATTCCTGCAAGCAAGCCAAATCCATCCCCCAGTTGGTCTGCTTTGGGTCAACGTGGTTTGAATATCATGGAATTCGTAAAG  
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AAAAGCCCGCGTTTGCAAAAAGGTAGTTCTAATCTCTGACAAACAGGTAGGTAAATGACCCGTCGCCAGTTGGAAGAAATTTGCTAAACTAAAGACCTGATTTGACTGCTGCTGAC  
TTGGATGCGCTGTTCTGACTATAGCAGGTTCTGCTCGCTCAATGGCTTGGACGTGGAGGCTGTTGTA

**SEQ ID 7956**

VARKIIGYIKLQIPAGKANPSPVPGALQRLNIMEFCKAFNAATQGMESGLPIPVVITAFADKSPFVMKTPPASILLKKAAGLQKSSNPLTNKVGKLTQRAQLEBIKTEPDLTAAD  
LDAAVRTIAGSARSMLDVEGVV

**SEQ ID 7957**

ATGTCGAAAAATGTTATGTTGATCAGGCGTATTCGGGTTTGAAGAATGTCCAACGAATATTGGAAGACGGAATGCCCCGTGAGGAGATGGGAGATTATTTCGCAAAATTCGTGTGC  
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CACTCCCGCTGTTCTGTTTTATTGGAGGAGGGCTAATAGACCCAGCGGATTAGTCAGAGAGAGGCTGAAATTTATTTACAGCAGGTTGACAGCGGCTAGAGAGCCGAAACCAAAA  
GTTGAATTTGAGTCTGCTCAACAGGTTCTGTAAATGAAGACCGTTTCGGGATTTTACCGGGGTGTTGAGGAGGTCAATTATGAACGGAATAGTTACGCGTGTCTGTCAGATATTG  
GTAGAGAAACCCGTTGAGCTGGAGTTTACGCAAGGTGAGAAGATTAAC

**SEQ ID 7958**

MSKMYVQAYSFPEKNVQRILEERLAREMGDYFGQILVPVEKVVDIRNGRTISERKSYPGYVLVEMETDDSWHLVKSTPRVSGFIGGRANRPTISQRBAEILLQVQGTGIEKPKPK  
VEFEVQGVVNEGPFADFNGVVEVNYERNKLRVSVQIFGRETFVLEFSQVEKIN

**SEQ ID 7959**

ATGACAGACATACCGCTGAAAAAAGAATGTTAAAGTGAATCAACTGGTTGTTCAAGATAAAGAACTGCATCTAAATCCGGTAAGGAGGGTTTTTTGTCATATTCTCAAAATCTTGGT  
CCGAATTCAAAAAGGTGTTTGGCCTAAGCGTGAAGATGCCGTGAGATGACTGTATTTGTTATAGTGTTTGTGCTGTGCTTCTATATTATCTATGCGGCAGATACAGCAATTTCTGT  
GTTATTTTTGATGATTGCTGAGAAGGAAGGT

**SEQ ID 7960**

MTEHTPEKKNVKLVQVVDKESASNSGKEGFFAYFNSNSWSEFKKVVWPKREDVMTVVFVAVLSIFTYAADTAISHLFFDVLRLREG

**SEQ ID 7961**

ATGCAACCGATTGCGACGTATTGATTCGGGAAACGGGCTGGCGGCACTGACGCTGCGCTGTGCTGCTGAAATCGCTTCCGCATCGTCATTTTGTGCAAAAACCGGCTGGACGACACCG  
CCAGCGCTCATGCGCAAGGCGGGATTGCGCGCGGTGGTCCGGAGAGGACGACATCGGAAACACGCTGCGCGATCTTTGGAAGCGGGCGCAGGTTTGGCGAGCAAGCGCGCTTCGCAC  
CATCTCTGCGCAGGGCAAAACCGCAATCGAATGGCTGCTGGCGCAGGGCGTGGCGTTCGACCGGAATCATAACGACCTGCACCTGACGCGCGAAGGCGGGCATACCTGCGCGCAATCGCC  
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GCCTGTACCGGACTGCACGGAGCCAAACCGCTCCGCCAGCAACTCCCTGCTCGAATGGCTGTTACCGCCAGGCTTCCGCCCAAGGCATCGCGGACGACAAAGCGTTCCAAATCGAACCAAT  
TCCAAAGGCCGCTGTAAGAGCCCTCCGCCGAAACAGACATCTTTTCAAAGCAGCTCCAAACACATTCAGCGCCCTGCTCTGCAACGTTCAACCAACGCCATCTCGGCATCTCCGCCAA  
CGATACCGACCTGCACCGGCCATCGACCAACTCGCGCTTTGGAAGCAAAACCAAGCCGACCCGACCGCTCGGAATACGAAACCGCAACCTACTCGAATGCGAGCTCCGCCGCTCGCC  
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## SEQ ID 7962

MQTDCVLIAGNGLAALTLALSLPESFRIVILCKNRLLDTASRHAQGGIAAAWSGEDDIGKHVADTLEAGAGLCDEAAVRTILSQKPAIENLLAQGVAFDRNHNHLLHRTREGGHTCRRIA  
HVADYTGEAVMQSLIIQIRRRPNIRVYERQNALDVQTESGAACGLTVLDCRTQETRYIRARHTVLAGGLGQIYAATTTPECTGDAIAMAIRAGCAIENLEFIQFHTGLARPSSENGRTF  
LISEAVRGEGGILTNQSGERFMPHYDRRAELAPRDIVARALAAETAKQTDVSLDISRQPAFVRRHPSIHRHCLSQGLDITRQAIPIVFPVQHYTCGGIQTDPGRTSLPQLYALGET  
ACTGLHGANRLASNLLECIVVTLAAQGLADGQAFQIEPFRPSPESAETDIFSNLQNTFSRVLQTFNQRLHGLILRNDTDLHRAIDQLRLNKNQNAEPHTASEYENRNLLECSLAVA  
QAAYRRRNQNGAHPNSDC

## SEQ ID 7963

TTGAGCTATTTGCCCTCTAAACTTAAGCGATAACAGAAGAAACACGCCGCGACCCACGTAACGCCGCCCTTCGGAATCGCAAGCGCAGACCTTCTTCCATAGCGATAGCGCAATCAGT  
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GGGTATGGCGCCGCCCTCTCTTCTGCTCAATACGTACACTTCTGCTTGAACCTTGGTGTGAGGAGTGATAGTACCCGGTTTGCCCAATACCTGACCGCGTCTACGCTTTCACGTTTGTG  
ACCGCGCAGCAATACGCTACGTTCTGCGCCCGCTGACCTTCTGTCAGAGTTTGGCGAACAATTCACCGCGGTCAGGTGGTTTTCGGGTTCTTTCAGACCGACGATTTCAATCTCG  
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CGTGTGCGTAGTGGCGGGTTTCGGTTTCGTATCTACGTCGAGGTGTTAATGGTAATACCGCGTCTTTTCTTCGGGTGCGTTGCGATTTGGTCGTAAGCTTTTCAGCGCGCCGGA  
TTTTTTAGC

## SEQ ID 7964

LSYWLPLNSLNRNHAHTGTAAPANRKAQTFHSDRRNQFYSNGYVLRHYHFHTTQSNRAGVYSGTEVELGTGVVGEKRGMAAALFFAQYVHFCFELGVRSDSTRFGQYLTAFFVTFPG  
TAQQYAYVVARLTFVQQFAEHPNAGTGGFLGFFQTDNFWLWVNDTSLYTAGDYTAGNGEHVDFRQENFVHGTLSRDAVAVQCSQFEDFPFVSGIAPQGFQCGTLYDRAVVAGEV  
AGQQVADPHFNQFQGLIVDHVAVHEHDDVRAYLTGQDVFAGLRHRAVGRSFTQDCTVHLGAGNHFVNVVGVTRTYVVCVAGPGFVYVGVGNACACFFPGCVVDLVVFSASAE  
FFS

## SEQ ID 7965

ATGGCTAAGGAAAAATTCGAACGTAGCAAAACCGCACGTAAACGTTGGCCACCATCGGTACGTTGACCATGGTAACCAACCCCTGACTGCCGCTTTGACTACTATTTTAGCTAAAAAATTCG  
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## SEQ ID 7966

MAKEKPERSKPHVNWGTIGHVDHKTTLTAALTTILAKKFGGAAYKDIDNAPEEKARGITINTSHVETETETRYAHVDCPGHADYVKNMTGAAQMDGAILVCSAADGPMPTREHIL  
LARQGVFPYIIVPMNKCDMDVDAELLELEMEIRDLSSYDFPGDDCPIVQSGALKALBGDAAYEEKIFELATALDSYIPTPERAVDKPFLPIEDVFSISGRGTVVTVGRVERGI IHVGE  
IRTVGLKETQKTCTGVEHFRKLLDEQAGDNVGVLLRGTKREDVERGQVLAKPGTITPHTKPKAEVYVLSKEEGGRHTPPFANYRPFYFRITDVTGAVTLEKGVEMVMPGENVTITVEL  
IAPLAMEBGLFAIREGGRTVGAGVSSVLA

## SEQ ID 7967

GTGTTTGGGTTTCGATGTCGAAGGAAGGGCTTTTTCGAAAGCCCTCAACCAACTTACGCAACCATAAAACTGAATGCCAATCTCTTAACCATGCTATTCAAATTTATTTGAACGATT  
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## SEQ ID 7968

VFGFRMSKEGLFCKGLNPTYATIKTECQSLNHAQIYLNDPFLTSQF

## SEQ ID 7969

ATGTCGCTTTTATTACCGACGAGTGCATCACTGCGAGGTATGCGAACCCGAATGCCCAATGATGCCATTTCCCAAGGCGAGGAAATTTACGAANTCAACCCCAACCTCTGCACGCACT  
GCGTCGGCACTACGATGAGCGCAGTGCAGCAGGTTTCCCGGTGACTGCATCTGATTGACGAAGAACATCCCGAAACCCATGACGAGTTGATGGCGAAATACGAAAGATATCCCA  
GTTTAA

## SEQ ID 7970

MSLFTIDECINCDVCEPCNDIAISQGEIYEINPLCTQCUGHYDEPQQQVCPVDCILIDEEHPETHDELMAKYEKIIQFK

## SEQ ID 7971

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CGGCGCGGATTA

## SEQ ID 7972

MGFGHFFVNDQAVHRANLLALRLIVVSDALRAEVGVDFVNFIALGNGIIGAFGAYAVDALVGNKKRHFFSFSTKLKPGGRGL

## SEQ ID 7973

TTGGGCGAAACAGCTGAAACCTGTGTTTGGGTTTCGATGTCGAAGGAAGGGCTTTTTTTCGAAAGCCCTCAACCAACTTACGCAACCATAAAAAC

## SEQ ID 7974

LGRKQLKTCVWSDVEGRAFLQRPQPNLRNHN

## SEQ ID 7975

ATGGCATCATTTGGGCACTTCGGGTTTCGATACGTCGCACTGATGACCTGCTCGGTAATAAAAAGCGACATTTCTTTTCTTTTCCACTAAATTTATCAAAACCGGCGGCGCGGATTA  
GCACAAGGTTTTT

## SEQ ID 7976

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## SEQ ID 7977

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CATCACCCGATCGGTTTCAACCTGTTTTCGCTTTTGACGGACCGGGCATCCCGGTTGCAGCACTTATGCCGCTACCGTAAATTCGCTATCGCGGGCAGCCTATTTCGGGCTGCTC  
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## SEQ ID 7978

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KVGAGSHLKAMCINLLKAANRLSAPAAA

## SEQ ID 7979

TTGCCCATCGGCGTGGGCAAAACCGAAGACTTGGGCAGCGACATCGCGCTGGTTCGGACACCGCCGAGCTGACCTACGCTACTTGC AAAATGTGTGGGAACAGTCGGGCAGA

## SEQ ID 7980

LPFGVKTEDLGSIALVSDTAEILTYATLQNVNEQSGR

## SEQ ID 7981

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## SEQ ID 7982

NRFDNHFRVNNIRLQPSGSKPKCAIIRARPVLII

## SEQ ID 7983

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## SEQ ID 7984

LPIPSAIAVSVRAMVFAHLCSCMGRLSGYLAI

## SEQ ID 7985

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## SEQ ID 7986

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## SEQ ID 7987

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## SEQ ID 7988

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## SEQ ID 7989

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## SEQ ID 7990

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## SEQ ID 7991

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AAGTGGCTGAA

## SEQ ID 7992

LSFASADGLRPTDPSVREKLFNWLQDLTGKTVLDLFGGSGALGMEASRNAKRVVIADNNRQTVQTLKNSRELGLGQVQTVCSDLGAYLANLKEKFDVVFLLDPPFAWQSWESLFWLGT  
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## SEQ ID 7993

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## SEQ ID 8007

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TGCTTACGGCATCGAATCCCTTTCT

## SEQ ID 8008

VPSDIGRPAVLQAGRRRISITYSRNLVIFTAAPPDFARHDAGVYDALATEAQTLPSLHWPFGNIRLNKGDTRATIAYGIESLS

## SEQ ID 8009

GTGCGGCGTTCGACATCAACGGTAGGACTTACCGCGTGGAGGCCAACGAAGCAGGAACCGCTGCACGCGGTTGCAACGGCTTCCCGTTTCAACGCGGTGGCGGCAGACGG  
CGACGGTTATCCCAACGATTGGATATTTCTACCGCTTGGACGAGGACGGCGGCTTACCGTTACCTATCGCGCCACCGCGCTCGCGCACACGGTGTTCGACCCGACGCTGCACATTTA  
CTGGCGGCTGGACGCGGGCTGCACGATGCGGTTCTGCATATTTCCGAGGCGGACATATTCGCGCGGATGCCGAAAACTGCCCGCTTTAACGGTTTCAGACGCGCTCGAAGTATTTGAT  
TTCAGCGGCCCAAGCGCGGATGCCCGCTTGCAGCGCTGCCCGCGGAAACGCGCGGTTT

## SEQ ID 8010

VRRSTSTVGLTAWRPTKAGTRCTAVRTGWPLFVSTRWQTADGYPNDLDSYRLDEBGLTVTYRATALGDTVFDPTLHTYRLDAGLHDAVLHTPQGGHI PAAEKL PVLTVSDGLEVFD  
PSRPKPPDAVAALRRETGRF

## SEQ ID 8011

ATGAGCGATACCCCGCTACCCCGATTTCCGCGCTGATCGACGGCGGGCGGTAACCGGCTATGTCTGTCCAACCGCGGTGGTACGTGCGTCTTCGTGCTGGACTTGGCGGGATTGTGC  
AGGAATTTTCCGPTTTGGCAGACGGCGTGCAGCAAAACCCCGTGGTCTGCTTCGACGATGCGGCTTCTTATCGCGACAATCCGTTTACAGATTAAACAAGCAGATAGGGCGCGTGGCGGACG  
CATCCGCGGTGCGCGCTTCGACATCAACGGTAGGACTTACCGCTGGAGGCCAACGAAGCAGGAACCGCTGCACGCGGTTGCAACGGCTTGGCGGCTTCCCGTTTCAACCGGTGGCG  
CGACGCGCGGACGCGTTATCCCAACGATTGGATATTTCTACCGCTTGGACGAGGACGGCGGCTTACCGTTACCTATCGCGCCACCGCGCTCGCGGACACGGTGTTCGACCCGACGCTG  
CACATTTACTGCGGCTGGACGCGGGCTGCACGATGCGGTTCTGCATATTTCCGAGGCGGACATATTCGCGCGATGCCGAAAACTGCCCGCTTTAACGGTTTCAGACGCGCTCGAAG  
TATT

## SEQ ID 8012

MSDTPATRDFGLIDGRAVITGYVLSNRRGTCTVFVLDLGGIVQFVSVLADGVRENPVVSFDAAASYADNPPQINKQIGRVAGRIRGAAPDINGRTYRVEANEGRNALHGGSHGLAVTRFNAVA  
ADGRRLSRQFGLPLGRGRPAYRYSRHRARRHGVPRDAAHLAAGRGPARGCSAYSAGRTYSGRCRKTARLNGFRPRSI

## SEQ ID 8013

TTGTTTATACGGATTGTCGTAGTTACGATGTATCAGATTGTAAGCGGATTGGCGGTTTCCGTATCAATCGCGGCACACATTTTCCGGAACCGGCAAAACCATATCAACGCAATTGGGAAC  
TTTGGAAATCGGGCAACCTCATTTGCGCAAGTTTGACGGCATTTCCCAAGAGCATTTCCGGCTGTATTTGAAGGAGTGGGACGGCGTTTGAACAAGTGGGGTAAAGTTCGAATTTT  
CATTTTAAACAATTTGGTAAAGCAGGATTATCCCGCTGGCGGGATTTTAAAAATAAATACATCTCT

## SEQ ID 8014

LFIRIVRSYDVSDCKRIWPPYQSRHTFCRTAKPYQRNWLLESCKRLKFDGIPKEHFGLYLKECGRRFDNSGVKVRISILKQLVKQDLSRLAGILKNKYIL

## SEQ ID 8015

GTGAACACGCTGCGTCAAAATCGAACAGCATCGAATTTCCCTTATGGTCGCGCTTGATAAAGTTTGTATGAATGCAAAATATGAAGGAAGTTTCTTAACAAAATAGGGAGGGATCATA  
TTATTCGGTACACAAATACTCAACCGGTGTGAGATTGGCAATAAAGTCTTAAATACAGGATAATAGCCCGTGAGAAATTTGATGGGATAAACAATACGATCATTTTATTTTGAAGA  
CAAA

## SEQ ID 8016

VKHAASKSNSIELSLMVALDKVLMNAKYEGSFPNKLGRDHI IAVHKYSTGVPRGNKVLKIRI IAREKFDGKHYDHFILKDK

## SEQ ID 8017

ATGCCCTTTCTTAGGACGCAATATATAAGGTTTATACCGTCTGTGCCCTAATGCGCAATCAGCGACATTTGTGCCAATTAATCCGAAAGAAAGTTAAGCCTGATGGCATTTGTATACAGG  
ATACCTTTCTGATGTTATGATGTGCTTGATGTAGTGAATTTAGCCATTACGTAAGTTTAAACGGCATTTCCCAAGAGCATTTGGGGCTATATTTAAAGAAATGCCAATGGCATTGTAA  
AAA

## SEQ ID 8018

MPFLDAIKYVTVVVVNAQSATLLPIIRKKVKPDGIVYTDTRSYDVLVSEFSLRKFNGIPKEHLGLYLKCKQWHLK

## SEQ ID 8019

ATCGTTGGTATTTCGCGTTACCTCTTCCAATGAAGTAATGCCCTGCATAATTTTCAAAAATACCGGCCCGCGGCAAAATCCACCATAACCTCCTTATAGGCAACGTCGCAAAATACCCACTTCC  
GTACCGTTGTTTCAATACACGCTGCATTTCTTCCGTGATGGGCATAACCTCATACACGCCCGCACCGCCCTTATAACCTTGCCCGCGGCAACGTCGCAACCGACGCGCGGTAAGTT  
TCCAATCTTTGCAAGATCTCATCGGTGAACCGACTTCCCTTCAAGCAGAGGACAGCGGGCGTTCCACTTCTGTTGACGCTGCAACACAGCTGCGTAAAGAGCGCTGCGGCATAAT  
CAGGCTGACCGAATGGCAATTAATAACGCGCGACACCCATATTCAGCATACCGGACACGCTGCGCGGCGCATTTCTGCTGTCAGTGTGGAACACCATATGCCCTGTTTGTCCGCG  
TAACTCGCAATATCGCGAGTTTCCAAATCAGAACTCTACCGACCATATGATGTGCTCGGCTCTGAGCAGGAAAGACTTCAAGCAGCGGCAAAAGTCAGACCTGCTTATCATTTGACGT  
CGGACCGGTACAGCACCATTCCGTAAGGACGCTGAATCGCTTCCAACAACAATTTTCTGGAACGCTCAAAACCGAGCTGCTGATGTTCAAGACGCGGCATCGGAATTCAAAATC  
CGCATCACGACCTTTTCCGCAACAGCGTCGCAATGTGCTGACACGAAATCGACAGGCTTGCAGCGCTTTTGAAGAGTCAGCTGCATCCACCGCTTCCGCTGCGGTATCCGTTTTCGGAA  
TGTCCAAACGCGACATTACCTTAATCCGGAAGCAAGCTGCCCTTACCGCAATGGCGGCTGAACCACTCGCGAGCTGCCGTCACACGGAACCGGATACGCGCATTTGTGTGTA  
AACTCGAAATGGATGTCGATGCCCGCTACGCAAGCATCCGACAAAGTTTATGATAAACTCGGAACAGGCGGCTCTTCTGCTCTCTGTTGTCATATACAGGGTGTGGCTTTCC  
TCTTCTCTTGTCCCTCCCAAGCTCCTGAAGCAGCATGTGCAACGCAACCCCAATCGAGCAAAACCGGCACTGGTATCTCGACAATGACCACTCAACCGCAATCCCTGCGG  
CAGAAACGGTTTCTGAATTTGCGGCATCTGGTGGATCGGAAACCGCAAAATACTTTGTGCGCCGACGGAACCGGACACAGTGGAACTCCACCATCTGCTCTCCGTCACAC  
CCCCATCAGCACCTGTGGCGCGGATAATGACGCAATCAAGAAATCGAATACTGAACACCTCGCAATCAATGCCGCAAGCGACTTGGGCGAAATGACACCGCTGTAACACGACATCGG  
AACACTTCTTACCGCGCTCGACTCATTTGTAGTAATGCTCGCCCGCTCAACAGTAACCACTGCTTTTGAACAGAAATCTCAGCAAACTACGCTCAT

## SEQ ID 8020

IVGICRYLFQ\*SNALHNQNTGPAQIHHTLLIGNVQNTHTFRTVVHNHTLHFFADGHNLIHARTPLITLPPATVATDGAVKPPIFCILIGETDFLQSRGRRAHFLFAARTQPA\*KTLRHN  
QADRTGNIKRRDTHIQTRQRRRRIIRVQCGKHNPCLRLNRNIGSFQITNLTDHNDVRLVQERLQSSGKSQTLIIIDVNLIDARQVNLGRVPRNCNIRLNIQITQIERHRLTRTR  
RTGYQHHPVTRVNRQQQFFLERLKTELVDVQRRGIGIONPHDLFAKQRQCADTEIDRLAALLKQLHPTVLRYPFGNVQTRHYLNPGLPPYRNGRLNLHAEIPVHTETDTRIVFV  
KLENDVGCPTAQIRQSFMDKPRNRAVFLVVDIQGVAFLPLPLKLLQRCRTRTHPIEQTRQLVLDNDQLNRNPGRNGFNLRLHGRIGNRKYPVAPENRHTVELHLLLRQH  
PHQHPVARIMTQIKNRIEHPNRQCRKRLGRNDTV\*KQHRQHFLRLRLIVVMLGPLSNHNLVNLQNPQQTAYH

## SEQ ID 8021

TTGGCACATCATCGGAAACTTCCCTTACACGCAATTTGGACGAAATCTGCGAAATATGAGGAGCATACGACATATCGTTTACGATTACTTTATCCGTCAAAACAGTCCGCATTTGGAAATG  
TA

## SEQ ID 8022

LAHRENFLYTHLDRICKIMEAYDISFTTTPSKQSAFGNV

**SEQ ID 8023**

GTGATTGTTCGTTTATTCCTGCGAAAGATACCGAATAAATACCATAAGGCGGGTTATTTGGCTGTTTGGCTTTGGGCGCGCTCGGTTTCTTCTCTATCTTCTTCATCTACAATCAATACG  
CACTCATCTCTGCTTATATCTTAATCGGCATCGCTTGGGCGGGCATTTATCACTTATCCGCTGACGATTGTGGCCAAACGCTTTGTGCGGGCAACACATGGATACCTTATTTGGGCGCTGTTTAA  
CGGCTCTGTCTGTATGCGCGCAATCGTCGCTTCGCTGTTGAGTTTCGTGCTTTTCCCGATGCTGGGCGGCCATCAGGCAACCAATGTTCTTGTTGTCAGGCGCAGTCTTCTGCTGCGGAGCC  
TTCTCAGTCTGTCTGATTAAAGAGATCCACGCGGGGTT

**SEQ ID 8024**

SEQ ID 8024  
VICSFILAKVPNKYHKAGYPGCLALGALGFFSIFFIYNQYALILSYILIGIANAGIITYPLTIVANALSGKEMDTYLGIFNGSVCMQIVASLLSFVLFPMLGGHQATMFLVAGAVILLGA  
PVSCLIKEIHGGV

**SEQ ID.8025**

SEQ ID no. 8025

TTGGCAGCATGTTAATCAAAACACGGCAGCCTGTTATTTTTCATGGCGAAATAGTGTTTGGCACATCATCGGGAACCTTCCTTTACACGCATTTGGACGAAATCTGCGAAATATATGGAGGC  
ATACGACATATCGTTTACGATTACTTATCCGTCAAAACAGTCCGCATTTTGAAATGTATGACGGCGAAGCAGGGGGCGGTGAAGTGTATTCCGTPAAAGCGACAGCGGGCCGAGTGGCCGC  
CGGCAAGCCGCCGTATTTCGGGCTTTGAAGCGCAACGGCAAGGTTTGTACGGTTACTGTCTGGCACTCGAACCGCATTTATTTATTCCTATCTCCCGGACGGGTGAACCCCGCGACGAT  
TGTTTATACGGATGTTCTGTAGTTACGATGTACAGATTGTAAGCGGATTTGGCGGTTTCGCTATTCGCGCGCACACCATTTTGGCAACATGTCACCAAGCAATTTGGAAGT  
TTTATGATTCGGGATTAATCGTATTTCGCGAAGTTTGACGGCATTTCCCAAGAGCATTTTCGGGCTGTATT

**SEQ ID 8026**

LAAVNONTAACYFLWFRNSVWHIIIGKTSPTIIRWTKSAKLWRHTTYRLRLLIRQNSPHLEMYDGEAGAGESYFRKGRRGRSAAGKAAVFGLLKRNKGKVCVTVVGHNSNRYFLIATYPRTGETRQH  
C1YGLFVVTWYQIVSGFGRPRINRGTHFAERQNHINAIGNFWNRANVICASILATAPKKSISCCI

SEQ ID 8027

SEQ ID 8027

TTGCGGTGCAGGCGGTTTCGATTGTGTTCTTTCCAGCCGCATTCTTTTCCGGGCAGACTTTTCCACGCCCCGGCGTTTGGTAGTTTGTATGCCAGTACCGGCCAATGGCAGTTTCGGSCAT  
TCTTTCGCGAAGCGGGCGGTTCCAAAGTGGCGTAGTTGCAGTCGGGATAGGTGCTGCAACTGTAAACAGTTTCCGCTAGCGGGATTTCGCTCGACGAGTTTGCCTTTTTCGATTTCGGGC  
ATTGGACGCCGATATCTTTGGGTTTTCACAGGCTCGACGTGTTTGCAFTTGGGGTAGTTGGCGCAACCGATGAATTTACTGCCGGTGGCGGTATTGTTGACACAGCCGTCGCCGCCA  
TTTGGGCAATTTCGACACGTCGAGTTTCGACCTTCGCGTTCCGCTTTTGGCGATGCGTTTCGGCAGCTTCTTCGGCGGTTTCGTTGACGTTTCGGGTGTAACATGCACCTCGGGATAACGGCA  
CACGCAACGAACCGGCCAATTTTCGCGAATTGATTTCGAGTTTGTGTTCCGCGCATTTTCGGCAGGTTTCGTCGAAGTTTCCTGATGTAAGAAATTTGGCGCGTTTCGATGCCCTCTTTTCTT  
CCACTTGTGTTGATGCAACGGTTTCCAGAAATTTGTCATCAAGGGAATTCAGCGCGATTTCGCGTCGCGCAATTCGTCGAAGCTGGCTTCCTGAGTTTGGCGGTGAAGTGGTAATCGACGATTG  
GGCGAAGTTTTCGGTCAGGAATTTTATTCAGCATGTCGCTGTGTGCGTGGGCATGAAGCGTTTTCGCTCAAGGTTAACGTATTCGCGCTCTTTCGAGCGTAGAAATTAATGCTGGCGTAGGTC  
GAGGGGCGGCCGATGCCGTATTCCTCAGGGCTTTAAACAGTGTGCTTGTGTTAGCGGGCGGGGGGTGGTGAAGTGTGTTTCGCGGTAGAGTTTTCGACACGGCAATTTGTCGCCCT  
CGCTCAFTTCGGGCAAGTTTTCGCTGCTTCGCTCTCTTCATCGTCGCTGCTTCTTCGTAAACGCTGAGGAAGCTTCGCAAGTTTTCGACTTTCGCGGTACCTCGGAACAGGCTTTGCTG  
GACGGTAATATCGACGCTGGTTTCGTCGAATTTGGCGGGCGCTCATCTGACAGGCAACGCTGACCTGCAATTTGTAAGAGTTTTCGATAGAGTTTCGACTGCGACACGAGGCTTTGACGCTT  
TCGGGCGTCCGCTACACGGAAAGTCGGGCGGATCGCTTCATGGGCTTTCGGCGATTGGTTTGTATTGTTTTCGCGGCACTCGGCAGATATCTTTCGCCGATTTCGTTTCAC  
TGTAAATGGCGGATTCGGG

SEQ ID 8028

SEQ ID 8028  
LRCRRFDLFFPAAFFLRADFFHAPAFGSDGQYRPMVAVRFAFFNGNRVPSGVVAVGIGAAATVKQPAVAGFALDEVAFFALRALDAGIFGFFQRLDVFAPFGVVGATDEFTAGAAVVFHQPSAA  
PGAFATVPEPDLFGFRFGDAPGSGFFGGPVDVAGVTALGITGTRNETAHPAELDLQPVFAAPRAGFVKFLRSEFGAFDALFFPHLFDERFPEFVHEGHPAAFAVGDVFKLVFEFGGEVVIDVL  
GEVFGQEFIDDVACVGGHEAFLKLGKNVFAVFERRRNAGVGRGAADAVFFEGFNGQCGFVARRRGGEVILFAVEFVDQRFVFAHFPGQFFAVFALFTVAAPFVNAEEACEGLHLSGYSKEHFA  
DNTDGTGGLVEFGGRHLFGNGTLPENHLIEFLVCTOEGFDAGRAVHGSRADRFMGFLGVGFGFVLFGGTRQIFADDFVFNVMADFG

SEQ ID 8029

SEQ ID 8029  
TTGGACGGGGATTTCGACGATTAAAGAGGTTTTTTCGCCATTTCGCTCTCTGGATGGTGGTTTTCAGCGCGGTGTTTCAGACGGCATCGGGCGGGCGGGCGCGGTC

SEQ ID 8030

LDGDSTIKRFFAICRSLDGGFDAGVSDGIGRAGAV

SEQ ID 8031

SEQ ID 8031  
ATGTCGGAATATACGCCCTCAAACAGCAAAACAAGGTTTGCCCGCGCCGGCAAAAAGCAGCATTTGGATGTTGAGCTTCGGCTATCTCGGCGTTCAGACGGCCTTTACCGTGCAAAGCTCGC  
AGATGAGCCGCATTTTTCAAACGCTAGGCGCCAGACCCGCACAATTGCGGCTGGTTTTTCATCTCGCCGCGCTGGCGGGGATGCTGGTTCAGCCGATAGTGGCTACTACTCAGACCGCACT  
TGGAAGCCCGCGCTTGGGCGGCCGCCCTGCCGTATCTGCTTTACGGCAGCG

SEQ ID 8032

SEQ ID 8032  
MSSEYTPOTAKOGLPAPAKSTIWMLSFGYLGVOQTAFTLQSSQMSRIPQTLGADPHNLGWFFILPPLAGMLVQPIVATTQTALGSRWAAAAACRICFTAR

SEQ ID 8033

SEQ ID 8033

ATGATAGGGGATCGCCGCGCGGCAACCACTTTCCGGATTTTCCAAAGCAAACTACTTTTCAAATCAAAAAAAGGATTTACTTTATGTGCGGAATATACGCCCTCAAAACAGCAAAACAAGGTTTG  
CCCGCGCGCGCAAAAGACAGCAATTTGGATGTTGAGCTTCGGCTATCTCGCGGTTACAGCGGCCCTTACCTCGCAAAGCTCGCAGATGAGCCGCATTTTTCAAACGCTAGGCCGAGACCCG  
ACCATTTGGCGGTGGTTTTTCATCTCCGCGCGCTGGCGGGGATGCTGGTTACAGCCGATAGTGCTACTACTACAGACCGCACTTGAAGCGCGCGCTTGGGGCGCGCGCGCTGCCGTATCTG  
CTTACCGGCACGCTGATTGTCGGTCACTGTCATGATTTTGATGCCGAATCTGGGACAGCTTCGGTTTCGGCTATGCGTTCGCTGGCGGCTTGTGCTTCGGCGCGCTGATGATTGCGCTGTTTG  
ACGTGTCGTGCAATATGGCGATGACGCCGTTTAAATGATGATGGTCGGCGATATGGTCAACGAGGAGCAGAAAAAGCTACGGCTACCGGGATTCAAAGTTTCTTAGCGAATACGGACGCGGTTTG  
GGCAGCGATTCTGCCGTTTGTGTTTCGGCTATATCGGTTTGGCGGATACGCTGCCGAGAAAGGCGCTGTGCGCAACCAACCGTGCTGAGCACTCTATGTGGGTGCGGCGTTACTGATTATTACC  
AGTGCGTTTCACAATCTCCAAGTCAAGAATACGACCCCGGAAACCTACGCCCGTTACCAACGGCATGCGGCTGACCGCGAATCAGGAAAAAGCCAACTGGTTTCGAATCTTAAAAAACCGCGC  
CTAAAGTGTGTTTGGACGGTTACTCCGGTACAGTTTTCCTGCTGGTTTCGCCCTCCGGTATATGTGACTTACTCGGCAGGCGCGATTGACAGAAAACGCTCGCACACTACCGATGCGTCTTC  
CTAGGCGCATCAGGAGGCGGGCAACCGGTACGCGCTTTTGGCGCGCGTG

SEQ ID 8034

[illegible]

SEQ ID 8035

SEQ ID 80355  
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GCAAACTGTCGATGCGATTGTTGCGCGCTGCGCAAGAAGCGCGAAACATCTACTCTCGCAACCGACCCGGACAGGGAAGCGGAAGCGATTCTTGGCATCTTTTGGAAATCCTCAAATCCAA  
ACCATGCTGAAAAACATCAAGCCGACGCGCTGTTCCACGAGATTACCAAAAACGCGGTGCTCGATGCCCTGCGCCATCTCTGCGGAAATGCAATGGATTGTCGATGCGCAACAA  
GCCCGCGCGCTTTGGCATATCTGTCGGTTTCAACCTCTCGCGCTTGCTGTGGAAAAAATCCGACGCGGTTTGAAGCGCGGGCCGTGTGCAAAAGTCCCGCCCTCGGGCTGATTTGCGAGC  
GCGAAAAACGAATTCGCGCGCTTTGAAGCGCAGGAATATTTGGACGGTGCATCTCGACGCCATAAAGGCGCGCAGCAAGTTCACCGCCAAAACCTCGCCCAATCAACAGCGCGCAACTCGAACA  
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ACATCCACCATCGACGAGATTCGCGCTGCGGTAACTGGGCTTACCAACCGCGCCACCATGCGTACCGCCACGACGCTTTACGAAGGTATAGACGCTAGGGCAGGCGCCATCGGTCTGATT  
CTTATATCGCTACGACGACGCGTGAATTTGGCTGACGAAGCGTTAAACCGAAATCCGCCATTACATTTGAAACAAAATCGGCAAGAAATATCTCGCGAGTGGCGCCAAACAATACAAAACCAA

ATCCAAAAACGCCAAGAAGCCCATGAAGCGATCCGCCGACTTCCGTGTACCGCAGCCCGAAGCGTCAAACCTTCCTGAGTGCAGACCACTTCAAACCTCTATCAAATGATTGGCAG  
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GCCGCGCTACACGAAGCCACACTGGTTAAAGCCCTCGAAGAAATACGGCATCGGCCGCCCTCGACCTACGCCAGCATTTTCTACGCTCAAAGACCGCGAATACGTTACCTTTGACCAA  
AAACGCTTCATGCCACCGACACAGCGGACATCGTCAATAAATTCCTGACCGAACACTTCGCCCAATACGTCGATTACCACTTCACCGCCAAATCGAAGACCGACTTGACGAAATCGCCG  
ACCGCAAAACGCCGCTGGATTCCCGTGTGACCAAAATTCGGAACCGCTTCATCAAAACAGTGGGAAGAAAGAGGGCATCGAACCGCCAAATTCCTACTACGAGAACTTGACGAAACCTG  
CCGAAATTCGCGCGAACAACATGCAAAATCAAGTTCGCGAAATGGGCGCTTTCGTGCGGTGTCGGGTATCCCGAGTGCAGTTACACCCGCAACGTCAACGAAACCGCCGAAGAGCT  
GCCGAACGCATGCCAAAGCGGAAGCCGAACAGGTGCAACTCGACGGTCCGGAATGCCCAATCGCGCGGACGGCTGCTGACAAATACAGCCGACCGCGAGTAAATTCATCGGTTCGCG  
CCAATACCCCAATGCAAAACAGTGCAGCGCTTGGAAGAAACCAAGATACCGCGCTCAATGCCGCAATGCAAAAAAGGCAACCTTCGTCGAGCGCAAAATCCCGCTACGCGAACTGTT  
TTACAGTTGCAGCACTATCCGACTGCAACTACGCCACTTGAACCCGCGCTTGCAGGAAGTCCCGAATGCCATTGGCGGTACTGGCCATCAAACCTACCAACCGCCGGCGCTG  
GAAAAAGTCTCGCCGCAAAAGAAATCGCGTGGAAAGAACAAATCGAACCGCTGCACCGCAAGAG

## SEQ ID 8036

LGSDFEILASYGHVDRDLVFKSGAVDPDNGFAMKYQLISRNKXHDVAIVAAKEANIYLATDPDREGEAISWHLEILKSKRGLKNIKPQRVVPHETKNVLDVAHPREIEMDLVDAQQ  
ARRALDYLGVFNLSPLMLKIRRLSAGRVQSPALRLICERENETRAFBAQBYWTVHLDHSHKRSKPTAKLAQYNGAKLEQFDLPNEAAQADVLKLEBGRVAVTAIEKKKRSRNPAPPT  
TSTWQDQAVRLKGTPTDRMTAQQLYEGIDVGGQAIGLITYMTDSVNLADALTEIRHYIENKIGEYLPAAQYKTKSKNAQBAHEAIRTPSYVYTPESKPFSLADQFKLYQMIWQ  
RTVACQMTPAKFDQTVDTITVGKGVFRVTGQVQVTFAGPLSVYEESDDSEDSKLLPEMSEGDPLVDKLYGQHFPTPPRYNEATLVKALEYIGIRPSTYASIISTLKDREYVTLBQ  
KRFMTDTGDIWNKFLTEHFAQYVDYHFTAKLEDQLDEIADGKRRWIPVMDKFWKFFIKQVBEKGIERAKFTTQELDETCPKCGEHLQIKFPGKMRFPVACAGYPECSTYTRNVNTEAEEA  
AERIAKAEABQVELDGRBCKPCGGRLVYKISRTGSKFIGCANYPKCKHVEPLEKPKDITGVQCPQCKGNLVERKSKYKGLFYSCSTYPCNYATNPNFVAEECPNCHWFLAIKTKRRGV  
EKVCPQKBCGWBKEIPEPAPQE

## SEQ ID 8037

ATGACCGAAGTCATCGCTACCTCATCGAATTTCCAAGATTTCGATACCTGCCGCCGCCGCGAAGACTTGGGTATGCTGCTTGAAGAAGCGGGTTTCGATACGATGGAATCGGCAACA  
CCCTGATGATGATGAAGATTATGCTCAACAGCTCCGAATTTTCGCCGGAACCGCGCGGACGCGGCATTCGCGGTGTACAGCAAGAAGAAACCGCAACCTGCCGAGGAAGTATGGG  
GCTGATGACGATATCTGATTGAAGAAAAAGCCGTCAGCTGCGAACAGCGGGAATCATCATCCGCGCTCATGACATCCCGCGGACGAAATTACCGTAGATACCGCAAGTGTCTGACC  
CTGCTGCTTTTATGGCAACAAGAGCGAGCTGCCCGTATTTGTCGCGGACGAGCTGATGAGCGCGCTTTTACTCGACAAACACCCACGATGAAC

## SEQ ID 8038

MTEVIAYLIEHFQDFDTCPPPEDLGMILLEAGFTMEIGNTLMMHEVLNLSSEFSAPAGSALRVYSKEETDNLQEVNGLMQYLIIEKAVSCBQRIIILHALMHPGDEITVDTAKVLIT  
LLLWANKSELFLVVGDELSALLLDNKPIMN

## SEQ ID 8039

ATGAACCGGGTCGAAACCCATTTTATCCAGTATGCCGCCGACGGCTGTGCCGCTGCCGCCCTTCAGACGCAATTTTGGCGGAGCGCGGGCGGTATGCCGCTCGAACCGCGCGCGG  
CCCGTGTCCGGCGTATCCTTATTTATAGAATA

## SEQ ID 8040

MNRVETHFIQYAADGCAACRPPRRHFCGRRRGVCRNLNGAAARVGRILYRI

## SEQ ID 8041

ATGCAACCGCTCAAACCTCGCCAACAGGAATCGAACCTGTATTTTACCGTTAGAGGCAATAGCTTCTATCCGTTGAACATATGGCGAGCCGAA

## SEQ ID 8042

MTFVKPRQESNLYFTLRRHTFPLNYGEPK

## SEQ ID 8043

ATGAAGATACACACTGCAAAATTAAGAAAGAAAGTACAGAAAGAACCGCTCCGTTCTTTGTACCGGAAGTTACCGCCCGTCTGCCGCCGATATTTGGGTATCCATCCCGATTCCGGCG  
CACTGTTTTCACGTAAATCCGACAGGTTTACCAACCATCGCTTTGGCTTGGCTGCGGATGAGGTTTTCGAGGGCCCGCGCGGCGCGGCGCAAGCTGTTTCGCGGACGCGCGTAAAGGCA  
ACGCGGTTCGCGCGCGCGGAGAAAAGCGGTTGCTTCGCAATTCGGAAGCAACGGCGCGGCTATACCGTTGCCGCGACGATGCGGAGCTTGAACGTTGCTCCCTGCGCTCAAAAAG  
AAAAATCATGCGCGGAGTATTTGTTATCGCATAGCCCGGACGCGCGCAAGTCCGACGCGCGGCGGTTTATCCCGTTCGCGCATCAACCGTTCCAAGGAATTTGAGAGCGCTCGGAAC  
ACATTAACGCGCATTTGGAACCTTTTGAATCAGGCAAAACGCGCTTTCGCAAAATACACAGGAATCGACCGCAACCTTCCCGCGCTTCTTGAAGGAATCGGAATTTGACACTTAACCTCGG  
CACACCGTCCCGGACGTAATAATCCTCGCGGATTTGGTGTGAAT

## SEQ ID 8044

MKITHCKLKKEVQKEPLRSFVPEVTARSAADILGIHPDSAAFYRKIRITVTNHLALAADEVFEGPAGPGASCFGGRKGRRGGAAGKAVVFGIPKRNGRAYTVAADDAEPETLLPAVKK  
KIMPDGIVYADSPGRSKSDAGGFTRCRINRSKEFADRRNHINGIGNFWNAKRALAKYNGIDRKPFPPLKECEFRINFGTFSRQLKILADWGI

## SEQ ID 8045

TTGTTTACCGAATCGAAGAAATATGTCCTCAACAATACGCTATTCTATGCTGCGCGTACGAAAGTTGTGCCGCCGAGAAAACCATCATTAAGATAATTTCCCTTTCTTTCTCCCG  
GCGCGAAATCGGCTCTTTGGGCTTGAACGCGACGCGCAAGTCCACCGTCTGCGGATTTATGGCGGGCTGGATAAGAAATTTGAGGGCGAAGCCGTCGCGATGGCGCGCATCAAAATCGG  
CTATCTGCGCAAGAGCCGAGCTTGATCCGGAATAAACCGTGCAGGAGGAAGTGAAGAGCGGTTTGGCGAAGTGGCTGCCGACAGAAACGTTTGAAGAAGTGTATGCCGAGTACGCC  
AATCCCGATCGGATTTTGACGCGCTGCGGGAAGAACAAGGCCCTTGAAGCGATTATCGCGCGGTTTCGTCACCTGCGCGCGGTGCGGAACCAAGTGAAGATCGCTGCCGACGCGC  
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CTCGACCGCGGACAGCGCATTCGTTGAAGGCAATTAATCTGCTTGGCTGGAGCAGAAAGAAACGCTTGGAAAACGAGGCGAAATCGAAGCCGCGCGGTGAAGCGATGAAGCAGG  
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TATCCCTGTTTCCGAGCGTTTGGGTAAAGAGTATGATTTGTAATTTGTAATTTTCAAAATCGTTCGCGGATAAAGTGTGATGACGTTTGAAGTCCGCGCGGCGCGGATTTGTC  
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AAAGCGCGAAGGTTTGAACAGCAAAACCGGTTCGACAACTTCCGAAGGTGCGGATTTTGGCGCGTTTGAAGAAATGAGCAACTACGAAATACCAAAACGCAACGAAACTCAGGAAATCTT  
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GATCTCGACGTTGAACCTTGCAGCGGTGGAAGAGCGCATTTGTTGAATTTGCCGCGCGGTGATGTTGATTTTCGACGACCGCTGTTTCGACCGCATAGCCACGCATATCTTGGCGT  
GTGAAGGCGATCCAAATGGGTGTTCTTCGACGCAACTATCAAGAAATACGAAGCGCAAGAAACCGGCACTCGGCAAGAGGCGCGAAGCAACCGCATCAATACAAACCGGTAAAC  
GGT

## SEQ ID 8046

LFDRIEKTHSQYVYSMLRVSKVVPQKTIKDISLSFFPAKIGLLGLNGTGKSTVLRIMAGVDKEFEGEAVPMHGIRKIGYLPQEPEDPEKTVREEVESGLGEVAAQKRLEEVYAEYA  
NPDAFDALAEQGRLEAIAGSSSTGGAGHELEIAADALRLPDWDAKIGNLSGEGKRRVALKLLLSKPLDMLLLDEPTNHLDAESVEWLBQFLVRFPGTVVAVTHDRYFLDNAEWMLE  
LDRGHGIPWKNYSWLEBQEKRELEAKSEARVANKQLELWVRNKAQRQAKPKARLARFEMSNIYEQKRNTEQEIFPVAERLNEVIEFVNVSKSPGDKVLIDGLSPKVPAGATV  
GIIGPNAGKSTLFKMIAGKEQPDSEVKIGQTVKMSLIDQSRGLQNDKTVFDNLAEGRDILQVQFEIPARQYLGRFNFKGSQSKLARQLSGGERGLHLAKTLGGGNVLLLDSEFN  
DLDEVTLRALEDALLEFAGSVMI SHDRWFLDRIATHILACBGDSKWFVFDGNYQYEADKKRRLKGBGAKPKRIKYPVTR

**SEQ ID 8047**

ATGGATTTTTATGACAGGAGCAACGTTTCGCGTGGCTGCAATTGGCGTTTACGCCCTATATCGCGCGGAAAGTTTCTCGTCTGATGCGCAGTTTCGGCAGCGCGCAAAATGCCTTGT  
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GCGGGACGATGCGCGCTGATGCTGCTTCAGGATGAAGATTTCCTCCGAAATGCTGACGACAGGGGCTGACGCGCGCGCGCGTTTGTGTTTTGCGCGGCAACGTGCGGCTGCTGCACAGCGCT  
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AGGGCTGATTGTACGCGAGTTCCCCATCGGCACGCGCGGTATGCGCGGCAACTTTCGCGCGCGCAACCGCGCTGATTGCCGCGTGTGCGCAGGTTACCGCTGGTGGTTCGAGGCGCGCTTGGAA  
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SEQ ID 8048

MDPMTEDERFAWLQLAFTPYIGAESFILLMRSPGSAQNALSAPAEQVAPVNRHKHALPAWRNAEKRAIARQAAEALEWRDGCRIMLLQDEDFPEELTQGLTAPPVFLFRGNVRLHKP  
SAATVGSRHATPQAMRIAKDFGRALGGKGIPITVSCMASGIDTAAHQGALEAGGTVAVWGTDIDRIYPANKNLAYETAEKGLIVSEPTIGTRPYAGNPPRRNRLIALAQSQVTLVVEALE  
SGSLITAGLAAMGREVMAVPGSIDNPHSKGCHKLIKDGAKLTECLDDILNECPGLLQNTGASSYSINKDTPDTGRRAVQTAYAPPPAAKMPSEGAAGGTAVGGILDKMGFDPVHPDVLG  
QLAMPAADIYAALLEKLDGSAVAMPGRYQRIIT

**SEQ ID 8049**

TTGGCTGATTTTAAACCTGACTTTGGCTGGCTGTGTAAACGGCCGCTGTGTTTTTGGCTTTCGGCTTCGGCAGCGGGCTGGTTCCGTTTGGCCGGGCACATTCGGCACTTTGGCGGCAC  
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CAGCGACCACGGTGGGATTGTTTGGGACGAGATTGTCGCCATGCTGTTTGTGCTGGCGTTTGTGCCGTTACAGGTGGACGTGGTGGCTGGCGGCATTGTGTTCTGTCCGCTCTGTTTGAATGCC  
CTCAAACCGCCCGCTGGTTGGTTTGACAAGAATCTGCACGGCGGTTTGGGCATTATGGCGGCAGATATGGCGGCTGCGGTGATGACCTTGATTGTCTTGAGGATTGCAATGCTGTTT

**SEQ ID 8050**

LADFKPDFAWLLKRPCLFLAFGFGSGNVFPFAGTGTGTLAALPLAFVLLILGIDGILLAFVCIVLPMGIRICACAERETGVSDEGGIVWDEIVANLVLVAFVPPFWNTWLLAFLVLERLFDA  
LKPPPVGVFDKNLHGGLGIMADMAAAVHTLVLRIAMLF

**SEQ ID 8051**

ATGCGTAGCAGCGATATTTTAATTGTAGACGACGAAGTCGGCATCCGCGACCTGCTGTGCGAAATCCTGCAGGACGAAGGCTATTTCGGTCGCGTTGGCGGAAAAATGCCGAAGAGCGCGCA  
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CGGCGGAGCGCGGCTTTCGGCTGTTTGAACCGCTGGCGCGCTAATTTCCATAAAAAACCGTAGCCGCTGGGTGAGTCCGCGCAAGGGTCGAATATCTGATCGATATCGCGATGGAACCTGTTCAGAA  
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**SEQ ID 8052**

MRSSDILIVDDEVGRDILLSEILQDEGYSVALAENAEARKLRHQARPAMVLLDIWMPDCDGITLLKEWAKNQNLMPVVVMSGHASIDTAVEATKIGAIIDFLEKPIISLOKLLSAVENALK  
HGAQIETGPVFDKLGNSAAIQEMNREVEAAAKRTSPVFLTGAGSPFETVARYFHKNGTPVWSPARVEYLLDHPMELLQKABGGVLYVGDDIAQYSRNIQTGITTFIIGAERCRRVVIASC  
SYAAGSDGISCEEKLAGLFSVSVRIPPLSMQHEDIPFLIQIACINVAESQKITPTAFSDDALAVLSRYDNPNGNFQOLQNVVTLLEADQOEIGIGAASSALGRGVPADGTGHMACGDF  
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SEQ ID 8053

TTGCAAAACAGGTACGGATAAGGATGTCGTATTGGCGCATAGGCGACGATGCGCGGATGTGTCCGCCCGCGCAAGGCTTCGATTGTGTGTTTCAGTCCGGATATGCTTTTGAAGGACAGGCAATT  
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GCGCAATTTCGCGAAGGGTAGGCGCTTTCGCCGCTGATGCGCGGTTTGGCGGCGCATATTTGGGTGTGCGGGCGTGTGCGTATGGCGCGCGCGCTTTGAACCTGCCGCTGTAACAGCGTGTG  
TGTTCGCCGATGATGTGTTTCGCCGAATCGGAACAAAAGCTGCTCCGTCCCGAGCCAAGGTTTGGCGTGGGCTGTGCTGCTGTGCCCTTTGCCCGGGCGCACAGGATGTTTCAGACGGCGCT  
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TAGGATGCCGCTGAAGGTTTTAGATGCCGGCGCAGGGAATTGGAACTACATTTCTTTAGGATTTCGATCATTTTGGC

**SEQ ID 8054**

LQGTGDKDVVLIGIDDAIVRPREGFDLCSADMLIKDRHFFADVKEPLGLAWKVLAVNISDMAAMGAIPIRWVLLSALPELDEWVLERFCGSSFPGLAKKFGVTLLIGGDTTKGDMAFNVYII  
 LGTPKGALRRDDAAGVDDTIWVSGRVGMAAAALNCRKRCVLDDVFAECBQKLLRPEPRVGLGLALLPFARAAQDVSDGLAQDLGHILTASGVGAETWADSLPSLSVLKDLILPRAQHSY  
 TIAGGGDYELVFTAPESCRSRVLDAAERCGVPVTCIGKINGGCRLEKVLDAAGGRELEHSLIGFDFHG

**SEQ ID 8055**

TTGGAAACCTCTAAACATCATCGGGAACAAATAATGCGCGCTTCTACCGATCGACCCATATGCGCGCTGCTCTGTACGGATTGACGGGGGCGACCGGCAGACCAAGTTGCTGTG  
CGGATTAATTCTGTGTGATAGTCTGTTACGCGCAATGCTGCTGCTGTGTGTGTGCGCGTTTGGACAGTTATGTGATPATPTGCTGTGTGAAGACAGCGCGCAACGGCGTGTCTGGTTTCGCA  
GATTTGCGCAACACCTTTCCGGGATGTTACGCTGTGCGCGTACTGCGCCGCTTTGCTGCTGCGGATTTCCGCGCATTTCAACGGCGACGATTAATTCTGTGTTTCGGCAGACGACAC  
CAGCAAGAACCTCGAACCGCATTAATTGTGAGCAAGTCCGACATGGAATTTGGCGGCGAGACAAGTCGCGCTCAGCAACGGCTTCCGTACAGATAGACTCATTCGGCACCGCCTCCCTGTGCG  
GCAATATGGGCAGTGTCTGGAACACTACGCCGGCAGCGGTTTTGCCAGCTTGCCTGTACAATGCCGCAAGCGGGAATTCGAAAAAGCATCAATCCGCACCAATTTCBACCAGCGCT  
TCCGACAAAGAACATTTGGGAACAGATTCAGCAGACCGGTTCCGGTTCCGGATTGTGAAGCATAGCGCGCTATTGTACGCCAGCGAGTGGTTGTGCGCAGGTACGACACACGGCGCGAT  
TACCGCGCTGTTCTTCCGCCAGCGGATTTCCGGAATAATGTGCACAGGATCCGCTTCTGATTGAAAGGCGCGGAATATCCGGAATTGAGTTACGCTAAAAAGGTTTTCAGACACTTTT  
TCTGTGTAAGCTCTGCTGAGCTCGCTGCTGTGTGATTTTTCTTCCGCTGATTAATGGACCTGATTTTGGCCGCGCTTTCGTGCAACCAATTTCAGCTCAAGAGGGGCGCGCGGT  
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AGATTTTGGGATGACCGCTCGCCCCCTGTGGGGCAGCAGCGCGCACGGTTGCGACGGCGTTTCGGCGCAGCATCTCCCTGCTTGCAGGAAGTTTTCGCCCATATGGTTCGGCGCGGAGGT  
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GCGGGAAGCTGGACGATCAGGACGCGCAATCTGACGCGTTCGACCGACACCATCATCAACAGGTGGCGCGTTAAAGAAATGGTCGAGGCATTCCGCAATTACGCGCGCGCCCTTC  
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TGACGCTTTCGCAACGCGCAAGGATTCGCAAGGAAATGCTGCAATGCTTTCGAGCGTATGTGACGGATAAGCGCGCGGAGCGGATTCGCTGCTAGTGAATAAATCAT  
TGGAGAACGCGCGCGCATCAGCTGAGCAATCAGGATGCGGCTGGCGCTGTGTCAGAAATCATCTTCCAAAAACGGTAGAACTTATGCG

**SEQ ID 8056**

LETSKHHREQIMRRFLPIAAICAVVLLYGLTAATGTSSTLADYFWIVSFSAMLLVLAVLARYVILLKDRRNGVFGSQIAKRLSGMPTLVAVLPGLFLPGISAQFINGTINSWFGNDT  
HEALERSLNLKSKALDLAADNAVSNVAVPVQIDLIGTASLSGNGSVLEHYAGSGFAQLALYNAASGKIEKSNPHQDQPLPDKHEWQIQOTGSVRSLESIGGVLYAQGWLSAGTHNGRD  
YALFPQPIPIENVAQDAVLEKARAKYAEYSKGLQTFPLVTLILASLLSIFLALVWALYFARRFVEPILSLAEGAKAVAQDFSTQTRPVLNDEFGRLTKLFNHMTQELSLAKEADER  
NRRREAAARHYLECVLDGLTGVVVVDEKGRKLTFFNKAABQILGMPLAPLWSSRHGWHGVAQSSLLAEVFAATGAAAGTDKPVQVEYAAPDDAKILLGKATVLPEDNGNGVVMVIDDIT  
VLIRAKKEAANGVEAKRLAHEIRNPLTPIQLSAERLAWKLGKLDQDAQILTRSTDTIKQVAALKEMVEAFRNYARAPSLKLENQDLALIGDVLALYBAGPCRFEBELAGEPLMMAAD  
TTAMRQVILNITFKNAEAAERADMPFVRVKSFTGQGRIVLTVCDNGKGFPGKEMLHNAPEFVTDKPAFTGLGLPVVKIIGEHGRISLSNQDAGGACVRILLPKTVETYA

**SEQ ID 8057**

ATGGCTTTTATTACGCGCTTATTCAAAAGCATTAAACAAATGGCTTGTGCTGTTCGCGTACTCTCCGTTTTCGCGGACGCGCGCGCGGAGGCGATTCGCGCGACCCGCGCGGAGCGAGGA  
TAACCGACGCGCGCGCGCTTTCATCAGCAGCGCTTCAAAACGAGCTGCGCGACGAGCTTCAACAGCGGCTTCGCGCGCGCGGCGTACCGCTCAACTTTACCTTAAGCTGGCAGCTTTCCGC  
CCGCAATTCGCTTCTTATCGCTTAAATGCGGCACTGATGCGGATGACGCAATATTGACTACAACTAAGTTTCCATCCGCTGACCAACCGCTACCGCTTACCGTCCGCGCATTT  
TCCACCGATTACGACACTTTGATGCGCGCATTCGCGCGACCGCGCGCTTCCCACTGGAAGTCTTGAACAAAGCGCGCTTTCGCGTGGCGAAGCAGCGGAAACCAAGCGGAAATCC  
CGCTGACGCTGTCCACTTCAAACTGCCAAGCCTTCCAAATCAACGATGACTTCTCAAACTGGCATTTGGATTTCGGTTGGAACTCTAAACATCATCGGGAACAAA

**SEQ ID 8058**

MAFTTFLKSIKQNLVLLPILSVLPDAAEGIAATRAEARIIDGRLSISRRFQTELPDQLQALRRGVLPNFTLSWQLSAPTASYRFLKQLIGDDNDIDYKLSFHLTNRYRVTVGAF  
STDYDLDALRATGAVANWVKLVNKGALSGAEGETKAEIRLTLSTSKLPKFPQINALTSONMHLDSGWKPLNLTIGNK

**SEQ ID 8059**

GTGTTTCAGCGTATTTCACCTTTAGCTTTAGCCATACCGTACCGGTATGACCGACCACTGTTTCAACACAAACGGCATATCAAGCACCGCACTGCACGCCGCCCGCAATGCAAG  
CGCAACTTCCGCCACCGAT

**SEQ ID 8060**

VFQRISLLALAIPIYPYPTTLFQHTNGISKHRTARRPECKAATSATD

**SEQ ID 8061**

TTGCGCGCTTTCGATTCGCGGCGCGGTGCACTGCGGTGCTTTGATATGCGCGTTTGTGTGTGTAAGACAGGCTGTCGCTGATACCGGTACGGTATGGCTAAAGCTAAAGTGAAATACGCTG  
AAACACTGAATGAGCGCTTATTGTTTGTACGACCTTTGCTGCTTTGCTATGATT

**SEQ ID 8062**

LPLCIRGGVQCCALICRLCVETGWSVHTGTWMLKLVKYAETLINEPLYCLTDLCCFAMI

**SEQ ID 8063**

ATGAGTATGGCACTTGCCCAAAACTTCCGCGCAGCAGCATTCGCGCGGTTGCCGAAGGCGCAACCTTCAGGACGTGTTGCCGCACATCCGCGCGCGCATCCGCACTGACGGCGCAGG  
AAAACGCGCGCTTGCAGGATATCGCTACGCTGCGCAGCTTATTGCGGCACTTTGAAACATATGCTGCGCGAGATGCTGAAAAGCCATCGACAATCCGCGAGCTCGAAAAGCCTGCTTTT  
GCGCGCGCTTGTACCACTGCAATACAGCGCAACCGCGCCACGCGGTGTGTCACAGAGCTGTTGAAAGCATAGCCAAATCGCGCGCGCGGAGTACCGTTGCTTTGCCAACCGCGCTTTG  
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ACAACATCGCGCGCGCTGCAATCCATCCGCGGATGACGTTCGCGCTCAACCGCGCGCAGCGCAATGCCGAAAGCTATTGGAAAACTGGTGGCGGAGGATATCGCGCTTAAGCGGCT  
GGAGCAATATGCGGTACGTGGAAGAAGCGCTGCGGTAAACCGTTCGCGCGCTTTGCCGAAGGACATGCTGTGCTACAGGACTTCGCGCGCGCAGCGAGCGCGGTATCTCTTAACCG  
AAAAGACGCGCAACGATTTTGAGCGCTGCGCGCGCGCGCGCGCGGCAAGACGGGCGCATTTTGAACCTGGCGGACTGCCCGCTTACCGCTTGGACATCATGATGAGCGCTGTAAGCGCT  
TGGAGGCAATATCGCGCTTTGGGCTTTGAGCGCATCGCGCGCTGTCGCGATGCGCGGATTTGGCGCGCTGATGATGGAAGGCTTTGCGAGCAATCTTTCGCGAGCTGCGCGT  
CAGCGCTTCCGCGCTGCGCGCGCGCAATCCGAGCTGAAATGCTGCGCGCAGCGAGCGCGCTCAAAACCGCGCGCAGCAGGAGCGCTGCTGAGCGCACTTTGGCAGCGCTTGA  
CAGGCGCGCAGATGCTGCTTGCACCTGTTCCGTGTTGCTGGAAGAAACGAGCGGCACTGCAAAATTCCTCAACCGCATGCGGATGCGGAACCGATGCGCGGTGCTTTTAC  
CGAACAAACCAAGATGCTTTTATTACGCGCTTATTCAAAAGCAT

**SEQ ID 8064**

MSMALAQKLAADSTAAVAGRNLDVLAHIRAAHPQLTAQENGALQDIAYGCRYLGSLSKHLMAQMLKKPIDNPQLESLLAALYQLHYTRNAPHAVVNEAVESIAKIRGRQYRSFANVL  
RRFLRERELKLAASCKDDVAKHNLPLWWWATLKNHYPKHWHNTAALQSHPMPTLVRNRHNGNAEYLEKLVABGIAAKALDEYAVTLEAVPNRLPGFAEGLVSVQDFGAQQAAYLLNP  
KDGERILDAADPAGTKGHLLELADCRVTALDIDAGRLKRVENIARLQFPQTASAACADARDLAANYDGPFDALLADVPCTASGVARRNPVVKWLRPTDALRTARQQEALLDALWQALK  
QGGEMLLATCSVFVEENDGQLQKFLNRHADAEPITSRVLLPNKHQDGPYALIQKH

**SEQ ID 8065**

ATGATGATAAAACCATATCCGCGCATACAGTCCGCGCACATCGGGCAGGATTCATCCATTTCCTAATGAGGGGAAAGGCGTGAATTTGTATGAATTAATCCCTTTCGGGGCTTGATACAG  
AAAGGATTCCTTGTATGCGGCAACCCACATCTACCGCTTAAATACAGATTTCACCCGATA

**SEQ ID 8066**

NMKFPYPYSAAHIGHDSIHFPMRGKGVNLYELSLGLDTERIPLLNANPHPTALKSEFPQI

**SEQ ID 8067**

TTGTTAATCCACTATAAAGCGCGGCAATGGGACACAAACATGAATTCGAATCCGAATCCGAACCTGCACCCGATTCGACGATAGCCGTTTCAGAAAACCAACCAAAAAACAAACCCG  
CAAAAGCGGGTTTGTTCACATCATCGATACCGCGGACGCTTTCAGCAATATTCGAACGATACCGGTTACAAAATCCG

**SEQ ID 8068**

LLIHYKARQNDTMNLNPNLHPDSDSRFRPKKTNPAKAGFVSHHYRPTFHEYCNSTRYKIR

**SEQ ID 8069**

TTGTCCGACAACTTTACGACACGCGAGGAACAGCTATGAAAGTATCTTTGCGCGCAGCGCGGATTTGCGCGCGCGCGCTTAAAGCCGTTGCGCGCGCGGTTTGAATCCCGCTGG  
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CGAAGCCCTGCAAAATGCTCAAGAGGTGAGGCGGACGTAATGTTGTTGCGCGGTACCGCTTGTATCTGCGCGAGGAGGTGTTGATATCGCGGAAACAGCGCTGCTCAATATCCAGCT  
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CCGCTGCTGCGCGCTGGGTGCAATATCAGGCAAGCGGATGAAATCCGCGGTGCCGAAGTGGTGGCGCAACAGGTACCGGAGCGGAGTGTGCTGCTGTCGCGGACGCTTGTGCTG  
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## SEQ ID 8070

LSDNFTHTQEHAMKVIAGTDFAAAAKAVAAAGFEIPLVLTQDRPKGRGMLTAPPVKQAALELGLRVAQPEKLRRNNAEALQNLKEVEADVHVVAAYGLILPQEVLDTPKHGCLNIIHA  
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PVPAAWVEYQKPKIRRAEVVAQGTAGEVLSADGLVACGESALKITELQPAAGRRMNLAAFAAGRSIRAGAKL

## SEQ ID 8071

ATGATATTTGAAAAATCAATAACCGCTGGAATACCGCGCGTAATGGAATCAGAACCAGCAAAGGAGCTTGCCCTGAACAGCCTTTATACAACAGACAGGATTTGAA

## SEQ ID 8072

MIPEKSINGWKYRAVMEIRTTQKELAINSLYTTDRIE

## SEQ ID 8073

TTGGGCGGTTTGGCGGAAGAAGGTGCTCATGGGAAATCCCTTAAATGCCTTGGTGGGAATTTAGGGGATTTAGGGGAATTTTGCAAGGTCTTCGGGTTTGTATTATAAGATTGGGAAG  
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GGGTATGCCGCCATGATTATGGAACCTTTGTGGCAAAACATAAGCACTTCACGAAGAGAACTTACCAAACTGTTTTATATAAAAACTTTTGGGTTGTACTAGA

## SEQ ID 8074

LGGLPEGAHGSFKCLGNNLDFRGIQJRSSGLYKIEWEGWRMPALPFFRTSIPMLVONRMSIFNHNKDAIFLEGWSLGDAAHIMELLWQNI STSRRELTKLFLYKNFVGTBR

## SEQ ID 8075

ATGGGCTTAAAGTGTCTGCCCCGAAAGACGTTTAAATCACACAAGGAAACAAAAATGAACATCCAACCTTCAAGGCCACATCGTCGGCGTTAAAAATTCACCGGCAAAATCGAAGGCAAGA  
GCTTCGACATATTGCCCGCTGATTTGTGCCACACCTTTAGACAGCTTCCCAAGGCAACGCATTTGGGCGAGCTTACTACTGAATACGATTTCCGGCGCTCTGCCAATTTCCGAGCAGTTCCGAAA  
CGCCCAATTTCCGATCGAAGCAAACTGAACTGGAATCGTCACTACGGGCAAACTCAAAACTGAAAGTCATCGGTTTCAACTCGTTAAGAAAGGC

## SEQ ID 8076

MSLKLPERRLITQGNQKNIQLQGHIVGVKFNQIEBGSFDYCRILIVATPLDSSQGNALGSSTTYDFGGSANFBQFRNAQFPIEANLNVIEVITGKTQKLKIVIGFQLVKKG

## SEQ ID 8077

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## SEQ ID 8078

LQPETLEKELGLKKNDDLLILGCSPCQYWSVIQTDKRSKSKSLLEFQRFVEYFNPYVVVENVPGILSRMKESGLDNFIKLEEKGFVHFHGHNTADYGI PQSRKRFTLIANRITK  
KSNWQSSIRANGLRYAMPNEWKTAFFKLWQDIKTRILICIVVDYPI SI

## SEQ ID 8079

TTGTTTCACATCATCGATACCGGCGGACGTTTACGAATATTGCAACAGTACCCGCTACAAAATCCGCTAACCTCATGCATCGGCAAGATATTACC

## SEQ ID 8080

LFHLIDTGRRTNLIATVPGTKSANLMHRQDIT

## SEQ ID 8081

ATGACCAAAACAGCTGAAATTAAGCGCATTATTCGTTGCATGCTCGCTTCGGGCACTGCTGTTCCGGGCGAGGCGTCCGTTTACGGGTTACACCGTAAGCGGCCAATCGAAGCAAAATCGTAC  
GCAACAACTATGGAGAATGCTGGAAGAAAGCGCTACTTTGATAAAGCAAGCCAGGTGCGGTAGAATGCGGCGATGCGGTTGCCGTCCCGGAGCCGGAACCCGCGCTGTCGCCGTTGTGGA  
GCAGGCTCTCAATATGTTGATGAAACATTTCCCTGCTGCCAAACCCCTGTTCCGTTTCGATAAGGATTCATTGCGCGCCGAAGCTCAAGACAACCTGAAAGTATTTGCCGCAACCGCTG  
AGTGAACCAATGTTCAATCTGTCGCCGCTGCAAGGCCATACCGACTTTATGGGTTCTGAAAAATACAATCAGGCTCTGTCCGAACGCGCGCATACGTAGTGGCAAAACAACTGGTCAGCA  
ACGGCGTACCTGCTTCTAGAAATTTCTGCTGTCGGCTTGGCGGAATCTCAAGCGCAATGACTCAAGTTTGTCAAGCGGAAGTTGCCAAACTGGGTGCGAAGCGCTTAAAGCCAAAAAGC  
TGAGGCTCTGATGATGATATCAAGCTGACCCCGCGCTAGATGTGAAAATCCGACGATCGTAACCCGTCAGGTTGTGCCGCGCACCAATCATCAACCAAC

## SEQ ID 8082

MTKQLKLSALFVALLASGTAVAGEASVQGYTVSGQSNIEIVRNNGECWKYAFDKASQGRVECDGAVAVPEPEPAPVAVVEQAPQYVDETILSLARTLFGFDKSLRAEQDNLKVLQRL  
SRTNVQSVRVEGHTDFMGSEKYNQALSERRAYVANNLVSNVGPASRI SAVGLGESQAQMTQVCQAEVAKLGAKASKAKKREALIACIEPDRRVVKIRSVITRQVVPARNHQH

## SEQ ID 8083

ATGAAAAACAGCGCGGCTATCCGCCGAGGAAAGAGAAAAATATGGCTTTACTGAATATCTTGCATATCCCGACGAGCGCTGTCACACCGTGGCAAGCCTGTCGAACAAAGTTGACGAGC  
GCATCCCGAAGCTGTGTCGCCGATATGTTGAACGATGTACGAATCCCGCGGCATCGGCTGGCGGCGACGAGTGCATGTCACGAACCGCTGCTGATGATTTGACCGAAGACCG  
CAGCGAACC CGCGGTTCATCAACCCCGTCATGTTGAAAAAGACGCGGAAACCACTTACGAAGAGGCTGCTGTCGCTACCGGGCATTACGACCGCGTTACCCGCGCGAAGCGGCTC  
AAGGTCGAGGCTTTGAACGAAAAAGCGGAAAAATTCACGCTGGAGCGGACGCGCTGCTGCGGATTTGCGTGCAGCAGAGTTAGATCACTGATGGGCATCGTGTGTGCAACGCGCTTT  
CCCAACTCAAGCAGGGCGGATTAAGACCAAACTGAAAAACGTCAGAAACATACGATT

## SEQ ID 8084

MKNRRRIIRRRKINALINILQYDERLHTVAKFVEQVDERIRKLVADMFTMYESRGIGLAATQVDVHERVVMDLTEDRSEPRVF INPVIVEKGETTYEEGCLSVPGIYDAVTRAERV  
KVEALNEKGEKFTLEADGLLAICVQHELDHLGIVFVERLSQLKQGRITKIKKRQKHTI

## SEQ ID 8085

ATGTTAAATGCGGAACATTTGTTATCACACGACATCCCGAGGGCTGCCCGCGCTTTTCCAAACCAATCAAGCAAGACAAACCGAAATTTATCAGATAAGGGGAACGGTTATGCAAC  
GTCGATTTATAACCTGCTCTATATTCAG

## SEQ ID 8086

MLACGTFVITRHIPRCRRFPQPNQARQTEIYQIRGTVMQRRIITLLYIQ

## SEQ ID 8087

GTGTGGGCTGTGTGCGGTGGCTGAACATTTGTTATAATTTATCATATTTCTTGGCGGTACGGTATGGGGCTTTGCCGTTGTGTTGTGTTGTTTGTGCAACGCGCAATCGTCGATATGG  
AAAAATCCCTTAAAG

## SEQ ID 8088

VWVCVGLNIVNLSYFLAGTVWGFVAVVVFVQVQSCDMEKIPK

## SEQ ID 8089

ATGGCTTTACTGAATATAGACGAGGTTTATAACGACGTTGCATAACCGTTCCTTATCTGATAAATTTCCGTTTGTCTTGTGATGGGTTGGAAAAAGCGCGGACGCCCTCGGG  
ATGTGCCGCTGTGATAACAAATGTTCCGCAATT

## SEQ ID 8090

MALLNTEBQYNTTLLHNSPYLINPGLSCLIGLEKAAAAAPRDVPCDNKCSAF

## SEQ ID 8091

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AAGAAAGAAATCGGCATTCAGATTTTATTCGCGAGCGGCAAGCGCGTGGTTTCGGTCTCGCAGCGCGGCAAGGTGGTTTGGATATTGCGGAACGTAATTTTGGCCGATGTACAGAACATTAA  
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GTCAATCTGACCATCAAACAGGGAAGCCCTGCCGCCATCGCCAAATGGTTACTTCGGGAGAAATCTGATTGCGGATTGTTACGGAAACGATAGACACCCCGAGTTGGGAAGGCTTT  
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CAATCGCGGCGAGCAGATCGCGCGGGCATTCGCGAAAGCCGTTTGAACGCGCGGATGTCGATTGCGCGGCGGCGGATACCGATGTATTGAAGACTTATGTCGCTTGGGTTTGGCGGTG  
GGACTGATGCGCAAAATGGCATACACCGGATACGAGCGGATTTGACAGCTTGTGGATGCGGCACACCTGTTGAGCGCTCGCGGACGTTGATAGCTTTGCGCAGCGATACCTATTTCG  
GCGGATATGCTTACACTTTATCCAGCGTTTGCGCCACCTGACACGCGAGAGGTGATAGGATCTGTACACGCCATCAGCGAGGATTTTTCGATT

## SEQ ID 8092

MLKQQLKYALEVYRHNINLSEAAELFTSQPGISQIKLLEEBIGIQIFIRSGKRVSVSQPGKVVLDIAERILRDVQNIKNIGSEFTGQDSGLTVATHTQARYALPLIVADPVKRYPK  
VNLTIKQSPALIAQMVTSGESDLAIVTERIDHPELGRISCYDNTHAVIVPNDHPLLECRNPLRIEDLARFPLITYEPFVAGSSIAARAFKARLERPDVALAADTDVLKTYVRLGLGV  
GLMARMAYNPDTDGLQDLVAALHLEPSPFWIALRSDTYLRGYAYDFIQAFAPHLTREKVDRLTYTPISEDFSI

## SEQ ID 8093

ATGTTCCGCAATTTAAACATCGAATTATCCGTACCATCAGGTAATTATGAAAAACAGGCGCGTATCCGCGAAGGAAAGAGAAATATGGCTTTACTGAATATAGACGAGGTTA

## SEQ ID 8094

MFRILTSNYPYHNGYKQAAYPKRENYGTFYRAGL

## SEQ ID 8095

ATGTTAAATGCGCAACATTTGTTATCAGCGGCACATCCGAGGGGCTGCCCGGCTTTTTCCAAACCAATCAAGCAAGACAAACCGAAATTTATCAGATAAGGGGAAACGGTTATGCAAC  
GTCTATTATAACCTGCTCTGCGCGGAGTATGCAATTCCTCAACACAACTTTGGCGGCAATTCGAGGTGCGCCCGGATCGCGCGCAACGCTACACGGTCAACAGCGGCGACACCT  
GTGGGTAATTTGGGCAAAATACCTGTACAGCCCGTGGCAATGGTGGCCGCTGTGGGCGCGAACCGGGATCAAAATCCACAATCCCGACCTGATTATCCGGGCGAGTATGGTGTGGCC  
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GGCTCTTTATGACGACCCGCAAAATCGTTTCCGCAAGAAACCGCTGCCGCGCGCGCTGCTCTCGGCGCGGAAGCGAGGCTGCTGTACACCAAGGCGCGGAGGTTTACACCAAGG  
CCTGAAGAAGACCGGCGCTTATCTGACCTACCGAATCAATAAAACATCACCGATCCGGATACGGTAAATTCCTCGGACAGAAAGTGCATTACGCGGATCGTGCCTCCCTCGACTAT  
ACCGACTCCGCGCTCGAAACAGCTCGAAACAGGCTGAAGAAGCGGTGAAGACACGAATACACACCGCACCATCTCTTGATTACCCCGGTGCGCACCGCTTCGATACAGCCGCTGG  
TGGTGAAGAACCGCATTTCCGAAATACAGCAGGCGACTACCTGATGAAATGCGGAAGACACCGACCGCTTCAATATGGTGGCGACGAAACCGTCCCGCGGTTTCAGGCAAAATCGT  
TTCCGCTTTGAAGCGCTGGGGTGGCGGAGAGTTCAAAACCATTCAGATAGACAAAGCGCGGACGAGGTTTGGACAAAGGCGCAGTTTAAAGCTTTACAAACCGCAAGAAACGATG  
CAGGTCACCTCTCAACAAATTTGACCGAAGAACCTAAAAGCAGGATACCGTTCGAGCTGATTTCGACACCTGCCGAAGAAAGTGGGCTTGGCAATGGTTTACCACTGCGCGAAACTGG  
CTTACGCGCATTTATTTGAAACACATCTCCGATATTTCCGAAGCGACACCGCGCAATCCGGGACGGGATTGGAACAATATGCCGATCAGGCGCGCGCGCGCTGATTCGACACCTTT  
CCAA

## SEQ ID 8096

MLKCGTFVTRHPRGCRFFQPNQARQTEIYQIRGTVMQRRIITLLCAAGMAFSTQTLAANLEVRPDAPQRYTVKQDGLWGISGKYLSWPQWCLRWGANRDQIHNPDLYPGQVLVLR  
YVGGEPRLGLEQTDGI PVVKISPDKEVSGYIPDAIDVNFYRVMQHPQIVSRKETAAPRLLSGPEGRLLYTKGARVYTKGLKEPGRYLTYRINKNITDPDTGKFLGQEVAFSGIVRSLDY  
TDSALEQRSKQAEERLKDNEYTRTHPLITPVRTRSIQPLVVETAISEIQDGYLMKPNEDTDRPMVHPHPSRPVQAKIVSVFEGVGVGGQPKTTITDKGGDDGLDRGAVLSLYKRKRTM  
QVNLSENILTEPKSRDTVELISTPAAEEVGLAMVYHTAPKLAAYITLENISIDISEBDTAAFPGRDLNMPDQGRARVDSDFPQ

## SEQ ID 8097

ATGCAAAACCTTGATTTAGTCGGACAAAATGCTTTTATCCGATGGAATCGGTTTCCGCGGAAACGAAATCACAGCGGCTGTCTCCCTTCGAGACAGATATAGCGAATTAACAAAACCG  
GTACGCGGTTGCCCGCGCGCGCTCAAGGGAACGATTCCT

## SEQ ID 8098

MQNPDLVGNFAPYPMESVSARTEITAAVSLADRYSELTKGTALPRPGSKGTIP

## SEQ ID 8099

ATGTGTCACAAGCACATAATCGGGATGGGGCAAAACACACGAAAAGGTACGGTATGGCTTCGCATAATACTACACATCAGATGAAACCGCTGTGTCTTCTCTGTTTGGCGGAACTCT  
GCCTGCGCTGTGGGCTGCTGCCCAACGAGTTTCAGCCAACTCGATGCGGTCTATCCGCCAAAGCGCGCGCTGAAAAAAGGCGAATACCTGTTCCGTCGCGGCGGAGTTTACCTCGCTCTT  
TGCCATCCGTTCCGGCTTCTTCAAAACACCGTCCGAGTCAGGACGCGCGGATCAGGTAACGGGTTTCTTTATGTCGGGCGAATCATCGGCATGGAACGGCATCTGTCTCTATGTGCAC  
AGTTCGACGCGGTCGCTTGGAAAAACAGCGAGTATGCGAGTTGCCGTTTACCCATATCGAAGAGCTCGGTGAGAATATCCCGACCTGCTACACACTTTTCCGATGATAAGCGCG  
AAATGTCGCGGATCAAGGTGTTATGCTGTTGTTGGCAATATGTCGCGCGGAGAGCGGATTCGCGCTCTCGTTGAACCTTTCCCAACGCTTTATTTCCGAGGTTTTCGCGCGCAACGA  
CTTCATCTTAAGATGTCGCGGAGAAATCGGCACTTATCTCGGGCTGAACTTGAACCGCTCAGCGGCACATATCAAGTTCATCAGGAAGGATTGATTTCCTGCAACACAAACAC  
ATCAAGATTTCTCAATCTGACGCTGCTGAAAAAATGTTATCGGTTGTTCCGACCCATT

## SEQ ID 8100

MCQAHNRDGAHKTRKYGMAHSHNTTHQMKLTCSSSLRELCLPVGLLPNEFSQDLDAVIRSRRLKKEYLFRAGGAPTSFPAIRSGFPKTTVASQDGRDQVTGPFNSGELIGMDICSYVH  
SCDAVALENSEVCELPPTTHIELGQNIPLRTHFRMISREIVRDQVMILLGNRAERETAAFLNLSQLYSRGFANDPILRMSREITGSYLGLKLEFVSRTLSKFHQBGLISVEHKN  
IKIILNLQVLKRMVSCSHAI

## SEQ ID 8101

ATGATGATGACAGCTCTCTGTCCAAAGTCGTTTGCACCGATACCTTTATGTTTGTATTTCTTTGCGCGTPTTTTGACCGCGCAAACTCGGTTCAATCAGAAAGCCTATACCTGAAGAGCTGC  
CTCCGCTCTGTGCGCATTTGTCGCGCTGCGCTGCTGCTGCGTGGCGGCTTCGTGTCGCTGCGTTCAAGGCTAAGGCGAAGAACTTCTACCGCGAAAAAATGATACAGAACGAAAG  
CATACACCCCTGCTGCACGCTTCTTGAACACTTGAACACAAAGCGCAATGCTCGCCCTGCTGCTCAAAACCACGCGCAAGGCAATGGCGGAACAGGTCAGGTTCAAGGCGGAAGTG  
CTGCCGACGACGAGAACGCGCGCAGATTCGCGCGGAGTTGGCAAAATGATATGTTCCGATTGGGACGAGACGCGGCTCGCTCGGCGAAACCTATGGCGCGCTGCTCGCGGATATTT  
TCGAGTTGTCGCGCGCTTTGGAAGGCGCGCGTTCAAGGGAATCTGAAACTGACGCGGGAATATAAAACATCTTCGCGGATGCTCCGCTTGGAAACGCGCTTGAATTTGGCGCGC  
TCAATCAGCGCTTGAAGGAAATCTCGAAACACCGGAAAGCC

## SEQ ID 8102

MMHVASVQSRFAPILYVLIFPAGFLTAQIWFNQAYTEELPILLSALSAVALVWLAWAFVSVRSKAKAEKFFYREKMIQNESIHPVLHASLQHLKHPQLALLVKNHKGMAEQVRFAEV  
LPDEEDARTIAELAKMDPALTDAVASGETYGRVFADIFELSAALEGRAFKGLIKLTAEYKHLRCLPFGNGVGFRAQSGVBENLENTGKA

## SEQ ID 8103

TTGCAAAATCTGTTCACTTATACCATTTATACAGACAGGAGCAAAACCAATGACGAAAGTTATACGCGAAGATCCCGGAGATGGAGGCGCAGGACGACGCGTCAAAAGTTTGGGTTTATG  
CCTCAAGCGAGGCGGTGATTTCGACGCGCAAGTCAATCGCGCGGCTATGAAGCGCGGATTCGCCGATTATATGAAGTTCCGCGAGGTGCGCGAGATGACGCGCAGCAACGCGCGCGGAAAC  
GCCGATTGAATTCACGTTGGAAGACGACGCGCAGAACCTTTTCGGGCGCATATCGTCTGATCCCGTTGCACTGAAGAAAGTCAAAACGCGGCTTTACAAAGGCTTTTCCATCGCGCGCAGC  
GTTACCGCTGCTCTTAGGT

## SEQ ID 8104

LQILFSYTTITDRSKPMKLYAEIAEAEQAQDDGVKVGWYASSEAVDSGEVIAAAHKAAPDYMKFGEVREHGSNAAGTALEINVEDDGRITFFGAHIVDPVAVKVKVTVYKGFPSIGGS  
VTAVCLG

## SEQ ID 8105

ATGAGCACCTTCTTCGCGCAAAACGCCAAGCCATGACTGCCAAACACATCGGCCGCTTCCCGCTATCGGAGTTGGACAGGTGATTGATTGGCAGCGGATCGAACAAATACCTGATCGGTC  
AAAAAACCCGCTTACCTCGAGACCGCCGCGCCGCTCCGCCCATCCCTGTGCTGCCATGTTCAAAGCCGCTCTGCCCGACAATGGACAGCCCTCCGATCCGCAACTCGAACACAGCCT  
CATCACCGCATCGGTTTCAACTGTTTTCGCGTTTTCGAGGACCGGCGCATCCCGGTTGCAGCACTTATGCCCTACCGTAAATTCGCGTATGCGCGGGGAGCGCTATTTCGGGCTGCTC  
AAAGTGGTCCGCAAGGCCACTGAAGCGATGTGTTGAACCTGTTGAAAGCCGCGCAACAGGCTAAGTGCGCCGCTGCCGCC

## SEQ ID 8106

MSTFFRQTAQAMTAKHIGRFPFLSELDQVIDNQPIEQYLIRQKTRYLRDRRGRPAHPLSMFKAVLPQWHSLSDELEHSLITRIGFNLFCRFDGPGIPGCTFLCRYKRFYARAAYFGLL  
KVGAGSHLKAMCLNLLKAAANRLSAPAAA

## SEQ ID 8107

ATGAAATCATTCAGATACAGAACAATCAATGTAACGATGACCGCCCCGAGTTTGACCGCGCGCTGATTGCCAGCTGCCGCCAGCGCGCGGCTATCTTCTACCCCTAACCGCG  
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CTACTACTGCGGCTGCAACAAATCATCAACAAAGCAAAAGCCGCGCGATACCTACATCGAATATCTTGAAAAAGAAATGGAATGCTCGCTCCACATCTGAACGAGCGGACCGAGCTT  
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AAGCTACGAAGAAACCAAGAGTCAATCGATGCCGCGCGTTCGAGGAGGTTCAATTCGTCAGCGTGCATTTGATTACGCTTCCCGCATCAGACTTCGGAAGCATCAAAACCCATA  
GATACCGTTTTCGCTCGATCCGACCGCGCTGCCCTTTTACCACTACGCCACCTGCCGACGCTGTTCAAACCGCAACGCGCATCGATAACGCGCGCTGCCGACAGCGAAGAGAGC  
TCGATATGCTGCAATACTGCTCAAAACCTGACAGAGCGCGCTAGCTCTTCATCGGCATGGACCATTTCCGCAACCTGACGACGAACTCTCCATCGCCCTCAAGAGGCTTCTCCCA  
ACGCAACTTCCAAAGCTATTTCGACCTACGCGGATTTCGATTTGCTGCCATCGCGCTGCTGCTTCCGCAAAATTCGCGAGCACTTATCCCAAAAGCAACGCGACATCGATGCTACTAT  
GCGGCCATCGACGAAGGAGACTGCCCATCATCGCGCGCTACCACTCAATCAGGACGACATCTCGCGCGCAACATCATTCAGGATTTAATGTGCGCGCTTCGCGCTCGACTCAGGATTT  
ACGAAATGATGTTGCGCATCCGTTTCGAGCCGCTACTTCAAGACGAACTGCGGAGTTTGGAAAACTCGCGGTTTGGGATTTGGGCTGAGCGGCTGACCGCTTACACCGAA  
AGGACGCTTCTCATCCCAACATCGCATGCTTTCGACTACCACTCGCGCAACAAAGAAACCAAGGAAATATTCGCAAAACGCTG

## SEQ ID 8108

MKI IQI QNNHNVNDRPEFDRLIASLPASGPRYSYPTADRFHDGPREGEVILVHLRGMGALNKPLSLYTHIPFCNTICYCGCNKIITKDKSRADFYI EYLEKEMELLAPHLNHRHQL  
AQLHPGGGTPTFLSDQIERVFRMIRKHFELIPSGEYSIEIDPRKVSRTDVLMLGRIGFNRMSVGIQDFPKVQAAVNRIQSYESTKEVIDAAREAGFKSVSDLIYGLPHQTSSEIKFTI  
DTVLSLDPDRALYHYAHLPHVFKPQRRIIDTAAPVDSSEKLDMLQYCVQTLTERGYVFIGMDHFAKPDDELSTALKGFLQRNFGYSTYADCLVAIGVSSIIGKIGSTYSQNERDIDAYT  
AAIDEGRLPIMRGYIQLQDDILRNIIQDLMCRFALDYRIYESHFGIPFDRYFKDELADLEKLAGLGLVRLNSHGLTVPKGRFLIRNIAMVDYHLRHKETKAKYSQTV

## SEQ ID 8109

TTGCGGCTAACGTACAAAAGCGCTCTGAAAGCGTTTTCAGACGCGCATTTTGTCTGCCGAGGATAAGTGTTTTCAAGAACAGCGCGCGGCATATCATAACTTTGTGTCCGACCGCTTCGAA  
ACCAAGATACCAACAGCATATCCCGACAGAACAGATTGTGCATAAGCCACAGCCGCGCACATTCATCAACAAAATGCCGTC

## SEQ ID 8110

LRLTYKSRLLKGFRRHFAAEDKCFQEQAAAYHNLVRPFRNQDTRQHIPTQIIVHKAQARTFHQONAV

## SEQ ID 8111

TTGCACTACGCAACCGGTAACCGTGGGCTTCAACCTGCCAGCAAAACCCAGGCGAGCAAGACATCATCAAAATCAAAGCGGTGCTTGGACGATAAAGCCGCGGACCGCTTCGCC  
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CCAGCGGAGCGGTCAAAGCCGCTTTATGTTAAGAACCAACAGCGGCGAGCGCGCTGAAATGCCACTACTCGGAAAAACCTACAACCGGATTCGGTGGCGGAAGCC

## SEQ ID 8112

LHYGNVTVGFNLPKSTQGSKDIIRIKGVCLDDKAADRLALFAPEAVVNTIDNFVVKRHLTLFDEIAEVFRCPNFCAGHGEFVKSRFYVKKHNGQTRLKHCHYCKEYTNRDSVAEA

## SEQ ID 8113

TTGTTGATGGAATGTGCGGCTTGTGCTTATGCACAATCTGTTCTGTGCGGATATGCTGTTGTTGATCTTGTGTTTGGAAACGGTTCGACACAAAGTTATGATATGCCCGCGCTGTTCT  
TGAAACACTTATCTCGGACGCAAAATGCCGCTGAAAAAGCCTTTCAGACGCGCTTTTGTACGT

## SEQ ID 8114

LLMECAGLCIMHNLFCRDMFLGILVSESDTKVMICRRFLKTLILGSKMPSEKAFQTAQVR

## SEQ ID 8115

ATGCTTAATCCGCTTTACAGACAGACATCATCTCCATTTCCGATTTTGTGCGCGAACAGTTGGAATACCTGCTTCAGACGCGCATTTGAAGCTGAAGCGCATCCGCGCGGCTTTGTTGG  
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TGCCAAAAAGGCGAAACGCTTGCAGATACCGCCGCTATCATTTCCGCTTACCGAGCGGATTGTCACAGCCCATCCCAAGACGCGCGCGCGGTGGCGCGGAGTTTTCGCGCGTC  
CCGCTCATCAACGCGCGGACGCGCAAGAACACCCAGCCAAACCTTGTGGAACCTGTAACGATTTATGAAACGCGAGGCGGTTTGGACAGCTTAAAAATGCCATGCGCGCGACT  
TGAAATACGGGCGCACCGTGCATTCGCTGTGTGAGCGGTGAAACGCTGGGCGTGCAGATTTGCTTCTGCTCGCGCGCGGCTTCGCGATGCGCGCTTACGAGGTTTGGCAAGTGAAGA  
AGCGACTGCGGATACCGCGCGCTCGGCACTTTGAAGAGCGCGCGGAATGGCGGACATCTGTATATGACCCGCGTCCAGCGCGAAGCTTTCGACGAACAGGAATTTGCCAAATCCAA  
GGCAATTTCAACCTCGAAGCGCTTATGCTGCGCGCGCGCAACCGAACTCGCGCTGCTGCACCCCTGCCGCGCACGAGCAAAATCCACCCGATGTCGATGCGCGCGCACGCGCTATT  
ATTTGAGCAGCGGACCAACCGGCTTATGCGGCTATGCGGATATTTGCTGCTGCTGTTGAACGAAGAAGTG

## SEQ ID 8116

MPNPLYRQHIIISIDLSREQLLEYLLQTPALKLKAHPRGDLLEGKLGSCFFEPSTRIRLSFETAVQRLGGKVIQVSDGANTSAKKGETLADTARIISGYTDAIVQRHPKDGAAARVAAREFSKV  
PVINAGDGNQHPSTLLDLVTIYETQGRILDKLAMAGDLKYGRTVHSLQALKRWGCEFAFVSPSLAMPDYITFELEERADCRYALGSLERAEANADILYHTRVQRERFDQEFAKIQ  
GRFNLASHLARAKNRLNVLPLPRTDEIHPDVAAPHAHYFQATNGVYARMAILSLVLNREV

## SEQ ID 8117

ATGGTCGATAACCGTCCCTTTTCGATGGCTTCGACACTGAGTTTTCGCGCTTCATATCCGTTCTCACTTCTTCTGTTCAACACGCGCAATATGCCATACCGCGCATAAACGCGG  
TTGGTCCGCTGCTCGAAATAATAGCGGTGCGCGCGCGCATCGACATCGGGGTGATTTCGTCCTGCGCGCGGAGGGGTGACGACGCGCGAGGTTCGCTTTGGCGCGCGGAGCATAGAGC  
CTTCGAGGTTGAATTTGCTTGGATTTCGCAAAATTCCTGTTGTCGCAAGCTTCGCGCTGAGCGCGGCTCATATACAGGATGTCGCGCCATTCGCGCGCTCTTCAAACTGCGGAGGCG  
GCGGATCGGCGAGTCCGCTTTCCTCAACTCTTCGTAATGATAGTCGCGCATCGGAGGCTGGGCGCGGAGACGAAGGCAAAATTCGACGCCGCGGCTTCAACGCGCTGACACAGCGAATGC  
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CGCGCGCTGTATGACGCGGCGCGCGGAAATTCGCGCGCGCGCGCGCTTTCGGGATGGCTTGGACAAATCGCGTGTAGCGCGGAAATGATACGGCGGATTCGCGAG  
CGTTTCGCTTTTTCGACTGTTATTCGCGCGCTCCGAAAGCGGATGACCTTACGCCCAACGCTGCACCGCGCTTCAACGACAGCGCTGTCGCGGTGAGCGCTCGAAAGGAC  
GAACCGATGAGTTGCTTCCAAACAAATCGCGCGCGGATGCGCTTCAGCTTCAATGCGCTGTAAGAGAGATATTCCTCACTGTTTCGCGCGCAAAATCCGAAATGAGAGATGATGCTGCTC  
TGTAAAGCGGATAGGCAATTTTTCGCCCTTCCGTAAACAAACCGCGCTCAGCGGGTATCGGTTATAGCTCCACGCGCGCGTATGTTTTCGGAACAGCTTCGCAAAAGCGCGGACAG

GC GCGTATTATCGC A CATTGCGCTCC A AAGTTT TACCGCAGGAATCCTGTATT TTTTCAGACGGC ATATCAA AACACG CCGGCAT AAGCATAA AGGTATAATCGCGCCAGACATTTCTTTT  
CAGGAAGCGCCCATGTGTTAATCTGCAACCCCTACGAAGTGTGTCATCCACGGCA CAACGAGTTTCGGGCAAGATTTTCGCGCCCGGCGACTGGCGGAAAGCCCTGTGCGGCATCCTGTCTCTGT  
TCACCAAGACACAACCGCCCTCCTATTTCGAAATGGGTGCGCCCATGCTGGTGGACAACATCCGCTGCGTCGCGTGA

**SEQ ID 8118**

AVNDRAFFDQTFITFLRPHIGSSSHFFVQHQRVQRHTRINAVGRLLIEIGVRRGDIGVDVFRARQGVQHAQVRPGAGEHRRFEVEFALDPKGLFVETFPALDAGHITQDVRPFRRLPQTAE  
AVSAVGFFQLFQGNVVGHREAGRRDEGKFAAPAFQRLTQRMHGAVPVQVARHGDFKLVTPLRFINRYQVQQGLAGLVRAVAGVDDGDARKLRRHARRAVFGMALINRVGVAGNDTGGIGK  
RFAFFGTGIRAVRKADDLTAQTLHRRFKRQPRARGLEKARTDEFAFOQIAARMRLQCLRLKQVQLFPAQIRNGDDVSVKIRIHFCPPSVKNPQAGIRLYVHAARMAEQLRKSGOT  
ARIITAHLPPOSPTARILYFSDGISKHARISIRYNRARHFFSGSRHVNLOPLRSRHPHNEFRODFFPRLGGTPVRRHPLVHQROPPLLFEMGAPHAGGOHLRRR

**SEQ ID 8119**

ATGTTAATCTGCAACCCCTACGAAGTCGTATCCACGGGCACAACGAGTTCGCGCAAGATTTTCGCCCCGGCGACTGGCGGGAACGCCTGTGCGGCATCTCTGCTCGTTACCAAAGACA  
ACCGCCTCTCCCTATTTCGAAATGGGTGCGCCCCATGCTGGTGGACAACATCCGCTGCGCTGCGCGTGCATATAAAACCTGGAAACCGGACAATCCGCAGATGTTCGCCCTCTCTGATGGCACTTTGC  
CGCCGACAACGACTCTGGCGGTATCGACTGCAAGCCCTGCTCGAAGAACCGGAACAGGGCGGACAAACAGCACCCTGCCAACGAACGCGTCTCTGTGGCAGCAGGCAATCGAAGAAAACAC  
GCCGCCGAGAAAAACAGGAACAGACCGCCTCTGGCGCATCTACGTTTACGCGAAATCGGCGCGGACGACACCGCCACCGCTTTGCAAGCTCTTGAGCGCTTGAGCGTTTGTGCGTTCCCTCCGTCGCG  
ACATCGGCGCGCTTTACCGAACAGATCAACAAAATCCAACGCCGCCCAAGCTACCGCGCTGCTGGGTATTTTGAAGATCTGCAAAACACAGCGGCTGCGCGCTCTGCGCGCTTTCGCGAAGCGCTG  
CACCCTCTCGCGCGCGCGCCGACATCCATCGACAGCATGTGTTATGCTGGCGCAACGCGCAAGCGCGCAAAAGGCTACGCGTGCGCCCTTTGGAGAGAGTCCGCAAAATCGCGCGGAAACAGG  
GTATTACCAAAATCCACCTTTAACGCTCCACGTCAACCAGCAGCGTACCGAGCGCGACCGCTGTATTTCAAAACAGGTTTGAAGATCTGCGCCTTACCCTCTCCGTTGCGACCCCAA

**SEQ ID 8120**

MLICNPYEVVHIGTSSGKIFRPGDWAERICGLISPTKDNRLSYKSWVRPMLVDNIRCVAVDKKLETDNPMQFRPLMDFAADNDLRLVIDCKALLERREPGGQNDPANERVLLAQATEKH  
AAEKTQEQTASGASYVLREIGADDTATAPAAFLSVLRSSLDIGRFTQINKIQRPQGYRLLGIFECKHNAVAVCGPREACTLAGGRHIHDDIVTLPSQRRKIGYASRLLEEVRKIGAFYC  
VTKTHLNVHVNHDRDTAHRLYFKNGFEICAYHFRCDPK

**SEQ ID 8121**

ATGTCGTCCAAATCCAAATGACGCGCAAATGTTAAACCATCAACGCCGCTCTTTGCCGCCATGCTGTTAGGTACAGTCGGCTATTTTATTATTATGGGGCTTGGGTTATACCCATTACAATTACG  
CCGCCCTTATTCATTATTGCCACGATGTTCTGGTGTTGTTATGGCGTTCAAACATCGGGCGGCAACGATGTGCCAAATTTCTTTCGCGACACAGCGTCGGTGGAGCGACCGCTGACCAATCCCCGAGCG  
TTTGCTGATTTGCGGCGGTTATTTAGGTTGACGCGCGCGGTGATCGGGCGGGGCAACGATACCATCAAGCTCAAAGGCATCGTGATTGGAAGGTTGTGATTTCGCAACCCCATACAGTTT  
GTGTTTATTATGATTCGCGGCTTTTGGCGGCGGCGTTGTGGCTGCTGTGCGCTGCCGCAAGGCGCTGCCGGTTTTCGACGACGACGCGGATATTGCGCGGATGTCGCGGAGTCGGTGTTG  
GTATTTGGCTTTTACGTCATTAATTCGCGAGCGGGGTGGCGTTGATACGTTGGGCAAGCTGGGCGAAATCGGGATGTCTTGGGTATTGTGCGCCGTGTTGGGCGGCGGGTGTCTTATTTCCGTGTT  
TTGCGCGCTCAAGAAAAACGTCTTAGATTACAACGCTTGGCGGGAAGGAACGCTCAAAGGCATCAAGCAGGAAAAAAGGCGCTATAAAGAACCGGACCGCGTTTCTTTTCGAGGGTTTGTGC  
GAAGCCGAAAAAGTCGATGACCTCCACAAAATGGCGCAGCAGCGCAAAATTACGACGAACCCGAATTCGATCTCAAGAGCTCGCAATCGGATATTACCGCGGTCCTTTATGCGTTTCGTCACA  
ACCGTAAAAACAATGTGATGCTTCTCAACAGGCGTCGATTTCTTGGAATCCCTTTATCGCTGCTTCTGCGCAGCATGATGATTTCCGCTATGCTGTTTCTCAAGGCTGTAAAAAATCCGTAATTT  
GGGATGAGCAGCACTCAACAGCTTCTCGACCACTTTTATGATAGGCGCGGCGGTGTGCGATGGGAGCGTTTGTGTTTGCCAAAAAGCCTCAAGCGTAAAGACTTTGGGCAAAATCGACCTTTCAG  
ATGTTTTCATGGATCGAGGTCTTTACCGGCTGCGGCTTCGCAATTCAGCCACGCGTGCBAACGATATTCGCCACAAGCCATCGGCCCGTTTCGCCGGAATTATGGATGTTTTCGCGACCGGCGAGG  
TTGCCGCGCAAAAGCGGCTCCCTCCGATTCGATGCTGACTTTCCGCAATCGCGCTGATTTGCGGTTTGTGCGTTTGTGCGTTAAAGAGGTGATTAACAACTCCGTCGATGACGAGTTTGGCGGAAT  
GCATCTGCTCTCGGTTTACCGCCGAACTTGTCCGCCGACATCGCTGTGATGGGCGCGTCTGATGGGCGTGCCCGTTCGTCAGTACGCAATATCTTGGTGGGCGGCTACTCGTATTCGGT  
TCGGTCAACCGCAATGCCAATGGAACTGATGAACCCATCGGTTTGGCGTGGGTATTACCTGCCTGCCGCGCTGTATTGTGCGATGGCCAGCTATTGATTTTTCGAGGACAGTGTTTC

**SEQ ID 8122**

MQIQMSANVKTINAVFAAMLVGTVGYYFLYWGLGYTHYNYAALFIATMFGVFMFAPNIGGNDVANSFGTSGVAGTLITPQALLIAAVFEVSGAVIAGGEVDTIRKGIVDLKGVDPEPIQF  
 VFIMMSALLAAALWLLFASRKGLPVSTHAIIGGIVGSGALCMFTFNADGVALIRWKGIGEIGMSWLSPLVGLGAVSYYFLSRVKKNVLDYNABAGTLKGIQKEKAYKSRHRLFPFEGLS  
 EARKVEYATKMAHDAIQIYDEPEFDPEIQSEYYRGLYAFDNRKNNDVSYKALHSWIPIIASFGTMMI SAMLIFKGLKNLHLGMSAGSTLPTIPMIGAAVWMGTVPFAKSLKRKDLGKSTFQ  
 MFSNMQVFTACGFAPSHGANDIANAGPFAAIMDLRNTSVAQSAVPPIALMFTGALITVGLMFGKEVIKTVGTSLAMEPAGSTFAELSAASVVMHGTLFPVSTHAILVGAVLGIG  
 LVNRNANWKLKMPGLAWVITLPAAAAVTNSMAYSLILOAVF

**SEQ ID 8123**

ATGATTATGGGTGTATTAAATTTTTTTTCTAATCGTCCAAATTTGGGATTATTTCGCGTACGATAAAATTATTTTATTATTAATAAAATTTAAACTTCCAAAAACATACATGGCGTATTACTCC  
CATCATCATCATTTTATTTTATTCATATTTATTCATGCAATAAAATTCATATGATTTTATTTTTTATGTTTCATGCGTTATTTCGCGTATACATATATGATAAAAAATCTTTA

**SEQ ID 8124**

MMGLVLIFFLIVPIIGFICATINYFIINKFKLPKYMAYLLPSLSILFIFIHAIKLHMLFFYVSCVYSAYTTYDKKSL

**SEQ ID 8125**

GTGGAAAAATATTATTAATCGCGCCGCAACATCCAGTAGTAGAAGTGTCATACAAACCCTTTCCGGCAGCAGTTTTGCAATTCGGTCAGGTTTGGGGGTATTCGGATCGGGTTCAGAAGGAAG  
GATGCTGCTCGCATATCCCGAAGCGCGAGTTCCGACCGGGGAGCAGCAATACAGTGTCCGCAACCTCATGATTTCCACCACATTAAAGGAAGATTGCCATGGCTCAAAATCCAAA

**SEQ ID 8126**

IRKYYNA PATSSSRSVTQTVSGSSPAFGVWGYSDAVOKEGCVCHI PKROFDRROOYSVGNTHDFHHIKGRLPNLKSK

SEQ ID 8127

TTGCGGGCGCATTATAATATTTTTCCACCCGCTTAAACATTTATTACACTTTATTACACTGCGGGCGGCAAAATCGGTATACGAGCGTCAATACACGTTAAAAATGGCGTTTTCACCAG  
TTTGGGAG

**SEQ ID 8128**

IRAHYNI PPPVLKHLFTLYLHCGGKSVYEROYTLKWRFPVWE

**SEQ ID 8129**

TGGCTTGGCCCTATGTTTGTGACCCCGCTCTCTACCAAAACATCCATGTACGGAGTTGGAAAGCAGCGGAGATTCCGGCATAGTAAACAAGATTGGATTTTCTTGC GGCGCGCGCT  
 CGATTGCCACGTTACTGAATAAATTTTATGCGCAGACATTATTCTGAAGCGGAAATCTTAGACAAATGGATAAAACCCAAATCGGTACTCTCTTTGATGATATGCAACGCATAATATGCCGA  
 ACTGGGTTTGTGAAGCACAAAGGTTATGCTTTGCCATTGAAACAGTTGGTACAACATAAAATTCCTGTAATTTGGTATATGAAATACCGCTAAACCAACCAATTTTTCGGTATTTGAACGGTAT  
 AACGGAGAAATCTGTTTCTGGCTGATGTCATCGCTGGGCGACGCTTCAACAGCACAATACCAATCTTTGAGCGGATGAAATACCGCTAGTGGCGAAATGGAAAGGAAAAATTTTAGCATCTG  
 TCCGCAAAAATCTGATTTTCTTTAGAAATTCAGATGTTTTTATCAAAATCCCGTTCGTCAACACACGTTTTACGGTAGAACAAATCCAAATGCGGCAAAAACGA

**SEQ ID 8130**

LLGLCLLPASYQNIHVRSWKARRDSGIVKQDLDFSCGAASTATLLANFYGRHYSEAILDKMDRTQMRTSFDDMQRIPELGFEEAGYALPFBQLVOLKIPVIVLYTKRKNHFSVLNGI  
NGETVILLADPSLGHVSTSKSOFLSAMWKTRDGEHGKILAIIVPKNFDVVRNOMPFKNKPNVROTRFTVBOIQMROKR

SEQ ID 8131

SEQ ID 8151  
ATGGCGTTTGGACCAAGTTTGGGAGTGATGATGGAAACACAGCTTTACATCGGCATTATGTCGGGAACCAAGTATGGACGGGGCGGATGCCGTGCTGGTACGGATGGACGGCGGCAAAATGGC  
TGGCGCGTGGCAAGGGCAGCCCTTTACCCCTACCCCTGACCGGTTCGCGCGCAAAATTGCTGGATTTCAGGACACAGGCACAGACGAACTGCACCCGACAGCAGGATGTGTGTCGAAGAAGCTCAG  
CGGCTGTACCGCGAAACCGCGCGGAAGTCTGTGTCAGTCAAAGCTCGCTCGTGCAGCAATTACCGCCCTCGGCTGCCACGGGCAAAACCGTCCGACACGCGCGGAACACGTTACAGC



ATACAGCTTCCCGATTTCGCGCTGCTGGCGGAACGACGCGGATTTTACCGTGGCGGACTTCCGAGCCGCGACCTTCTGCGCGCGGACAAAGGTGCGCGCTCGTCCCCGCTTTTCAGG  
AAGCCCTGTTCGCGGATGACAGGAAACAGCGCTGGTACTGAACATCGGCGGGATTGCGAACATCAGCGTACTCCCGCCCGCGGACCGCGCTTCGGCTTCGACAGAGGCGGGCAATAT  
GCTGATGGACGCGTGGACGAGGACACTGGCAGCTGCTTACGACAAAAAGGTGCAAAAGGCGGCACAAAGCAACATATTCGCGCACTGCTCGGACGCTGCTCGCCACCGTATTTTC  
TCACAAACCCACCAAAAAAGCAGCGGCGCGAACTGTTTGCCCTAAATTTGGCTCGAAACCTACCTTGACGCGCGCGGAAACCGATACGACGATATTCGCGACGCTTTCCCGATTACCGCGC  
AAACCGTTTGGACGCGCTCTCACAGCAGCGGAGATGCGCGTCAAAATGTACATTTGCGCGCGCGGATCCGCAATCTGCTTTTAAATGGCGGATTTCGCGAGATGTTTCGCGACACGCGT  
TTCCTGACACGACCGCGGAACTGAACTCGATCTCAATGGGTGGAGGCGCGCATTTGCGTGGTTGGCGCGGCTGTTGGATTAAACCGCATTCGCGTAGTCCGACAAAGCGACCGCG  
GCATCCAAACCGTGTATTCGCGCGCGGATATTTATAT

## SEQ ID 8132

MAPCTSLGVMMETQLYIGIMSGTMDGADAVLVRMDGGKWLGAEGHAFTPYDRLRRKLLDLQDTGTDELHRSMLSQELSLRYAQTAELLCQNLAPCDITLALGCHGTVRHAPHEGYS  
IQLADLFLLAELTRITVDFRSRLAAGGQGAFLVPAFHEALFRDRETRVLNIGGIANISVLPFGAPAFGDTGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPTF  
SQPHKSTGRELFALNWLETTLDGGENRYDVLRTLSRTAQTVCDVSHAADARQMYICGGGIRNPLVMDLAECFTRVSLHSTAEINLDPQWVEAFAFWLAACWINIRIPGSPHKATG  
ASKPCLLAGYGY

## SEQ ID 8133

GTGCTTGGCGCTTAGGAAACCGTTCCTTTGGGCGCGGCGGCGCAACGCGCTACTGTTTGTGTTAATCCACTATAAAGCAAAGAAACCGCATTAGCCTACACCCCCCAAGCTG  
CGGCTGCAAAACACATCGGCTGCTCTCGACGACCGCGTGAATAATCGCGCTATCGCGCGCGCTTGACCGCACCGCTGCTTTGCCACCGCTGCCGATGCGGTC

## SEQ ID 8134

VIGRLRBPFLGRGGATPYWFLIHYKSKETAISTTTPQAAAAXHIGCFSTHPLKNAFYPPALATAPAFATLPDAV

## SEQ ID 8135

AACCTTTCGCGCAACAAAGACAAGATGTCGCGCGCAATCAGCGGCGGACAGGGATACCGCCATAAATGCCACCGCATGACCGTACCGATCAGCAAGCCGTTACCAATACCGGCTGC  
CGTCCCATCAAAGGACGCGCATCCCGCCAGCCAGCAAAATACCGATAAAACCGCGGATATCATTTTAAATTCAAAAATTCGCGCAACAGGAGGAACCTGCGGCTTTCCTGAAA  
CCAACGACTCAAACCCCTATGGTCAAAGAATGATACCGAGGTTCAACCGGTGCTCTCGACCAACGGGACAACTGTACCAATCGCGTCTGCTCATCAGCAGCAATATGGTTGCCGA  
GACGTAATCGAATGTTGTGCTGACACCCCAACAGAACTCAGGTAACAGAAACAGGGGAACAAACTGAAATTCAT

## SEQ ID 8136

NLSGNKRQDVGRNRPDRDTHAKCHPDDRTDQARYQYRLPSHRHAASRQPSHENWIDKNGYHFKIKQFGRNRRLRLS\*NQRTQNPYGQKNDTVEQVPLLDQRDLQYCRLLHQDQYVGR  
DGNRIVADHPQONRQNRQGNKTEH

## SEQ ID 8137

ATGAAGGTTTGAACGGTTGGTCAGATAGGAAGATGTGCGGGGTTTGAAGTCTTTGCCGATAGGCGGTGTGTTTTTGAATTGATCTACGGTTTTGTGTTGAATGTGTGACGGGTTGG  
ATTTCAGCGTGCCTGCGGATTCGGAAGGCGGTGTGCGGGTTACGCGCGATATGCGTTCAACAGTTTTCAGATGTGCGCAACGCGGATATGCGCGCGGTGTGTTTCGGGTTTGGC  
GGTTGTGTTTTGCTCAACCGTTCGGTGCAGCGCGGCGAGGTCTGGAATCGGGGTGTTCCGGATGTGCGGCTGGTGGCGGTATGCGGTTTACCGCGCGCTTCGCTGCGGAGTGGCG  
AACCGCTGCGCGCTGCTGCTGCGTGAAGGCGCGGACGTGGTCAATACGGGAATCGCGTTATGTGCTGACGCGCTTGTGTATGCCCTTTCGCGCGGTGTGTCATCATCGGGCTGGTAGGCG  
GGTTACGGCTTCAGACGGCATCGGCGAGGTGGCAAAGGCGAGGGGTGCGGTCAAGCGCGGCGA

## SEQ ID 8138

MYVLNGWSDRKMVRVLSALPIGVVFFDLIYGFVLNVLQGLDLQRAVPDSEGLAVTPDIAFNLSLQIVANGMAAVVCFGLAVVFLNRSVRRRQVLEIGVFMGLGLVAVLAFSAPSLNEMA  
NALPILLKGAADVNTGNARYVLTAICMPFPAVSCIIGLVGRFRLQTASGRVAKAGGAVRAGG

## SEQ ID 8139

ATGAAACCCCTGCTCCTCCTATCCCCCTGCTACTCACCGCTTCGCGCACACTGACCGGCATACCGCGCCACGCGCGGCGGCAACGCTTTGCCGTGCAACAGGAACCTGTCGCGCATCTGT  
CCGCGCGCGCGCTCAAAGAAATGGACTTGTCCGCGCTGAAAGGACGCAAGCGCGCTTTACGCTCTCCGTATGGCGGACCAAGGTTTCGGCAACATAAGCGCGGAGCGTACTCCTATCGA  
CGCATGTATACCGCGCGGTACCAACAACCCCGACAGCGCCACCGGATACAGCTACCCCGCTATGACACTACCGCCACCAACAAATCCGAGCGCTCTCCGCGGTAAACACTTCCACA  
TCGCTTTTGAACGCCCGCGCGCGCTGACGAAAAACAACGAGCGCAAGGCGAAGCGTCCGCGCGGATGTCGCTCAACGCGACGCGGAGTACCGCAACGAAACCTGCTCCGCAAC  
CCGCGGAGCTTCTCTCTGACCAACCTATCCAAACCGTCTTCTACCTGCGCGGCTTCGAAGTCTACCGCGCGGAATACCGCGACACCGACGTATTCGTAACCGCTGACGTATTCGGGAC  
GCTCCGCGAGCGGTACCGAACTGCACTCTACAACGCGGAAACCCCTTAAAGCCCAAAACCAAGCTCGAATATTTCCGCGTACCGCGGACAGCGGAACTGCTGATTGCCCTTAAACCGCC  
GCTACGAATCCCAATCAAGAACAATACGCGCTCTGGATGGGACCTTACAGCGTTCGCAAAACCGCTCAAGCCCTCAGACCGCTGATGTCGATTCTCCGACATCACCCCTACGCGG  
ACACAACCGCCCAACCGTCCGACTTCAACAAACAAACGTTAAACCCCGATGTCGCGCAACGAAGTCAATCCGCGCGCGCAAGGAGGA

## SEQ ID 8140

MYTLLILLIPLVLTACGTLTGIPAHGGKRFVEQELVAASSRAAVKEMDSLALGRKAALYVSMGDQSGNISGGRYSIDALIRGGYHNPDSATRYSPAYDITATTKSDALSGVITST  
SLINAPAAALTKNNGKRSAGLSVNGTDYRNETLLANPRDVSFLNLIQTIVPYLRGLVVPPEYADTFVFTVDVFGTVRSRTELHLYNAETLKAQTKLEYFAVDRDRKLLIAPKTA  
AYESQYQBYALHMGPIYVSGRTVKASDRMLMVDSDITPYGDTTANQRNPDQKQNGKNPDVGNVIRRRKGG

## SEQ ID 8141

TGCTCTGCTTTCGCTACTATTGTACTGTCTCGGCTTCGCTGCTTGTCTGATTTAAATTTAATCCACTATACCGGACCGCAAGCGCGCGAACAACAAACAGGGCGCTGTCTAG  
ATAAC

## SEQ ID 8142

LPRLAVLVLSAASSPCPDNLHYTRPRKPNKQGPVLDH

## SEQ ID 8143

GTGTCGGGTATAGTGGATTAAATTTAAATCAGGACAAGGCGAGCAAGCGCGACAGTACAAATAGTACGCGAAGCGGAGGCAACCGCGTACTGTTTAAATTTAATCCACTA

## SEQ ID 8144

VVGYSGLNLNQDKATKPTQVQIVRQGEATPYHFKFNPL

## SEQ ID 8145

GTGAAACCGCTGCGCAGACTGACAAACCTCTTTCGCGCTGCGCGTACGCGCGGTGCGACTCATACGCGCGCGCTGCGCGCGGACTTGGCGCAAGACCGGTTCAATACCGATAACACCC  
AACCGGACGACTACGAAACCGCGCGGCAATATCAACCTCTTCGCGGACCGCGCGGCGGACGCTTTCGAGCGCGACCGGCAAAATCAACGTCATCCAAGACTATACCCACCGATGGGCAACCT  
GCTCATCAACAGCGCGGCAATCAAGGCAATCTTGSTTACACCGTTCGCTTTTCGAGACCGGACACGAAGAACAACGCGCCCTTCGCAACACCGCGCGGACAGCGCAAGCAAGAAAA  
GGCAACGTTGACGACGCGCTTACCGTGTACCGGCTCAACTGGAAGGACACGAACATCATCCGCGGATGCTACGACGCGCGGAGGCGGCAATTAACCCAAACCTACGCGCGGACGAG  
ACGAATACACCTATACGTCACCGGACAGCGCGGAGTATCAAACTCAATCCGACCGGACACCGCGGAGTACCGCAACGCAATTCGACAACTACAACACCTCGGCGAGCAATTTCTCGGA  
CCGCGCGGATGAAGCAACAGAAAAATGTTGAGCACAATGCCAAGCTCGACCGCTGGGGCAACAGCATGGAGTTGTCAACGCGCTGCGCGCGCGCGCTCAACCCCTTTATCAGCGCG  
GGCGAAGCTTGGGATAGGCGACATCTGTACGGAACCGCTATGCCATAGACAAGCGCGGATCGGCAACATCGCGCGCTTACCCCGGAGGCAAAATTCGCGCGCATCGCGCGCTGG  
GACGCGCGCGGCTTTGAAAAAATACGCGGAAAGCGTTCGCGGTGGATACAGGAAACCCCAATGCCCGGAAACCGTCAAGCGCTGGTCAACGCTCTGCGGTTTGCCAAAGTCAA  
AAACCTGACAAAGCGGCAAAACCGGGAAGGCTGCGGTTAGTGGGATTTTCTAAATCTTACACCTGCTCTTCCACCGGACGACCTTGGTCAAAACCGGACAGCGCTACAAAGCAAT  
GCCCATATCAAGCGGACAGCGCTCTTTCAAGGACGAGGCAAGCGGAGAAACCGGATACAAACCGCTTACCGCGGATACGGAATCCGATCAAGAAACCGCTTACATTTAAGATTT  
CAGACGCGATCGGCAACGCAACCCCTGATTTCACCGCATCCACCGCTTTTATTCGGAACGCAATAGGATTAAGCGGAAGATTTAAAGCGGGAAGCGCGCTGTATCCGAAAGCGG



CAAAACCAACCGTCGCAACATCGTTGTCAAACCAACCGCTCAAAGCCTACAATCTGACCGTTCGCGATTGGCATACCTACTCTCGTCAAGGGTAATCAGGCGGAAACGGAAGGGGTT  
TGGGTTCAATAGTATGTTCCGCTAAACCAAAACCAACCAATCATGCCCAACAAAGAAAGAAAGACTAAAAACGATTCTCATGAAGTGTGGGAGATTCCAATCGTGTCTCGCGAAG  
GAAAGCAATATTAGATTCCGACACAGGAAACATGTTTATGTAAAGGAGATAAAGTGGTTATTCTAACTCTGATGGAAGACAGGTAACCTCAATTTAAGAACTCGAAAGCCAAATACGTC  
AAAAAGGGTAAAAAATGGGAATGGACACCAAAA

## SEQ ID 8146

VKPIRLRLTWLLAACAVAAVALIQPALAADLAQDPFITDNTQRQHYEPGGKYHLFGDPGRSVSDRTGKINVIQDYTHQMGNLLIQQAIIQGNLYTVRFSGHGHEEHPDINHAADSASEEK  
GNVDDGFTVYRLNWEHHEHPADAYDGPFGKNYKPTGARDEYTHVNGTARSILNPTDTRSIQRIFDNYNLLGSNFSRDEANRKMFEHNAKLDWNGNSHEFVNGVAAGALNPFISA  
GEALIGDILYGTRYAIDKAAMRNIAPIPAEGKFAAIGGLSAGFEKNTREAVDRWIQENPNAETVEALVNVLPFAKVKNLTKAAKPKGAASVSDFSKSYTCSFHGSLVKTADGYKAI  
ARIQAGDRVLSKDEASGETGYKPVYARYGNPYQETVYIEVSDGIGNSTLISNRIHPYSDGWIKAEADLKAGSRLLSESGRTQTVRNIIVVKPKPLKAYNLVADWHTYFVRGNQAEBSGV  
WVHNDPCPKPKPTNHAQQRKEAKNDSHRSVGDNRVVRBGRQYLDSDTGNHYVYKGDVVLTPDGRQVTQPKNSKANTSKRKNGKMTFK

## SEQ ID 8147

ATGTTTGTATGGCGAAGTAGAAGCAGATGAAAGTTATTTTGGCGGACAACGCAAGGCAACGCGGTTCGCGGTGCTGCCGTAAAGTTCGCGGTATTCGCTCTTTGAAGCGAAATGGTAAGG  
TTTATACCGGTACAGTACCGAATCTCAACCGCTACTTTATTTCTATTTATCCGTGAACAAGTGAAACCTGACAGATTGTTTATACCGGATTGTTATCGTAGCTATGATGATTAGATGT  
GAGCGAATTTAGCAATTTAGCTTCGCTGAAACTTCGTTTTCGTATCAATCACAGCACACATTTTGGCGGAAACGCAAAACCATAT

## SEQ ID 8148

MFDGEVEADESYFGGQRKGRGAAGKVAVFGLLKRNGKVYTVTVPTQTATLPIIREQVKPDSIVYTDYRSYDVLVDVSEFSHFSFAETSFSVSQSHPTFCRTTKFY

## SEQ ID 8149

ATGGGAAATGGACACCAAAATCAATCTTCCTTAGAAAAAGAAATTTTATCTGAGCATTTCGGGCGAGTATCTGATGATTTCGCCCTATCGGATTACTCCAAAAATAACATACG  
TCGTTATGGCGAATTTCTCTATCCAAATGAAAAATGGATTGGGAAAAATTTAGATGATTGTTGTTCAATGAGTTGGTTTATAGGAATTACAGTCTTCATTATGAGATTGGTATCCAACTAT  
TGAAAGGCAATTAGCATCATTTAGAGACTTTTCG

## SEQ ID 8150

MGNHGQNNQSSLEKRIFFYLEHSGQYLMICALSDYSQNKHTVVMANFLYPNEKMDWRNLDLPLNELVLEELQSSFMWYPTIEKAISSHLEDPS

## SEQ ID 8151

TTGCAGGTAAATATCAAAACATTAATTTAAATCATATTTTACAGAAATTTCCGCCGCTTCACCAATGACATCAAAACCGGTTCCAAATTTCTGTAATTTGCAACAAAAACCGCAA  
AACCCGATTGAGACCGAAAGGACTTTCATA

## SEQ ID 8152

LQVKYQITINLNIPTFYSAAFTKWTNRFQISVILQONTAKHPIETERTPI

## SEQ ID 8153

TTGAGTTATCTCTGTAGAGAAAAATCCATACGCGAAGCCGTTGACCGGTGGATACAGGAAAAATCCCAATGCCCGCGAAACCGTCGAAGCCGCTCTCAACGTTGCCCGCCCAAGTCG  
CGAAGCTCGCAAGCGCGCGAAACCGGGGAAAGCTGCGGTTAGCGGGGATTTTTCGATTAGCTATAAAACTTTTCTACTGTCAAACCAAAAGTAATGCCAAAGGAAACGATTAATGGAAA  
GACTTTTAGAGATGTTAATCAAAGTGCAAAAATGGATCGCTGATTACCTACATTAATAGCCCAACGAGTTAATGCAAAAAATCCAAAGCCGAGCGTAAACCTCGTCCGAATGCAACCGTT  
GCTAATTCACATGCTGAAATTTGGTGTATCCAGCAGGCTTATAATGCAGGTGAAACGAAAGGGCATCTATGACAATGACAGTTTCAGGAAAGATGTTTGGCGTTATTGTAAGAGAGATA  
TTGCAGCTGCTGCTCAAGCTTCTGAGTGAATCACTGACTGTAAATGCGACAGATAATGTAAACAGGAAAAATAAACTACTATTGGACCGCTGTTATGAAATCAATTAAGGAGAGAAA  
A

## SEQ ID 8154

LSYLSIRENSIREAVDRWIQENPNAETVEAVFNVAAKVAKLAKAAGKGAASVSDFSISYKNFTSVKPKVIAKGTINGKTRFVUNQSAKIGSPDSPTLIAQRVNAKIADGKPRPNATV  
ANSHAEIGVIOQYAGNETKGAASMTWTSGKDVCGYKGDIAAAQASGLKSLTVNATDNTGKNTYTYWTPGMKSIKBRK

## SEQ ID 8155

ATGAAACATCAACAAATGTTTGGTGGATTTTTATTACAGATAATGGAGAAGCAATCCCAATCCCTATTTAGAAAAATCTAACATTAAGAAATAAACTTTTCTGTATCAA  
ATTTTGAAGAAAGCGGAGTCTTGTTCAGAAATATTCCTGAGCCTGAATTTGGCAATCTGAATTAACATCTATTTTGAAGAAAGATATATTATACCAATTAATCAACAAATTTT  
AGAAGATGGAGATATTGAATAAAAATCTTAAACAGAAAAATATAGTGGAATAACAATGAAATTTTGGGAGACGCTACCTATTGAGCATATCTCTAAAAATATTCTATATTCAA  
GATATAATTTCTGAATTTATTATGAAAAATAAACCAATCAATAATGATT

## SEQ ID 8156

MKTSTIVFGGFTITDNGRIQIPLENPNIKENINFFSVSNFEKKAGVLVFRIIPEPEFGNTELTITYPEKGYLPIIQTILEDGDI EVKKNLKTENYSGNTWELGDVUPIEHSKNISIIQ  
DIISEFINKNPITIMI

## SEQ ID 8157

ATGAACACGACAGCCGCGATCTGACCGCATCAGCCACAACCAAAATCGTCGCCACCTTTGGCGCGGCGAGCAACACGTCGAACGTTGGAAGACATGATCCGCGTCCGCGCCCTGA  
ACGTCGTCGCGCTTCAACTTCAGCCACGCGACGCGCGAATTCATCAGGAAACGCGCGCATCGTGGCGGAGGCGGCAAAACGCGCGGACAGGAAATCGCCATCATTCGCGATCTGCGGG  
CCCGAAATCCGCGTGGGCAAAATCGCGCGGCGCGCATCGAATGAACAAAGGCGAAACATTGGTACTCGATGCCGCGCTCGAAGGCGAAGGACGCGCGAGGCGGTCGTTTGGACTAC  
CGCGACCTGCCGACGACGTTGCCGCGAGCGATGCTTGTGGCTGGACGACGCGCTGCTGACCTGACCGTGAATCCGTCGAAGGCGAGCAGGATTATCAAGGGTGGAAACAGCCACA  
TCTTGAAAGCAACAAAGCATCAACAAACGCGCGCGCGGTTTGTCCGCGAGCGCGTTGACGCAAAAGACTTCCGCGACCTGAAACCCGCGATTGCCATCGGTTGCGACTACCTCGCCAT  
CAGCTTTGTGAAATCCGCGAAGACCTGCACATCGCGCGCGCAAGTGAAGAGGAAATGAAGGCGAGCACTGCCGTCGCGCCCGGTTTGGTTTCCAAAAATCGAACCGGTAGAAAGCGATT  
GAAACCTTTGATGAAATCATCTTCCGCGGCGAGCGCATATGCTTGGCGCGGCGACTTGGCGGTGAAAGTGCAGACCGCGCGCTCCCGCGCTGCAAAAAACGATGATCCGCGCGCGCC  
GCGAGTTGCCGCGCTTCAGCATTCGCGCGAGCGCAATGATGGAATCGATGATTACCAACCCGTCGCGCGGAGTGCAGCGATGTGCAACGCGGTTATGGAGCGCACCGATGC  
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ACGGAGTATCCGGAAGCCGTCAGCAACCACTTAGCGATTGCGCGCGCGCGGTGAGCGTGGCGCGCGCGGTTACGCGCAAGCCCATCGTCCGCTGACCGAAAGCGGTTGACCGCGCTTTG  
AAATCAGCGCGCAATATACCTGCGCGATTTCGCGCTGACCCGAGCGGTTTCGCGCCAAACCGCGTATGCGCGATGATACCGGGCGTGGCGCGCGGATTTTGGCAACGACGACCGACCA  
CGACACGCGGTGAAACGAAGTCGAACGATGCTGGTGGAACACAATCTGCAATTCGCGCGACGAGTACATCATCACCAGCGCTCGCAATGCGCGAATCCGTTTCGACCAATACGCGT  
GAAGTCTGCGCGCTCAA

## SEQ ID 8158

MNQTSRDLTRI SHNTKIVATLPGSNVVELLEDIMIRVGLNVVRPNFSGHTPEFHQENARIVREAAKRAGQETAIADLQPKIRVVGKIAGGGIENLNGEYLVLDAALEGGSTREAVGLDY  
ROLDDVAAGDVLWLDGLLTATVESVBSRIITRVENSHILSKNKGINKRGGSLAGALTEKDFRDLTATAIGCDYLAISFVKSAEDLHIAKVEEEMKGSFAVRPLGVSKIERVEAI  
ENLDEILLAGDGLMVARGLAVEVGAHAVPALQKRNI RRARELRPSITATQMMESMITNVPVTRAEVSDVANAVLDGTDVAVMCSAETAVGAYPTFETVSQMAIICAAAEKQDSLNGVABQ  
TEYPEAVSTNLALAGGAVSVARAVHAKIATVALESSTAFESRHNLITLPIPALTPSVAQRMMYRGVRPLILATSTDHDTALNEVETMLVEHNLHSGDQYIITSGSQMRBSGNTWL  
EVLEVK

## SEQ ID 8159

TTGAAAGTTCAACAAATCAAAGGTCGCGTGAATCGTGTAAATTTTCAGACGACCTATTTCTCTCATTTGAAACAGGATATTGAAAC

## SEQ ID 8160

LKSSTPIKRSPEIVFNQTTTFLHLKQDIEN

## SEQ ID 8161

GTGCAAAATCCGGCAACATCGGATAAAATCGAGTGCCTATACTAAAGCGAAACAAGGCAITTTCCGACTGCTTTTATTTGTCCACGTCGCGCTTTTACGGAACCGAAATGACCCCTT  
TCACACTGAAAAACCGCTCTGCTGCTGCGCACTGCTTTGCCGCGCATCTGTCCACGCACTCCGCTTACCTTGGCACACAGTCGGTCAACGCGCAAGACGCGAAATGCCGCGGAC  
GCGTCGACCATCTTCTACAAATCCCGCGGCG

## SEQ ID 8162

VQTRQHRKSSAYTKAKQGLSDCLFYLSVRLPTETETPTFLKPSCCSALPLPPLSLTHPATTSASRSSTRKARQMPPTRRPSSTIPPA

## SEQ ID 8163

GTGGTCGCGGACCCCGGATACGGGCAATGGCTTTGTAGCCGCTGCGCTTTTGACCAAGGTGCTGCGGTGGAAGGGCAGGTGTAGGATTTTGAAGAACTTAGTTTTCATATCTCTGTTTC  
AAATGAAGGAAATAGGTGCTCTGAAATTAACACGATTTTCAGGCGACCTTTTGATTGT

## SEQ ID 8164

VVADPTGNGFVAVCRFDQGAVERAGVGLKLVNLFQMKIEIGLIKHDPRFPDC

## SEQ ID 8165

ATGTCGCGGCAATCAGCGGCGGACAGGATACCGCCATAAATGCCACCCGATGACCGTACCGATCAGCAAGCGGTTACCAATACCGGCTGCGCTCCCATCAAGGCAACGCGGACATC  
CCGCCAGCAAGCCAGCAAAATACCGATAAAACGCGCGGATATCAITTTAAATTCAAAAATTCGGCAACAGGAGGAACCTGCGCTTTCTGAAACCAACGGAATCAAAACCCCTATGTT  
CAAAAGATGATACCGAGGTCAACCCGCTCTCTCGACCAACGGGCAAACTGTACCAATGCGGCTGCTGTCATCAGCAGCAATATGTTGCCGAGAGCGGTAAATCGAATTTGTTGCTG  
ACCACCCCAACAGANTCAGCGTAACAGAAACAGGGGAACAAACTGAAATTCATCGGTTACGACACCTTGACCAAGATTCCTTCGCCAGC

## SEQ ID 8166

MSAAISGPTGIPPINATPMTVPISKPVITGCRPIKGTTPHPASQATRIPIKTADIILKPKNSATGGTCAPPETNGLKTPMVKRMIPRPNPCFSTNGTCTNAVCCISSNVAETVIELLLL  
TTPNRISVTRNRGTCLKFIGYDTLTKDSFAS

## SEQ ID 8167

TTGCATCGATTCAITCCCGGATATAGCGCAGGTCTTTCTCCAGCCATTTCCCTTCCAAACAAAGAACAAAAAGCGCGCGGCGGCGGATGCGCCCTTCCTTTACAGGTTCCCTATTTTT  
TAACCGCAGGCGACCGGTTTGGCGGGGCTTTTGGTGGCGGCGGCGGACGGAAGCTGGTCTTTACGCTTCGCCAGCACCGCGGACCGATGCGCTTCACCTTGATCAATCGTCCAC  
AGACTTGAAACGCGCGCTTTTGGCGCGGCTATTCGCAATGGCTTCGCGGGGCTATGCCCGGCGAGCGCTCCAGCTCTCTGCTGCGAAGCGCGATTTGATGTTTACCGCGCGAAGGAGAG  
GCGCAGGAGAACAGCATACAGAAACATACAAACATTTTTTTCATGTTTTTCTTTAAGGTTTGCAAAACAAACCGCATCTTGCGACGATATGCGCGATTAAACAAAAACCGGTACGCGG  
TTGCCCCCGCGGCTCAAAGGGAACGATTCCCTAAGG

## SEQ ID 8168

LHRFIPRYSAGLSPAISLPNKQKSAGGSRCPFLYRFYFLTAGSTGLAGPFGAGAPTEAWSFSFSTAGPMPFTLIKSSDNLNAPFCARYSAMAFAGPMPGSASSSCCEALMFTAAREK  
AQENSIQNNINLFPVPLRVANNKPLATITWRINKNRYGVAPPRLKENDSLR

## SEQ ID 8169

GTGCTGCCGAGCATTCATTATGAAGCAGATTCCGCCACCGACTTTACCGGGCTTCCCGTCCAAGGTTCTAAAAACGCGCAAAATCAACAAAACCGGTCGACCCCCACATTTACGGCGCAT  
ACAAAGTCAACGACAATCTGACCGTGGCTTGGCGGTGTACGTCCCTTCGGCTCTGCCACCGAATACGAAAAAGATTCCGTGTTGGCGCAACATCAACAACTCGGTCTGACCAGCAT  
CGCGCTCGAATCTGTGCGCGGTGGAATCAACGAGCGCATTCCTTCGCGCGAGGATCATGCCCAACATAATTCGCGCAACTGCGCAATATGCGCGAC

## SEQ ID 8170

VLPSIHYEADSATDFTGLPVQSGKNKIKTTVAPHIYGAYKVNNDLTVGLGVYVFPGSATFEYKDSVLRNINKLGLPSLAVEFVAWKLNNRRSPGAGIIAQHNSAELRYAD

## SEQ ID 8171

TTGGGATATAGAAAAATAAAGAAAGAACGAGAAATGATGCTGCTATTTTTTAAAAAGGAAAGAGTTATATATACCGCGATGTAGATTACATAATGAGGGGCTTGAAAGAGCATCTT  
CACCCAAAAATCTGACAGAAAGAAACAGAAACGGTACATTTGATAAAAACCTAAATCGTATTGAGAT

## SEQ ID 8172

LGRIKIKERTNDAAIPKKGKSYLSRDVDSHNGAWKEASSPKNLNRKETRNGTFDKNLNRIGD

## SEQ ID 8173

TTGAGCAGCGGCGAGTAGGATTAGAAGGTGTGCTTGCAGCATTTGCGCTTTTTTGGGATTCTCTAGTCGGCATATTTGCCAGTTTCGGCGGAATATGTTGGCGGATGATGCTTGGCGG  
AAGGAATGGCGTTCGTGTAGTTTCCACGCGGCGACAGGTTTCGACGCGGATGCTGGTCAGACCGAGTTTGTGTATGTTGTGGCGCAACACGGAATCTTTTTCGTATTCGGTGGCAGAGCCGA  
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GGTAAAGTCTGGTGGCGGAATCTGCTTCATAATGAATGCTGGGCGACGAGATTTGGCGTTGACGGAATCTGGCTGCTGTCGAGTTTGGTCAGGCGCGGGAATTTAGAGATGTTGCGAC  
GCGTTCGGCGCATTTGCGGTGCTTTGCGGCTTGACCGACTGTGTGCGAAGTGTAGCGGATGCTGGACAGATGCGCGCGCAAGGCGAGTGGCGGACGAGGAGCGTTTTTCAGTGT  
GAAAGGGCTCATTTCCGTTTCCGTAAAAAGCGCGGACGCTGGACAA

## SEQ ID 8174

LSSGSRIRRCLOHLRFPWDSVGIQFQGLMLGDDACBGMFVEFPRGRFDGAGQTEFVDDVAHQHIFVFGGRAEGDVHAQHQIIVDFVCAVNVGCDRGDFAVFRTLDGKP  
GKVGCGICFIMNAGQHDVGVGDLAAVEFGAGGIVEDGRRVGGICRALRVDRICAEVVGACVDRCGGKSABQQDGFPSVKGVISSVSKRFRVDFK

## SEQ ID 8175

ATGTGCGAGTTCAGGATTTTGAAGAAACATCCCTTGTTTTGAAGATATGACGAAAAATTCATTTATGGCAAAATGGTATGATGACGGAGTGTGGGATGATGAAGAAATTTGAAATTTGG  
AGAAATGCTTTAATCGAGGTTAGAAAAAATATCCTTATCCGATGGATATACCAAGGACATCGTGATTGGAATCGGTACCATTTATGATTTTTAATGTTTCAAAATTTGAAACTTTTTGA  
AATTAAGCTTCTCTGTTGCTTAAAGTGTCAAAATTAATGAGCGTTATGAAGGTTTACAGATTAATGCTCCGTTATATTTTACTGATCTAGATGACAGGACTGGAAATTTTTTAC  
TTTCCATAACATAGTAAAGGTAGATTGAGA

## SEQ ID 8176

MCEFKDFRNI PCFREYDENSFIGKYYDDGVWDEEYWKLENALIEVRKKYPYPMADI PRDIVIGITLIDFLMVQNWKLFEIKASFWLPSVKINERYERFVMLRYIPTDLDAEDWKFY  
FPIQHSKGLR

## SEQ ID 8177

ATGCTGCAAGCAACACCTTCTAATCTCTACTGCGCTGCTCAAAATCAAGGCCGACGGACGCGGATGTCAAAGGCAGCGATTGGGGCGTGGCTTACCAACTGGCGTGGATGTGGGACATCA  
ACGACCGCGCGCGCGTGGCGGTGAATACCGTTCCAAAGTTTACACACGCTCAAAGCGGATGGCGCGGAGATGGCGCGGCGGCGGGAACACAGTGAATGACAAATATGCTCAC  
ACCGCTCGGTTACACGCGGAATGAAAAAGCCAGTGTCAAATCTGAACGCGCTGAGCTTTTGTCCGTACACGGCATGTACAAAGTGTCCGACAAAGCGGACCTGTTGGCGGACGTAACTTGG  
ACGCGCCACAGCGCGCTTCAATAAGCGGGAATCTTTTTTGAAGAAAGAAAAATATGCTTAATGGCAAAAAATCCGACCGCACCATCATCCCCAACCTGGCGCAACACTTACAAAGTGT  
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CTGGTCTCGCGCGGATGAAATACCATATCGGCAAAACACGCTGCTGATGCGCGCTACACCCACATCCACATCAACGACACAGCTACCGCAGCGGGAAGGCAAGCGGCAACGATGT  
GACAGCAAGGTGCGTCTTGGCAGCTTCAAAACACCGCGACATCATCGCGCTGCAATACACTACAAATTCAAA

## SEQ ID 8178

MLQATPSNPTAAAIKADGHDVKGSDWGVGYQLAWMDINDRVRVGVNYSKVSHTLKGDAAWADGAAAKQOWNMLTFLGYTANKEASVKIITPESLSVHGMKYVSDRADLFGDVTW  
TRHSRPNKAELEPFKEKNLANGKSDRTTITPNWRNTYKVGGLGSYQISEPLQLRWGLAFDKPPVRNADYRMSLEPDGNRIWFSAGMKYHIGKNHVVDAAYTHIHINDTSYRTAKASGNDV  
DSKGASCARPKNHADIIGLQYTYKFK

## SEQ ID 8179

ATGCTGTGAGTTCAGGATATTATAAGAAACGTTCCTATTTTGGAGGGTATGACGAAATTCATTATTGGCAAATGCTATGATGACGGGGTGTGGGATGATGAAGAATATGGAAGTGG  
AGAATGATTTAATCGAGGTAGGAGAAAAATATCCTTATCCGATGGATATACCAAGGATATCGTGATTGGAATCGGTACCATTTATGAGTTTPTAATGGTTCCAAATGGAAGCTTTTGA  
AATTAAGCTTCCCTTGGTTACCTGATAGCTGGGAATTAACGAACGTATGAAAGGCTTAAAACAATGCTCCGTTATATTTTACCAGAGAAAGACATAGTCAACGTGCAATTTGATTAT  
TACAACAAAAA

## SEQ ID 8180

MCEFKDILIRNVPYFEGYDENSFIGKWDGVDDEEYWKLENDLIEVRRKYPTPMIDIPRDIIVIGITIEFLMVPWNKLEIKASFWLPDSVGINERYERLKTMLRYIPTERDIVNVQFDY  
YNKK

## SEQ ID 8181

TTGAATATGGCGATGGCTTTGTAGCCGTCTCCGTTCTGACCAAGGTGCTGCCGTGGAAGAGCAGGTGTAGGATTTTGAAGAAGTTAGTTCCCAATATCTGTTTAAAAAAGGGGAA  
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## SEQ ID 8182

LNMGDGFVAVCRSDQGAVERAGVGLKNLVPNLFKIRGRSPEN

## SEQ ID 8183

ATGCCCGGCTGCCGACCGACTTGGAAAACTGTCTGAAAAATACCTCGAACAGTTCGGGCGGTATCGGAAAGTATCGAAGCCTGTACCGCCAACTGCAGGAGCAACCGTCTCTTCA  
ACAGGCTGATGAAAGCCAACGACAGCTCAACAGGAGATTGACGTGTTGCAGAACAGTCCGACGCCATCCACAAAGCCTATATCGAAATGAACACGCTGCTTTACCGCCATCGCGA  
AGTAGTTTCCATCCACAAACCGCAAGCAGATTATCGGAAAAAGGGCAAGAGCGGATTCGCGTGTTCGCCGCGGTTTGAACGGCATACCAAGCTGCTGCCGCGCTCTGTGCCCGAG  
CGTCCCTACCATTTTGATATGAAGGAGGTCTGTATATATTTCTCCGAATACCGAGA

## SEQ ID 8184

MAGCLTDLENCKEYLBQFPVSEIEACTAKLQEQSPFFNRIMKANDKLNQRQIDVLQKQSAAIHNEAYIEMNTLLYRHRREVSIHNRKADYAEKGERIALFPRLNGITKLPAAVILLPE  
RPTHFDMKEVLYIPSRIPR

## SEQ ID 8185

TTGAATAGGATCAAAAATATGGTCAAGTAAAGTCCGCTAATTCGGGTATTGAAACAATCCAGCCAAACAATCTATAAAAAATATTTCTCTACTTCAAAATGAAGACAAAGTATGATCATG  
TCATCCCTAAATCTAAGGGTGGTCAAGGTACACCTAAAAACGGGCAGGTATTATGACAGGGCTGCAACATTAAGAAGAGTAACAAA

## SEQ ID 8186

LNRIQNGNQVKCANCIETIPAKQSIKNI SPTSNERQVDHVIPKSKGGQGT PKNGQVLCRGCNIKKSNK

## SEQ ID 8187

ATGAAATCGAACTTACTGTCTCTATTACGATTTGGAAAGCAATATTGCAGAAAGAACTACTGTGACGAAACATAATGCCTGATGGAATTTTCTTATTCAAGAGATTCTCTTTTCGCAC  
CGAATTTGGCTTTAAACGACATTGTTGCCATAGAACGTGAGGATAAGATGCTGTTTTTCGACCACTTGATAAAGCTTCAGGAAATACCAGATAAACATCGTTGTTTGGATCATTTCCC  
AAGGATTTATTGGCAGCCATAGAAGAACACAGTGTGTAATAACGAAAAATGAGAGAAATATTATTATCGGTAAATTTCCGCCCAAAAAATATAATTCGATTAAAGGAATTTTAAAT  
AGATATGAGGAAGCAATATCTCTCAGTACAGGGAAGCTTGTPTTGGGCTTCTCT

## SEQ ID 8188

MKSKLTVVYVDLESNIAEELISGNIMPDGNFLIQEIPFAPNLALNDIVAIEREDKMLFPDHLIKASGNTTINIVLDFHPKDLLAAIEHSGKIRKNGENILSVNFPKKNYNDLKGLIN  
RYEENILSYREACLGFS

## SEQ ID 8189

TTGCCGTACTATCTGTACTGTCTCGGGCTTCGTCCCTTGTCTGATTTTTGTATTATCCGTATATTGTCCATTCGGCAGGGAAGCCTGAAGAAGAAATTTCCCGCAAGATGGCCGGCTG  
CC

## SEQ ID 8190

LPYLYCLRLRLVLFVNPFLYCPFGRESLKKMFARWPAA

## SEQ ID 8191

GTGGAAGGAGCAGGTGTAGGATTTTGAAGAACTTAATCCCAATATCTGTTTCAATGAAGAAATAGGTCTGTGAAATTAACACGGTTTCAGACGACCTTTAATCGT

## SEQ ID 8192

VEGAGVGLKNLIPNLFPQKEIGRLKIKHGRFRPFNR

## SEQ ID 8193

TTGACGGAATGCCGTCTGAAACCGTGTGTCGGTTTCAGACGGCATTTTGACCAATACGGTACGACGGGCAAAACAGCCGGCTTTCTGTGTTTCATGCTGATGTTTCAACACACA  
GGACGGCACATAAAGGCTGCCCTATGTGCCGTCC

## SEQ ID 8194

LTEMPSETLLSVSDGIL/INTVRRRKTAGFSCVSYADVSTHRTAHKASPYVPS

## SEQ ID 8195

ATGATGAGTGTAAAGAATTATTCAAAGTCATCTTAGATGAAAAATAAGATTTTCTATTAGAAGATTTCATCGTACCCCGATGGGATACCTTCCAAACCTGTTGCTTTAAGTATTGTTT  
AATATGAAATGACCCGGGATTTTATTGTTTATTGTTGATGAGACCGGTGAGGAACAAACGGATACCTTATCATGACACATAGATTCCGCATTGTAACAGGCTGAATTTGAATTTGGAAT  
CAGCAAGAGGAATGGATGCAAAAGTCTT

## SEQ ID 8196

MMSVKELFKVILDENKDFPIRTIERTFMGILFKPVALSIVQYENDPGFYLYLDETGEQTDYTHDTLDSAFBQAEFFGLSKEEMMQSP

## SEQ ID 8197

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GGCGAGGCCATTGCGGAATACCGCGCGCAAAACGGCGGTCAAGTCTGTGGACGATTTGATCAGGTGAAGGGCATCGGTCCGGCGGTGCTGGCGAAGCTGAAGAGACCGGCTTCGGTC  
GGCGCGCCCGCACCAAAAGGCCGCCAAACCGGTGCTGCTGCGGTTAAAAAA

## SEQ ID 8198

VILHILRESFPLSRGGATPYRLLIRHIVARCGLLFATLKGKTMKMFVLCMLFSCAPSLAAVNINAASQOELEALPGIGPAKAIABEYRAQNGAFKSVDDLKVKIGPAVLAKLKDAQSV  
GAPAPKGPAPVLPVAVKK

## SEQ ID 8199

TTGAACGGAGGACAAAAATGATTACACCGCAACAGGCTATCGAACGATTAATCAGCAATACAGAGTTGTTTACGATGAAATGACCGACTTGATGCCCAAAATGATGAGCGGAAAGTGC  
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GGACGGGCTGGTGCATATCGTCGGTACGGGCGGGATGGCGGAAAAACCTTCAATATTTGACGACTTCGATGTTTGTGCTGCAGCGGCGGCAAAAGTTGCCAAACACGGAGGCGCG  
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TGAAATGAACAGGCTACGACGGGAAAGAGGGGCGCGCGATATCTGTTTAAATACCGCGCGCGCTTATATGCCGGAATATCGCTGCTTTCAGACGGCATATCTGC  
CGCAGCGGAAGCATCGATTACAGTAGGGCGAAGCGAAAAAGAGAGTTTGTGCGTTTACACGGCAATTCGCC

## SEQ ID 8200

LANGGKMTTQQAIERLISNNELFYDEMIDLMRQMSGKVPPEQIAAILTGLRIKIVETVSEITAAAAHVCEFAKVPLEADGLVDIVGTGGDGATYNIISTSMFVAAAAAKVAKHGR  
SVSSSGAADVMEQGANLNLTPQIAQSIQTGIGFNPAPNHSAHRHAPVRRSLGRSIPNLLGPLTNPAGAPNQLLVFHTDLGILSRVLQQLGSKHVLVCCGEGGLDEITLTGKT  
RVAELKDKLSEYDIRPDEPGLSTRNLDEKIVANTQESLLKMNVELDKGEAARDIVLLNTAALYAGNIAASLSDGI SAAREGIDSGRAKAKKEFVGTRQFA

## SEQ ID 8201

ATGAATACCGTCCCAAAAGCAGGATTCCTGCAAAACCGTCCCGGAAAAACACAGCGAAGCCAAAGTCGAAAAATGGCGGAGCTCGTGCAGACACGCTTGTGCGGCGAATGGG  
CAGTGGCGCCAGATTGGCGGAAAAACGCTTTACTGAAGACAGATGGAATAATTCGCCAACCTGTTGGCGAGA

## SEQ ID 8202

MNTVPKSRIPVKPLPEKTABAKVEKWRQLQADHGLSGEWAVARLGENGTETEQMENIANLFGF

## SEQ ID 8203

ATGGATGCAAGATCCCTAGACGGCAAAATCAAGATGCCGCTTATTTTTCAGACGGCATTTCCTGCAATAAAAAAGTCGGTATTTGGAGCCCAAAACAGCTACGCTTGTCCGGGATAGGA  
TGAAATCTTTAAGAAAAATGATTATAGT

## SEQ ID 8204

MDAKSLDGKIKMPLFYSDGLSVNKKVIGAGQNSLRLAGIMKSLRKNDS

## SEQ ID 8205

ATGATTTATAGTTGAACATTTAGAACATTTATTTGGGTGAAATCGAAAGCGGTATAAAATGCTTGGATCGACGTTATCATCTCAGCGTTTCCTGCTTCCATCACAAACATATAAAGGGGTAA  
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GATGATGATTTTTCAGGCTCTGTTATGCGGAACACTACAATATCGTTTTCCTTTGCTTGTCTTGTATTAACAGGAAGCAGAAATTTGGTGGAAAAAGAGGTTGGAATGCTTTTACAGCACT  
TCTTGTGAATAATGAAGTTGACAACCTTTTCGATATGAAGCGGAAACCGTTTGTCTGG

## SEQ ID 8206

MITVEHLHYLGEIESGKICLDRRYHLSVSVFPSPQPYKGVTTSTLGLNRYDLYKSRFELFTCEEMNKENIAAFLSGVAEYLIDNRQPIRLGELIQLPRVIIIEGSKMDALVTSAPFFP  
IDDFQVCYGERHYNIPVLLVPLKQEAELVEKGNAPBQFLANNEVDNLSMKRPFAM

## SEQ ID 8207

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AAGAGTTGGTCCGCAACAGCGCAAGTGGCGCAGGAAAAATCAGCAACTGCCGACAAGCGCGCGCAGGACAGCGGAGGAATACCGCAATACCTCAAGCTCAATCGCACCGG  
GATGACGCGGCAAGCAGATACAGTATCTTCGCGGCTATTCATCGAT

## SEQ ID 8208

MYRKLIALPFFALLAACGREPPKALECANPAVLQDIRSIOETLTQEARSPAREDRQFVDADKI IAAAYGLAFSLHASETQEGGRTFCIADLNTVPSETLADAEANSPLLYGETSLA  
DIVQKRTGNNVEPKDGLVLAARFLPAKDARTAFIDNTVGMATQTLAALLPYGVKSI VMIDGKAVTTKEDAVRVLGSKAREEPEKPTPEDILEHNAAGDAGVQAEGAPEPEILHPDD  
VERADTVTVSRGEVEARVQNRASEITKLWGLDITDVQKELVGEQRKWAQEKI SNCRQAAQADQRYAEVLKLCQDTRMTREIRIQLRGYSID

## SEQ ID 8209

TTGGTAAGGGCTTCTTAAATTTGATTAAAGGTGCTGAAATTAAGCTTGTTTTTCAGATGGTCTTTCCTTCATTGAAGCAGGATATTGAGAAC

## SEQ ID 8210

LVRAPNLIKRGLSLPFRWSFLHLKQDIEN

## SEQ ID 8211

TGCCCCGCCGATAAAGCAGGCTGCTCCGTACTGCTATCTCACCATTACTTCTCCGCAATCGGCTTTTATCTCCCGGTTTACCCTTTTGGCAACTTCGCGGCTTTGGCGGTGG  
CAATGTTGAAGCGGCTTCGACGGTTTCGCGCGCATTTGGGTTGACCGCTACTCATCGCAACCGCAACACGACGCGGTGTTGCTTTTCAGCGCTTCCCGTTTGACCAAGGTGCT  
GCCGTGGAAGGACGAGTG

## SEQ ID 8212

LCRIKQVCLRTVPHIYPPAIGFYLPFTVFNFAALAVAMLKAASTVSAALGLTRTHPTATRTTFVAFQPSAVLTKVLPWKEQV

## SEQ ID 8213

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GTATCAGCTCGACAGAACCTGTATTTTATTCAAAA

## SEQ ID 8214

VKIKPLQFSNNHRFVYVDKICVTEQDVNIIASDRNYELNRIPIIDNI IHQITDESIVKVFSEYLFENKTENNSDGNPTANYFBEI IDOSYMDWLKEESPFPFEKKYKAYIFFFSDSVIE  
VISSTEPVYSK

## SEQ ID 8215

TTGACAGCCTTAACATTTCCCTAATATCTTCGCGCTTCGCTCCCTTCGGCGGATATAAAGAAAAACATTTTAGGAGGTCAACAGATATGGAATGGGCGTTTAAACAGTTATTACACCT  
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## SEQ ID 8216

LTSLNYSNIFALASPSGGYKEKHFRRSNDMEWAFNSYTLIAATLVLLVGKLVKKIRLLDFNIPFVAGGLIAAIIILFALHEAYGVSFKEKFLQNAFMLIFPFTSIGLSADFRLKAG  
GLPLVVFATVGGFVLVQNFVGVGLATLGLDPLIGLITGSVSLTGGHGTSGAGWPNFETQYLVGATGLGIAVTFGLVFGGLIGGPVARRLINMKRKPVENMKQDDNADDVFBQAK  
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## SEQ ID 8217

TTGACTCGCCTTGCCTACTATCTGTACTGTCTGTGCTTCTGCTGCTTGTCTGATTTAAATTTAATCCACTATACAATAATTTTTCACAAACAAATGCGCTC

## SEQ ID 8218

LTSLVLSVSVASSPCPDNLHHTTIFYKQNAV

## SEQ ID 8219

TTGCTGCCAACAACTTCGGCAAAATCAAGCCGGCAAGCCCTGCTCTGTCCTGTCGGAATCGGAGAAATGCGCTCTGAAAGCCGAATACCGCTTCAGACGGCATTC

## SEQ ID 8220

LRANFGKIKPASPCILQSEKMPSESRIPLQPAF

## SEQ ID 8221

TTGCTGCCGCTACTTTTTCGGAACAAATGGGTAAACATAAAATATCCTTAAAGATTTATTTTTCATAGGTTGTGCGCCCTCCAAATTCGCTGCCAACAACTTCGGCAAAATCAAGCG  
GCAAGCCCTGCTATCTGTGCTCAATCGGAGAAATGCGCTC

## SEQ ID 8222

LLPFPFGKLGKTNILNLFPIGCRPLQIACQQLRQNAQKPLHFPVIGENAV

## SEQ ID 8223

GTGAAGCAATCAAGCGTCCGACTTCACCGACGAACACTTCGGACTGCCGACCATTCCTGGACATCTGTCCGAGCTGGAAAAACCGCAGCCGGAACGGACAGCCGGCCGCAAAACCAAA  
CGCAACGAGCTGTGCCAACCAATTCGGCGATGGCGATGCGTTTGGCAAGTTGAAGCGTAACTCCGACAGCAGGATGTACAGCGACAGATGACAGCGCGGCTTTTCCCGCCGCTTTT  
CTGTATTTCAAATATGTGATTTCCCATGATGCCCTC

## SEQ ID 8224

VKQIKASDPTDEHFLPTILDILSELEKQPRTDSRPQTTTQACPNQFGDGGCVCEAVSPTAGMYSRCSGGFCPRFPCYFKYVYSHDAV

## SEQ ID 8225

ATGGGAATACACATATTGAAATAACAGAAAAAGCGGGGCAAAACCCGCGCTGCTCTGCTGTCATCCCTGCTGTGCGACTTACCGCTTCAACTTCGCAAAACGCTACCGCATCG  
CCGAATTTGTTGGGACACGCTGCTGCTGCTGTTTGGCGCGGCTGCTGCTTCCAGCTTCGGACAGAAATGTCAGAAATGTTGGCGAGTCCGAGTGTTCGTCGG  
TGAAGTCGGACGCTTTGATTGCTTACCGCGCTCGCGGTAACTGCCTAAATATGAAATCTTGGTCTCTCTG

## SEQ ID 8226

MGIHIFETEKAGAKPAASVAVHPCCRTYRNFANASAIJELVGRSLRGLRPAVRSRLRFFQLGQNVQNGRQSEVVFVGEVGRFDLLHALAVNCLNMKFLVFL

## SEQ ID 8227

ATGTTTAAAAAATCAAAACCGGCTACTGTTGTCATTTTTCGACTGTATTTGCTTTTGGCTGGGAACAGGTATTGCTATGAGATTAATCCGCGTGGTGTGAGCGATACGGCAACTG  
AAGTACTGAAATTCGAATGCTTTTGTGGGAACTTGGCGGCTGTTCGGAATGCGGACAGGGCGGTTGTATCGTGAAGGAATCGATGAGGACGAGGAAAGCTTGGCGGAGCTGT  
GGATGACGCTCCGTTGAGTGGGAGAGGATATCTCGCGCTCGCTATCCGCTCAGTCTGTTGAAAGAAAGGCGAAATGGTTTCACTGTAACGGACAGGAACATGGGGAAGAGGTTTGG  
CTGGATTACTATATCGCGGAGGGCGGTTTGGTTGCGGTTTTCGCTTTCGCAACGCTCGCGGAGCGGTTTGTAAATGCCGAATATCTGTATCGGAACGATCGTCCGTTTCTGTAAATGTGT  
ACGGCGGAGACGCTTACGGGGAATAATGAAACGACAGGAGATATCGGGTTTGGCAACCGGACGGTTCGGTATTGTATCGCGCGGCGCGGAAATCGGGGAAGATGTTTATGA  
GCATTGCTCGGGGTATGATGAGTGGCCAGGTATATTGGCGAAATACCGGGATGTCGCGAATGACGAGCAGAGAGGTTTGGGACTTCCGCGAAGAGAGCAACCGGATGTCATCGGACTCG  
CGCGATTATGCTTTTATCAGAATATCGGGGAATGATGCGCGGGGATGAAGCGCAACAGTCTTGTGTCGCTTATGATCGCGGAGCGTTCGCGCAAAAGCTTATTTGAGTTTCGACA  
ATGGAAAAACCGCGAGTTCGAATATATTGAAACAGGAAATCTTTTATGTCACAATCTTCGACGGTAGCATTTGAAACGGATGCGGTAAACCGGATATGACAGCTATCATGC  
GCAACAGACGTGTTTGGATGGCGGGCGGATATCGCGAAGAGAAACAGGAGACAGACTGCTGATTTCTTTGAACTTGAAGATTGGAAAAAGAGGTGAGCGGTTATGTCAGAG  
GCTCGCGGAGAGCTTCGGCGGCGAGCGCGGCTTCTCAC

## SEQ ID 8228

MFKFKPVLSSFFALVAFWLTGTGIAYEINPRWFLSDTATEVPEPNFPAKRLARLPNADRAVVIVKESMRTEESLAGAVDDGFLQSEKDYLAALRLSLRKEKAKFWHVTEQHEGEVW  
LDYITIGGGLVAVLSQSPFAFVNAEYLYRNDPFSVNVYGGTAHGENYETTGAYRVVWQPDGVSFPAAGRGKIGEDVYEHCLGCTQMAQVYLAKYRDVANDEQKVDPFRESNRIASDS  
RDYVYQNMRELPMFRMKANSLVVGVDADGLPQKVYVSFNGKRRQSFYLLKNGLFLIAQSSTVALKADGVTDMDQPYHAQQTWYLDGGRIIRERQGRDLDFPLNLEDELEKEVSYAE  
AAARSQGRGLSE

## SEQ ID 8229

ATGGGATTTATAGAACCGGTTTTTATCAAGCTATACACTTTATCAGGAGATTATGTACAAGCTGCTACTAACCGAAACGCAAAACCOCTACTTTCCAAATCGTATATACGCACTCTGGCT  
TTCAGCGTTCAGTAACGAAACTCTAATATTCGCAAAATAAATTTCTGATTAACAGCTGCTGCGAGCTCCACAAGGCAAGCTAAATAAAAAGAAATTTGCCOCCATGATGTTAGTAGA  
CTTAAACCTTTCAACAGATTTATCTAACCGAAACAGAAATGAATGATTTTCAACAGGGAATAGAAATCAGGATTTATGAAACGAAATACAAATCAAAATGATTTATGAAACCTA  
TTAGACAAATAGACGACTTAAACAGAGTAGGTGATGACTTATATTTGCTGAGGATGCCAACGTTATTTTGGTAATTTGGATGAAATTTACTGTAAGGAAACCGGACCCCTATTATACATC  
GCCTATACAAACCAACTTCAAGAAAGAGTGAAGAACATTACGGTAATGTGAATGTATGCTGGAACCACTTGCCTATCTGTTGATTTGACGAGTATTAAGCCTTTTCATCTGCTG  
GGATGATACCGAAGCATACGACCCAAATAACCGCTTCTGATTAAGTCTGATGAGCTTATTTGATTTGAAATATATTTGCTTTGATGATGAGGAAATFATGTTGAAATCTAAGCGG  
TTATCAGATGATGTTTGGCGAGCTTGGTGTGATGTGAAGCTAGATAAACAATCTGCTCAACGACAAACGTAATCTTACTTGGCATATCATGAGAGCTTATGCTACAGAAAGACCAAGAT  
TTCAATAT

## SEQ ID 8230

MGFIEFPLSSYTFPLSRDYQARTNRKQTLKSKIVYTHSGFQSVTENSNIQINFLIKTLVEHPQGLNKKKEIAAMMLVDLKTFFQDDYL/TETELNDYFQOGIESGPIERKYNQISYLMNL  
LDKLDLKRVDGLYFAEDAQRIFGNLDEITVRKRPYLRHLYKNQLQEESEHYGNVKMCKLEKLAIPVLIASHIKPFLISDDTFAYPDNNGLLSRLTDLDFDKYISFDDGNNMVKSR  
LSDDVWRWCDVKLDNLLNKKRSYLAHREMLQEDQEPHI





**SEQ ID 8242**

MHTFLTYIDLFSGAGGLSLGFEQAGFQQLLSVEMESDYCYPTRTNFRHQLLQKDLTTLTBQDLTNCLNGQSDVLVIGGPPCQGFSGNAGIKRPTTDDPRNHLKPEFVRIVKIQVPYFFVM  
ENVARLYTHNSGKTRIEIIQAFQNIIGYSVECKILSAADFGVPQIRSRVPIGRDDKGISFPEPLQISHQTVGSAIGHPPKLAAGESNPHVANHEAMNHSQAQMLEKMAFVKNGGNRNDIPE  
PLRPTGDIRKYIRYNSNKPACVITGDMRKVPHYEQNRALTVRELAALQSFNDNFTPCGSKIAQQQQVGNNAVPELLAKALAESILKNSENE

**SEQ ID 8243**

ATGAAACGCGTCAAACTGGAGCGTTTACTCTGATATTGTGTGAAAAACAGCGCTTCTATTGCGGTATCAGCCGAATCCGCAACAGCGGCTTGCCATCCACACAGCCGGAAAAAGCGCGAAAT  
ATACCCGCGTATTCAAACCGGTGGCGATCGGTATCGTTGCAGGCGCATGGATAAAGGCACCTGCGCTCAAAACAGGAAATCGCCGTCAAAAAACTGACCGCGGCACAAAAACGGCAATTGTG  
GGAACAGGCAGAAAAAATGCCGCTGTGAAACC

**SEQ ID 8244**

MNASNWSVYLILCENSAFYCGISPNPQORLAHTAGKGAKYTRVFKPVAMRIVAGGMDKGTALKQELAVKKLTAAQKRQLWEQAEKMPSET

**SEQ ID 8245**

GTGGCCGCGGTAATCAGGACGGTCAATAAACAACTTCCTTTTCAGATTGTATCGGGCAAGATATATCAGTATTATCTTCATCTTTTCCAAACGATTACCCACATITGGCCGCTCGGCTGTTC  
AGACGGCATCACGGAGGCAATTATTAACACATCACCGAACTCTCTCCCAAGAACTCTCCGCCACTACCGTGCAGAAATCAATGCCGCTATTCAGAGCTTTTGGACGACGGCGCGACCGCTCCCTTT  
TATCGGCGGTTACCGTTAAAGAGACCACGGGCGGGCTGGACGATACGCAAGCTGCGCCAGCTTGGCGAGCGGCTGCAATACCTGCGCGAGTTTGGAAAGACGCGAAGGCCGTTGTGTAAAAAGC  
ATTGAAGAGCAAGCAAGCTTTTCAGACGACCTCAGGGCGCAAAATCGAAGCCGCCGACAAACAAACCGGTTTGAAGACGCTTACTTGCCCTACAAAACCCAAACCGCCGACCAACGCGCAAT  
TCGCGCACGAACACGGTTTTCAGCGCCGCTGGCGGACGTGTGTGCTTGCAGAACACGCGCAGGACGCTGGAAGCGCGCGCGCAAGGCTTACTGAAACGCAAAACATCCCGACGAAAGCGCGCT  
GGATGGCGCGCGCGGAGTTCTGATAGGACGATTTGCGCAAGACCGGGAATCTCATCGGACGCTGCGCGCACAGCTGCGCAAGCTGCAAGCGGAAATCCACACGCAAGTTCGTTGAAGGCAAGAA  
ACCGAAGGCGCGCAAAATTCACGATTTATTTTCGACCTCCGCCGCAACCGGTGCGCGCCATGCCACGCCACCGCGCGCTGGCGGTTTTCGCGCGTTCGCAACGAAGCGTGTGAAACATCGCGCTCA  
AATACGAGCCCGACGACACGCCGATTACGCGAGCAAGCGAATACGAGCAAAATCATCGCCCGCGCTTCAAGGTTTCAGACGGCCACAAATGGCTGCGCGACACCGTGCGCCGTGACTTGGCG  
CGCGAAATCTTTTTGTGCGCTGGAACCTCGAAGCTCTCAATCTGTTTGAAGAAGCTGCCGACACTGACGCGATTACCGTGTTCGCGCGCAATCTCAAGAGCTTTGCTGCTCGCGCGCGCGCGC  
GGGCGGCTGACCACTTTGGGACTCGACCCCGGCTACCGCAACGGGCTGAAATGCGCGCGTGTGGACGACACGGGCAAACTGCTGGATACGGTTCATTGTCTATTTCATCAAGAAACAATA  
TGTGGCAACGCTTGTGCGCGCTGATTAAACAACACGGTGTGAAGCTCATCGCCATCGGCAACGGCACCGCCAGCCCGCAAACTCGCGCGCAACTCGCGCGGAACTGTGCGCGGAATCCCGCA  
AAGCAGCTTGCACAAATCTGCTGTTTCCGAAGCCCGGCGCGTGCATTTATTCTGCGTTCGGAATCGCGCGCGCGGAGTTTCCGAGCTTAGATTTTCCCTCGCGCGCGCGTGTCCATCGCC  
CGCAGGCTCGAAGAACCGCTTTCGCGAGTTGGTCAAAATTCGCAACCAATCATCGCGCTGGGCGACTATGACGAGCACTGAAACCAAGCGCGGCTGCCAAATCGCTGGACGCGGCTGTGTG  
AAGACTGCGTGAACGCCCTGCGCGTGGACGCGAACACCGCCTCCGCCCTCTTGGCGGGATTTCGCGTTTAAATCAAAACCTTGGCCAAAACATCTGCGCTTACCGTGATGAAAACGG  
CGCGTTCGACAGCGCAAAAAAATTGCTAAAAATACCGCGCTTGGGCGAAAAAACCCTTCGAGCAAGCAGCAGGCTTTTTCGCGATTAAACGGCGGCAAGACGCGCTGACGCGAGCGCGCTC  
CACCCCGAAGCTATTCGCGTCTGTCGCAAAATGCTGGCGCAACAGGCAATTACCGCGCGCGGAACCTCATCGCAACCGCGAGCGTGTGAAGCAAAATCAAGAGCATTCGACTTACCGACGAC  
GCTTCGCTTTCGCGCATTTTGGACATCTCTGTCGAGCTGGAAAAAACCGGCGCGACCGCGCGCGTTCGCTTTCAGACGCGCATCGTTTTCGCGAAGGCACTCCAGAAATCAGGCACTTGCA  
AGTCCGGCATGATCATTCGAGGGCGTGGTCTCCAACGTGCCAACTCTCGCGCGCTCTGTGACATCGCGGTCATCAGGACGGCTTGGTGACATCTTCGCGCTGCTAATAAGTTTCGCTCAA  
GACCCCGCGCAAGTGTGAAAGCCCGGACGCTGGTGAAGTGAAGTCTGGAAGTCTGATCGCGACGCGCAACGCACTGCGCTGATGAGTACGCAACCGGCGCGCGCGCGCAAAAC  
ATPAAATCGCGCTTCAAAACCCGACGCGGACGAGCGGCGGCGCAACCGCAACGCAACGACGCGCGCGCGGACCAATTCGCGCATGGCGGATGCGTTTTCGAGCTGAAGCGG

**SEQ ID 8246**

VPPVIRTVINKHSFQIVSGKVYQYLLHLFQITITHIAPSAVQTASRRQFMNITRILSQELSQTVPQINAAELTLDGDGTPFTFYIARRKEATGGGLDDTQLRQLAERIQYLRELEERKAAVVLKS  
IEEQGKLSDDLRAETAEADNKTHALDVLKYPKRTKATQIAHEHGLQPLADVLLEKQDPVEAAAGQYLNENIPDKAALDAGARILMEQFAEDAELITGLRUKLWNEAEITHTQYVVEGKE  
TEGEGFSDFYDRRREVPAMPSHALAVLRGNBEGNTIALKYPQDDPTITQQSEYEQYIARRFSSDGHKMLRDTVLTWRAKIFSLSELEARNLRKEADDTATVTFARNKLDILLAAAP  
GRLTGLDGLPGYRNGVKCAVDDTGKLLDVTYVYLHQENNNMLATLSRLIKQHGKVLIAIGNGTASRETKIAGELVRGMPSSLEKTVVSEAGASISASELAAREFPDLDVDLSLRGAVSIA  
RRLQDPLAEIVKLDPKSTGVGGYQHDIWVQSRKLASLDVAVEDCVNAGVGDNTASAPILARISGLNQLTQAINVAYRDEGDAEDSRKLLKVPRLIGKTFEQAGFLRINGGKEPDLASAV  
HPREAYVPVAKMLAQGGITAAELIGNRERVQIKASDFTDERFGLPITLRLDISELEKPGRDPGAFQTPASFAEGIEHISDLQVGMILEGGVSNVNFAGAFVDIVGHQDGLVHISALSNKFPVQ  
DPREVVKAGQVVKVVLVDVAARRKLMLTRLDEDPGAKHMMENSRERSTAGRRKQPNDRAPTSNADAPAKLR

## SEQ ID 8247

CCGCGGTTTGGCCGTTCCAATGCAAAATGCCGTC

SEQ ID 8248

LREKICPIKPDFDAVIVRTAKKQKPIVANIARLLKNAATRRRFAVFMQNAV

SEQ ID 8249

TGTGTTTATGACCGTCTCTGATTACCGGCGGCACCGGCTTTATCGGTTGCGACACCGCGCTCTCGTCTGCTCCAAATCCGGTTACGATGCCGTGATTTTGGATAATCTGTGCAACTCGTCTGCGG  
 CCGTCTCTCCGCGCGCTTTCGGCAAATTACCGCGAGAAACATACCGCTTTATCAGGGCGACATCCGCGAGTCTCAGATTTTGAGGCGAGATTTTTCAGAAATGAAATCGAATCCGTCATCCA  
 TTTTCCCGGTTTGAAGGCAGTGGGGGAAAGCGTTGCCGAGCGCAAAATATTACGGCAACAAFGTTTACCGCAGCCCTGTGTCTGGCGGAGAAATATGCGCGCGCGGGCGGTGTGTAATAATC  
 GTATTACGCTCTGTGCGCAACCGTTTACGGCGATGCCGAAAAAGTCCCTTATACGGAAGATATGCGCCCGGGCGATACCGCTAATCTTACCGTGCCTCCAAAGCGATGGTGGAGCGGATGT  
 TGACCGACATCCAAAAAGCCGATCCCGGTTGGAGCGTGATTTTGTGCGCTATTTCAACCCGATCGCGCGCGCACGAAAGCGGACTTATCGGCGAACAGCCCCAACGGCGTTCCCAACAATCT  
 TTTGCCCTATATCTGTCAAGTGGCTTCGGGCAGGCTGCCGCAACGTTCGGTATTCGGCGCGGACATATCCGAGCCCGGACGCTTACCGGGAATCGCGGCAATCATCCATGTGATGAGATTTGGCA  
 GAAGGCGATATCCGCGCAACGAGGCGAAAGCGCGCGCTTCGCGCGTACGATTTGTCACTTGGGTTGGGAGCAGCGGCTATCCGTTTGTGAAATATCATCGCGCGATATGAGGCGCGCATCCG  
 GTTTGCACATTCCTTACCGAATCCAAACCCGCGCGCGCGCGCATGTCGAGTGTCTTATGCGCACCGCTCCCATACCAACAACAACCTGGCTGGGAAACCAACCGCGCTTGCGAGCAAT  
 GATGGAAGATTCGTGGCGTTGGGTCAGCCGCAACCCCGCGAGATATGGGGAT

**SEQ ID 8250**

LPMFLVLTGGTGFIGSHSTAVSLVQSGYDAVILDNLCNSSAAVFLRLQRTGRTNPFFYQGDIRDQCILRLQIFSEHTEISVIHFAGLKAVGESVAEPKTYKGNMNVYGLSLVAEEMARAGVLKI  
VFSSSATVYGDAAEKVPYTEDMRPGDTANPYGASKAMVERMLTDIQADPRWSVILLIRYFNPIGAHESGLIGEQNGVFNLLPYICQVASGRPLQLSVFGGDYPTPDGTGHRDYTHVMDLA  
EGHIAAMKAKGGVAGVHFLNLGSGRAYSVLEITRAFEASGLHIPYRIOPRRAGDLACSYPADPSHTKQOTGWETKRGLOOMEDSWRWVSRNPGRYGD

**SEQ ID 8251**

AGCTGTGTCGTGATATTTTACGGGGGTTTGCCCTCGGGGCTGCCGCTGACTTTCTGTATTAACCTGATTCOGGCGTGGTTCGCAGCGAGCAGGTTGGATTGGAAGAGCATCGGGCTGATGGCGT  
 TGATCGGCTGCGCGTTTACTTGGAAATTTTGTGTGTCGCGCGTGTATGGACCGGTCAGGCTGCCCGTTTGGGACCGCGCGCGGTTGGATGCTGCTGACGACGAGCAGGGTTACTGGCGG  
 TTGGCGGCATATGCTTTTAAACCCCCGGAATCATCTGCCGTGATTGCCGCTTGTCGGTGCTGTGCTGCTTTTTCGCGCAGTCAGGACATTTGTAATGGATGCGTTTCAGGCGCGAG  
 ATTTTGTGGGACGAAGAATTGGGTTTGGGCACTCGGTTCAATGTGAACGCTTACCGGTTGCCCGCTGATTCCTCGGTTCAITGAGTTTGGTGTGGGACAGCAGGATGCCGTGGTCAGAAG  
 TATTTGTTATCACTTCATTTATATGCTGCCCGGCTTCTGATGACGCTGTTTCTCGCGCAGAACCGGTGTTCGCCCTTCCGTTCTCAAAACGTTGAAGCAGACCGTGGTAGAGCCGT  
 TAAAGAATTTTATGCGCAAGGGCATCGTTTCGGCGGTGTGCTGCTGCTGTTTATCTTCTTACAACTCGCGGACAGTATGGCAACCGCGTGGCAACCGCTTTATCTGTGATATG  
 GGTTTTCAGCAAGACGACATCGTTTGAATGCCCCAAAATGACGAGCTGTGGCGGCGATGTCGGCGGCGAGTATCTTGGCGCGCTGTGGATGCTGAAATCCGCGCTCAAAAGCGCTTGTGGC  
 TATTCGGCGCGTGCAGGCAATATGATTTTGGGGTTTGTATGCGTGGCAGGGTTGCGAGATTTTCGACACGCTCGGCACAGCGAGAGGCTGATGCTGGCGGCGAGTTATCGGCGCGGAAGC  
 GGTTCGGCGTGGGGTTGGGGACGGCGCGCTTCGTATCGTATATGCGCGCGAGACCAATCCGCGTTTACGGCAACGACGCTTGCCTGTTTACAGGCTGTTCGCGCGTGGCGCGCAGGTC

ATCAATTTCCTTTGCAGGCTATCTGATCGAATGGATGGGTATGTACCGTTTTTCCGGCTGTGTTTCATACTTGCCCTGCGGGTATGCTGCTGCTGAAAGTTCCGCTTGGAACGGG  
AAAAAACCCAGGATGCAGGCAGA

**SEQ ID 8252**

LKCDT0222  
 MLVCSIDTGFASGLFLYFLINLIPAWLRSEBVOLKSIGLIMALIGLPPTWKFLWSPLMDAVRLPVLGRRRGWMLLTQAGLLAALAAAYAFINPRNHLPLIAGLSVLVAFPSASQDIVLDAFRE  
 LNSDEBLGLGNSVEVHNAYRVAALIPGSLSLVLADRMPSSEVFFVITSLFMLPGLIMTLFLAHEPVLPPSVPTKLQTVVEPPKFFPMRKGIASAVCVLLPFLFYKLGDMSATALATPFYLDH  
 GFSKTDIGLILAKNAGLWPAVAAGILGGVWMLKIGVKNALWLFAGVQAITVLGPVWLAGFGHFDTVGTGERLMLAAVIGAEAVGVGLGTAAFPVSYMARETNPAFTATQIALFTSLSAVPTV  
 INSFAGYLIEWMGVVPFFRLCFILALPGMLLLKVPWNGEKTDAGR

**SEQ ID 8253**

TTGCTACTGAAACCCGACGGTTTACAGGCTGTAATACATTTCAAATTCCAGCGGGTGCGGCGCCATACGGATGCGCGCGACATCTTCCTCTTTAAAGGCGATGTAGCTGTGCATCCAGTCT  
TTGCTGAACACGCGCGCCGCGACAGAATTCGTGGTTCGGCCTTTGAGGGCGGCAAGTGCTCTTCTCCAAAGAGCGCGAGACGGTTCGGGACGAGCGCGCTCTTCTTCCGCGCGAGGTGCGTAC  
GGTTTTTATCCGCGAGGGTCGCCCGGATGGATTTTGGTTGAATGCGGTCACCAACCGCCGATCGAGCGGGTCCGCAATGCCAAATCTGGCGTTGGCGTTCGGGTCGGGGAACCGCTTCGAT  
CGCGCGCGCTGTGCTGCTTTCAACAGCGGGATACGAGTGAAGCGCAACCGTTTTTGGCGAATAGGCCAATTTTGGTGTGCTCTCAAAGTTCGGCGACGAGGCGTTTGTAGGAGTTGGG  
GACGATTTGGTAATTCGCTTTACGGCGTTTGGCGTGTTTGATGATGCCCGGATGTAGTAGAGCGCGGTATCGGACAAACCGGCATAGCCGTCGCTGCGAACAGGTTTGTACCGCTCTTCC  
AAATGGATTTGGTGAACGTGCATACCGCTGCGCTTGTGCGCCATAATCGTTTGGGCATTAAGGTGGCGGTTTTCGCGAAATTTGTGGCAACGTTTGGATGACGTATTTCAATATCTTGGG  
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CGGAGCGCGCAATCTTGACCGCGAGTCAATCGCGCGACGCGCGCTTGACGCGTTCGAGCGGGGCGTGGCGCGTTTGTGACCGTCCATATGACGCGGCTTGTCCCAACGCGCGCGCTT  
CGGACGTGATTTCTGATAACGGGTTTGTGCATGTGCGGTTTCAAATCTACGCGCTCGAAGACGAAGAATTCGGGTTTCGGGGCCGAAATAGCGGGTGTGCGCGATACCGGAAGATTTCAAATA  
GGCTTCGGCGCGACGTGCGATGGAGCGCGGGTCGCGTCTGAACCTGACCGCTCGCGAGGGTTCGATGACGTTCGACGGTAAATGACGACGGTAAACATCATATAAAGAGGATCGACGAAGCT  
GTGACGCGATCGGGGCGCAACTGCATATCGGAAGCGCTCAATGCCTTTCCAGCGCGCGATGGACGACGCGCTCAAAACGCGGTCCTGTTTCAAACCACTCTTCGCGGGTCTTCCAACACGATG  
CGCGAGGACAGGTAAAGTGTGCTGCTTGCCTTTGGTATCGGTGAAGCGCAATCGACAAAGGGGCTTCGCTTCTTCAATCAATTTTACGCGTTTAAATGGACATCTTCAGTCTCTG  
AAAAGGGGAAATGCGCAAAATGTTCGGGAAGCGCGCGGCTTGACGCAAAATGGCGACAGATTTTACCAACGCGCATGCGCTC

**SEQ ID 8254**

LLLPKDGLQAVIHFQKQVRNRHTDAADIFLFGKDVAVDPVFAZHAHAQOEFVVGLGEGGKCFORSADGRDERVFFRRQVVQVF I GRVARMDFVLNAVQTHGQQGKCQIRVGGKVGETRFD  
 AARLAAVHRRDYDSGTVFVGIGIQPGRCFKVRHEAFVGVGGRIGNRVGGVGFDPDAAADVBERIGIGTGIAVACBQVLTVPFNGLVDPVHTAAVVAHNRFGHKGGGFAETVGNVLDVDFPHLG  
 LVGAFDQSGSETGADFHILAAGTDFAVAGDFDFAESPQNHHGGAQILTAVNRNRDGRVAADFDDGAVAGVLTVMHQACPRAAFGRDFVTGTVHVGFKFYAVEDEEFGFGAEIGGVADTGRFQI  
 GFGATCDGARVAVVTLVGRVGDVAVDDNGNIIIKRIDGCGRI GAQLHIGSGPAADGRKASRVFVKPLFGVGFQHDARRHGKVVLLAFGIEGAQIDKAGFAFFNQFYGVFNHGLQLL  
 KKGNGKICQTRRLDAKARSYPHADAV

**SEQ ID 8255**

ATGCAAAACCGCAGGCAAAAAAACATCTCTGTTACCGCGCGCGCGGGTTTATCGGCTCGGCAGTCGTCGCCATATTTATCCAAAAACCCCGAGATTCGCTGCTCAACCTCGACAAGTTAA  
CCTACGCGGGCAATCTCGAATCGCTGACGACATTTGCCGATATATCCCGCTACGCTTTTGAAGCAAGTGGATTAATTGCGCAACCGCGGAATCGACCGCGGTGTTGCGCGCAATACCGGCCGA  
TGCGGTGATGCACCTTGGCGCGCGGAAAGCCACCGTGCAGCCGCCCATCGTTTCGCGAGGCAAGATTTATCGCGAACCAATATCGTCGGCAATTCGACATTCGTGGAGCTGCGCGCCTATTGCG  
CAGCAAAATCGCTGTGAAAAAGCGGAAGCTCTCGGTTTCCACATTAATTTACCGTAGAAGTCTATGCGCATTTGACAGCGGCACAGACGTTTGTGTACAGAAACACCGCATACCGCGCGT  
CAGCGCCCTCATTCGCGCTCCAAAGCGCGCGCGGACCACTTGTCGCGCGGTGGCAGCGGACTTACAGGCTGCCCTCCATTGTGCAGCAACTGTTCCANTAAATTACGGCCCCCGACAAATCCC  
CGAAAACTCATTCCTTTGATGATTTCTGAACGCACCTTTCCGGCAAAACCACTGCTGTTGACGGCGAGCGGGCGCGAAATCCCGGACTGGCTGTTTGTGGAAGACCAACGCGCGCGCGCTGTAT  
CAGTCTGTTACCGAAGGTGTTGTGCGCGGAAACCTACAATATCGCGGCACCAATGAAAAAAAACCAATCTCGAAGTGATCAAAACCATCTCGCGCCCTCTTGGAGAAGAACTCGCCCCGAAAAAC  
CGCGCGCGGTGGCAGCGGTGAAGATTTAAATCTTCTGTAAGAAGACCGAATCGCGGCGCATGATGTCGCGCTGATCGCGCGAAATACGCGGGATTTGGGCTGCTGCCCTTCTGGA  
AACTTTTGAATCCGCGCTTCGCGCAAAACCGTGCATATGTTATTTGGACAACAAAAACCCGCGCGCAAAACGCA

**SEQ ID 8256**

QVVTGCVGTFYNIHGHNKTNLEVIKTI CALLEELAPEKPAGVARYEDLITFVQDRPGHDARYAVDAAKIRRDGLWLPLETFESGLRKTVOHWLNDKTRRQNA

SEQ ID 8257

TGTGTGACAACTCTGCGGTTTGAAACTATATTTTCCGGCTTGGAATTTGACGCAAAACCGGTTTCAGACGGCATCGGCGTGGTAAAAATCGTGCAGCATTTTGCGTCAAGCCGCGCGCTTCG  
 CATATTTTGCCATTTTCCTCTTTTCAGGAGCTGAAGATGTCCATTAAAAACCGCGTAAAAATTGATGGAAGAAAGCAAGCCGCGCTTTTGCGATTTCGCGTTACCCGATACCAAAGCGCAAGCA  
 GCACCACTTTACCGTGCCTCGCGCGCATCGGTGTGGAAAGCCCGAAGAGTGGTTTGAAAGACGGACCGCGGCTTTGACGGCTCGCTCCATCGGATACCAAAGCGCATTTGAGGCTTCGCGATC  
 CAGTTGCGCCCGGATCGGTCGACAGCGCTTCGTGCATCTCTTTATGATGATGTACCGCTCGCATTCGACGCTCATGACCGCTTCGCGAGCGTCAGGGTTACGACCGCGACCGCGCTC  
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 TCGCGTCAAGATTTTCGCTCCGCCATGTGTGAACATTTTGAAGGACTCGGCACTCGAAGTCGAAGTCCACACACAGCAAGGTGGTACCGGACGCCAATGGAAATCGGCACCCGCTTTGCCA  
 CTGTTGCTCAACCGCGCCGCAATTAAGCAACAGATTAATAATCGCTCATCAAAAGCTGTGCCAATTTGCGGCAAAACCGCCACCTTTATGCGCCAAACAGATTTCGGGGACACACGGGACCGG  
 TATGCACGCTCCACCAATCCATTTTGAAAGACGCTGAAATCTGTCGACGGCAGCGGCTATGCGCGGTTTGTCCGATACCGCGCTCTACTACATCGCGGCATCATCAAAACGCCAAAGCC  
 CTGAACGCGATTACCAATCCGTCACCAACTCTTACAAACGCGCTCGTGC CGCACTTTGAAGCACCGACCAAAATTTGGCCTATTTCGCGCAAAACCTTCCGCTTCCATCCGTATCCCGCTCTG  
 TGAACACGACGACGAGCGCGCGCGCATCTGAAGCGCGGTTTCCCGACCGCCAGCCGCACTGCTGTTATTTGGCATTTTGC CGCGCTTCGTGATGCGCGGTTTGGACGCGCATTTCAAACAAATAATCATCT  
 GGGCGACCTTCGAGATAAAAAAATCTGTACAGCTTGC CGCGCGGAAGAACGCGCTCGCTCGGACCGCTTCGCTCTCTTTGGAAGAACCATTTGCGCGCTTTCGCGCGTCAAGGCGGACCGAAATTCCTG  
 TGGTGGCGGGCGGTTCGACGAAGAAGCTGATGACGACGCTCATGCTGCTTTAAAGAGGAAGATGTCGCGCGCATTCGTATGCGCGCGCCACCGCGTGAATTTGAAATGTATTACAGCTCTG

**SEQ ID 8258**

LILTLPFETPITSGLEFDKAPVSDGIGVVKSCRLCVKPPRSAYFAISLFQELKMSIKNAVKLIESEARFVDLRFTDTKGQHHFTVPARIVLEDPEEWFENGPAFDGSSIGGWKGIEASDM  
 QLRPDASTAFVDFPFDYDDVTVTTCDDVIDPADGGYDRDPRSIARRAEAYLKSSGIGDTAYFGPEPEFFVFVDGVEFTDLHMKTRYEITSSSGAWASGLHMDGQNTGHRPAVKGGYAFVAPID  
 CGQDLRSAMNTLLEGLGIEVEVHHSEVGTSGSMEIGTGFATLVKRADQTQDMKYQIVQNAHNPKGTATFMPKPKIMGDNGSGMHVHQSIWKDQGNLFAGDGYAGLSDTALYYITGGILKHA  
 LNAITPNSTNYSKRLVPHFEAPTKLAYSAKNRSASIRIPVSNWSKARIEARFPDTPANPYLAFALHAGLDGIGIKHPGDPAKKNLYDLPPEDALVPTFCASLEALAAKLAHEFTL  
 IARGVFSKWDYSYIAFHEFEDVRRIRINAPHPLEPFMYSL

SEQ ID 8259

SEQUID 8259  
ATGCTTGCACATCTTCAATTAACCTTTCGGCACCGGGCAGGGCGTCACACCTTATACGTCCACTTTCTGTGTGGCAGAGTCTGTGTTTTTAATAAACAGTCGACGCCACCTATTCTCTGGC  
ACCTCTCGGGGTTACCGAGCAAGTCCTTAACTTAGAGGGCATACCTTCTCCGAAGTTACGGTATCAATTTGCCGAGTCTCCTTCTCCCGAGTCTCTCAAGCGCCTTAGAATTCTCATC  
CTGCCACCTGTGTGGGTTTGGGTTACGGTTCGATTCAAACTGAAGCTTACTGGCTTTTCTCGAAGCGTGGTATCGGTTGCTCTCGTCTCCGTAGACACTCGTCATCACTTCTCGGTGTTA  
AGAAAACCGGGATTGGC

## SEQ ID 8260

MLAHLQUTFRHRAGVTPYPTSTFVLAECVFNKQSQPPILCDPPGLTBQVLNLRGHTFSRSYGINLPSSSRVLSSALEFSSCPPVSVCGTVRFLKLKSGFSWKRIGCFVSDTRHRHFSVL  
RKPGFA

## SEQ ID 8261

CGACACCCCTGACCAAGATTCTCTCGCCAGCTGAATCATAGCATCTCTACTTTCGCTGTGGACAGGCGATCCAAACGCGGCAACGGCAACAATCGACTGCTTTGCGCGCTCGCCATCGAA  
TATGCCAAGCATCCGAACGGACGACATAATCGCGGATTTTTTCAAATAGCCGCGATCTGCATTTTCAAAGCAGTACGCACATCGTTCCGAACCTGTTCGGAACCTCGACCATCAGAT  
AATCAAAGGCGAGGTTCGTTTCTCTCCGCAAAATCGTCGCCGAGCTTTTACCTGTTTCTTCGGTTTCCCGCAATAATCCAGCAGCATCGTCAATAATTCGGAATCGCGTACCGACGTA  
CATACCGTAGTCTTCAAGGCTCTGTCTGCCCGGGGGAAGCTTTGCCCAAAATTCGCGCGACTTGAGCGGCGAGCTTCAAACAATTTGCCGTTTATATTTGATGACTCGGATATATTGT  
TCTTCGGTATATGTCCTGATTGCGGATGTTTCATCAGCTGCATGACCTCTCCCTCGGCAATGATGTTGGTTCGATCCGCCATCACTTCCAAAACGCGCATCTGCCCGAGGCAACCATCAGTT  
GAAATGCACGGGTATATAAAAGTCGCCAACCAACACTGCCCGCCGATTCGCCAAGAGATGTTTTCGCTGTCCCGCCACGGCGCAAAATCGCTTTTCATCGACGACATCGTCTGCGAGGAG  
TGTGGAGTGTGGATAAACTCGACCATCGTCCGAGCAATACAGTTTCTCGTCATATAACCGACCGCTTACCGCCCAAAATCGTCAATCGACGACGAGGCTTTGCCCGCCGCGCTG  
ATGATATATGACCGATTTCGGAATCAGTGCACATCGGATTGCACCGCAGGTTGATGACTTTCATTGACTTTTGGCAAGGCTTTCAGGCAGATGCTGGAATAGGCGAGATTCTCGA  
GCAT

## SEQ ID 8262

RHPDQRLRLQNLHSLHFAVGQGIQRNGTIDCFARLAYRICQSIRTDIIADFFKIAAICIPQSSTHIVRNLFGLTHQINRQGRFSFRQIVADVFTCFPGFPRIQHIIVNLECRITDV  
HTVVPGLFVPGSFAQNCADLSGSKQFCRFLDSDILFPGNVRIADVHQLHLSLGNVGRIRHFNQANTARGNHQLKCTGI \* KVANQHCRRIAEQIVCRCPPTAQIAPIDDIVVQV  
CGSVDLKLRHCRIQFLVITTDRLTRQNRHRTQAFARADDICTDLNQCIDILHRTVDDFIDFGKVFRCMSLEIGQLLEH

## SEQ ID 8263

TTGTCAACAATATGCTTCGGTTTGTCTGTTCAAAGCGGAATGCCGCCCTTTTGTCCGAATGCCGACAAACAGATGCCGTCTGAAGGCGGTTTCAGACGGCATCGTTCCCATCTTCGCG  
CCGCCGTTATAAAA

## SEQ ID 8264

LSITCFGLSVQKRNARPFVRMPTKQMPSEGGFRHRSHLRAAVIK

## SEQ ID 8265

ATGACCGCCCGCCCTTTATGGAATATGACTATGCACGCCCTCCCGCGTACGCCGTTTTCGGCAACCCCGCGCCCAACAGCAAAATCGCGGAGATTTCATCAGCAATTTGCCCTTCAGGAAG  
CGGTTGACATCGAATACGACGCATTTGCGCCGACATCGCGGTTTTCGCGCAGCGGTTTCGACATTTTGAACAGCGGTTTCGCGGCAACCGTTACCGTACCGTTTCAAACAGGAAGC  
GTTTCATCTGCGCGGACGAACATTCGACCGCGCTTTGCGTGCCTGCGGTCATACGCTGTTGTTGGAAGACGCGAGAATACCGCGGACAAATACCGACGGTATCGGTTTGGCCAAAC  
GACATCAGCGAGTCAAAACATTTGCCATCGAGGCGAAACCATCTTCTGCTTTTGGCGCGCGGCGCGGTTGCGCGGCGTATTCCGCTTTTGAAGAACACCGCCCTGCCCGTATCGTCA  
TTGCCAACCGTACCGCGCCAAAGCCGAGGAATTTGCGCGGCTTTTCGGCATTTGAAGCGGTCCCGATGCGCGGATGTAACGCGGTTTCGATATCATCATCAACGGCACGTCCGCGCGCTT  
GAGCGGTACGCTTCTCCGCGTCAAGCCCTAAAATTTTCGCGACTGCGCGCTTTCGCTTACCGGCAAGCGGCAAAACCGPTTTAGATTTTGCACGCAATCGGCTGCGGAA  
AAAACCTGCCAGCGATGCGTATGCTAGTCTGCTAGGCGCGGCTTCTACGCCCTTTCGCGCGGTTTCAAACCGGACATCCGCGCGCTCATCGAACATGAAAGCCCTG

## SEQ ID 8266

MTAPPLNMTMALPRYAVFGNPAHKSQPIHQFALQEGVDIEYGRICADIGGPAQVSTFFETGGCGANVTVPFKQEPFLADEHSDRALAAGAVNTLVNLEDGRIRGDMTIGIGLAN  
DITQVKNIAIEGKTLILLGAGGAVRGVIVLKEHRPARIVIANRTRAKAEELARLPGIEAVPMADVNGFDIIINGTSGGLSQGLPAVSPKIFRCDRLAYDMVYGEAAKPLDFPARQSGAK  
KTADGLGHLVQAAAYALWRGFKPDIRPVIEMKAL

## SEQ ID 8267

ATGTTCCGCATCGTCAAAATGGCTGATGCGCTGCCCGTCCGCGCATCTTTATCTTTTCAATGCCATGTGTACGGCAACATCATCACTACCGCGCGCTCGCGCCCATCGGATGCGCTTGA  
TGTGATGCGGATGAAGCAGTTTGAACAGAAGTTCGCGATGTCGCACTGGATTACCGCTGGGTGCCCTACAAACCGCATTTCCACCAACCTGAAAAAGCCCTGATGCTTCCGAGAGTGT  
CCGTTTTCGCGGACACGGCGGCTTCGATTGGGACGGCATTTCAAACCGCATCAGCGCAACCGGAACAGCGCGGAAGTGAAGCGCGGCGGATCGACCATCAGCCAGCAGCTTGCACAAAAC  
CTCTTCTCAACGAAGCCGCAACTATCTGCGCAAGGGGAAGAGCGGCCATTACGGCAATGATGGAAGCTGTTACCGACAAAAACAGGATTTTGAACATGATTTAACTCAATCGAAT  
GGCACTACCGCGCTTTTCGCGCGGAAGCTCGCTCCCGTATTTTATAAAAAACCGCGCGAGACCTGACCAACAGCAGCGCGCGGCAAACTGACGGCACTCGTCCCGCGCCGCTCTACTA  
CGCTGACCATCCGAAAGCAACCGCTCGCAACAAAACCAATATCGTGCTCAGACGATGGGTTTCGCGAGAATTACCCGAAAGCGATACGGAC

## SEQ ID 8268

MPRIKWLIALPVGIFIFPNAYVYGNIIITYRAVPHRTAFMSMRKQFEQEGRDVALDYRWVPYNRISTNLKALIASEDVRPAGHGGFDWDGQIQAIRNRNNSGEVKAGGSTISQQLAKN  
LFLNESRNYLRKGEAAITAMMEAVTDKNRIFELYLNLSIEWHYGVFGAASRYFFKPAADLTQKQAAKLTAIVPAPLYYADHPKSKRLRNNTNIVLRMGSAELPESDFTD

## SEQ ID 8269

ATGGTATTGTGACACAAAACCCGCGGCAAAACGCATAAAACGGCAACTGCCCTTCGGAAACGCTTAGGTACGGGCAAAATAGTTTTCAGACAGCATCCCGACGCAATCCGCTCTGAAAAAC  
CATCGCAAGGAAGAAAGAAAAGATGAAGGCATCATACTGGCAGCGCGGACGCGTACGCGCTATATCGGATTACGCGCGCGTATCCAAACCACTGCTCCCGGTACGACAAACCGAT  
GATTTATACCCCTTTCGCTGTTTGTATGCTGGCGGAATCCGCGATATTTTGGTAATACCGCAACCGAAGACACGCTGCCCTTCCAAACCGCTACTCGCGACAGCGCTCCGACTTCGCGATC  
CGCTGCAATATGCGCTTCAACCCAGCCCGACGCGCTTGGCGCAGGCAATTTATCATCGCGGCAAGAAATTTATCGGCAACCGCAATGCTGCGCTGATTTTGGCGGACATATTTCTACGGTC  
AATCATTTACGCAACATTTGAAACAGGCGCGCGCAAGACCCAGCGCGCAACCGTATTCGGTTATCGGGTTAAAGACCCGAGCGTTTCGCGCTGGTGAATTTGACGAAACTTCAACGC  
CTTATCCATCGAAGAAACCGCAACAGCCCAATCCGATTGGCGGTAACCGGCTTGACTTCCAGCAACCGCGCGCTCGAGTTTCGCAAAACAGCTCAAAACCGCTCCGACGCGCGGAA  
TTGGAAATTTCCGACCTCAACCGGATGATATCGGAAGAGCGCTCGCTGCTGCTCAAAATATTTGGGACGCGGTTTCGCGTGGTTGGACACCGGACGCAAGAAAGCTGCACGAGGCGGCTT  
CCTTCGTCAAACCGTGCAAAATATCCAAACCTGCACATCGCTCGCTCGAAGAAATCGCTGCGGTAACCGCTGGCTGACGAAAAAGATGTGGAACACGGGCAAGCCTTTGAAAAA  
AACCGCTACGGCAATACCTGCTGCGCTGATCGGCAAA

## SEQ ID 8270

MVFGQONPAKRIKRIQLPFGTLRYGQIVFRQHPDAMPSENFSQRKKEKMGILLAGSGTRLYPTTRGVSKQLLPVYDKPMIYPLSVLMLAGIRDILVITAPEDNAAPQRLLDGSDFGI  
RLQYAVQPSFDGLAQAFIIGEEFIGWNVCLILGDNIFYGQSTYQLKQAAKTHGATVPGYRVKDPERPVGVEFDENFNALSIEEKQPKSDWAVTGLYFDHNRVAFKQLKPSARGE  
LEISDLNRMYLEDGSLVQLLGRGFAWLDGTGQESLHBAASFPVQVQNIQLNHIACLREIAWRNGLTKKDVEVTRAKPLEKTAYGQVYLLRLIGK

## SEQ ID 8271

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ATCGAACTTTCGTGACGAAACCACTCCAACTCCAGCAAGGCGGTATTCGCGCGGCTGCACTACCAACCGCAAAACACCAAGGCAAACTTCGTACGATAGTTGTCGCGGAGGTTCGGA  
CGTGGCGCGGATATGTCGCGAAGGTTCCCGACTTTCGGCAATGGCGGGCGCAACCTTTCGCGCGCAAAACCGATACCGAGCTTTGGATACCGGAGGCTTCGCACAGCGTTTTCGCGTT  
TTGGGCGACGCGCGAAGTCTGTACAANTGCACGGAATTTACAACCTGAAACCGCAACAGGTTTAAATATGGAACGACCGGCAATCGGCATAGGCTGCGCGCTTCAAACCGCGCGC  
TACTTTCCGCCAAAGACCTTCCCGCAAAACGTGGGCACAGCGCAAAAGCTTCGCGCTTACCGCTTTCGCGA

## SEQ ID 8272

MDIIDLTPDWLLKLPQVFTDGRGPFMETFRDGFKNLADRTFVQENHNSKSGVLRLGLHYQTEWQGLVRIIVVGEVFDVAVDAREGSPTFGKWAGATLSAQNRVQLWIPEGFAHGFCV  
LGDAAEVVYKCTDYNNPETBQVLWNPDAIGWPLQTAPLLSPKDLAKTWAQAKLRILTLR



## SEQ ID 8273

TTGTTAGAGCAACGAGTTGAAAAATCCGTGTGTCGGCGGTTTCGATTCCGCCCTCTGGCCACCAAAAAACGATTATAAGCGGTATTTTTTTCCTGCCGTTTCGGCAGCAGTCCCGCACCGC  
AAATACTGCCATGCACGACATGGTCTTTGCGGCTGTCCGGCAGGTTAGTGGATTAAACAAAAATCAGGACAAAGCCGAGAGGATACACATAGTACGGCAGGCGGGGTAAC  
GCCGTACCGGTTTAAATTTAATCCACTA

## SEQ ID 8274

LVEQRIENPCVGGSIPLATKKPILSGYFLPAVFGSSPAPQIPAMHDMVFAAVGQVSLTKIRKRRSRQYNIVRQGGVTPYRPFKNPL

## SEQ ID 8275

GTGCGTATTAAACAAATTTTCGGGACGACACGCAAGCGGATTGTTCGATATTTTTTACCACCGGACTAAGTCGATGTTTAAAGTTAAATTAATTCACAGAAAAATAGTCAAAATCGGT  
TTTTTTCGGCTTCGTTCCGGCAGTGTCTGCTTTGCAGACGGCAAAACGCTCAATATTTGAAGTCTTCGCCCAAA

## SEQ ID 8276

VRIKPNFGITRKIRICRYFLPNRLSRCPFKLISQKNSANRFFAVRSAMFCFADGKTLQYLKPSFK

## SEQ ID 8277

ATGAGCGCAAAACACAGCCCGCTCGTCTGCTCAAAACCTGCAGAAAAATTTCAAAAAACGCCAAGTCGTCAAAAGTTCTCCCTTGAGATCGAAAGCGGCGAAGTCATCGGACTGCTCGGGC  
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CCTGGGTGTCGGCTACCTGCCGAGGAAGCCTCGATATTCGCAAAATGACCGTCGAACAAAAACATCCGCGCATCTTGAAATCAGAACCAAGATAAAAAATCAATTCGACAGAGAAATC  
GAAAAATGCTCGCGCACTCAATATCGGACACTTCCGCGCAATCTCGCGCTGCTGTCGCGCGGGAACCGCGCGCGCTCGAAATCGCCCGTGTCTCGCCATGAAACCAACGCTTCA  
TCTTTTGGACGAACCTTTTTCGCGCGCTCGATCCATCGCGCTCATCGACATCCAGAAATCATCGGTTTCTCAAAATCGCGCGCATCGCGGTATGATPACCGACCAACGCTCCGCGA  
GACCTCAGCATCTCGGACCGCGCTACATCATTCAGACGTCGCGTCTGCTTCGCGCAAGCCGACGATTGGTCCGCAACGACAGGTGCGCGCGCTCTATTGGCGGAGAACTTC  
AAATAT

## SEQ ID 8278

MSANNSRLVQNLQKSPKKRQVVKSPSLIESGEVIGLGPNGAGKTGPFYIVGLIAADAGSVMLDGRHLRPIHERARLVGYLPQASIPKMEVQENIRAILBIRTKDKNQIDREI  
EKLADLNLIGHLRNPAFSLSGERRRVEIARVLAMKPRFILLDEFPAGVPIAVIDIQIIGFLKSRGIVGLITDHNRETLSDCRATYISDGAULASGKPDLDVNGEQRVAVYLGENF  
KY

## SEQ ID 8279

ATGAATAAATCTTTATCCGGTTCCGTAGAAAAATACCGGAAGTACGCTCCGAGGCATGACTCCGGCGCATTTGATCACTGTAATTTTTACTGCGTCTAACGTTTACCTCGGTTTGAAAG  
TCGGGCTGACCTTTGCTCGTCGATTCGGCGCGCGGTGATTTCGATGGCGGTTTTAAAAATTTTTCAAGAGCAGCAATATTTGGAAGAACACATGGTCAGACCCCAAGCCTCGGCTCGCGG  
TACGCTTTCAACCATCATCTTCGCTCGCCGGTTTTGCTGATGGCGGCTACTGGAGCGGTTTCCGTTTTCGACAGCAGCTTTTATGATTCGCGCGGGAATTTTGGGGGTGATTTTC  
ACCATTCGCTGCGTTACGCGATGGTGTGAAAGCGATTTCCTTATCCGGAAGGTGTGGCGGCTGCTGAAATTTTGAAGTGGCGGTCATGAAGAAGGGGATGACCGTCAGGCGCGCA  
GCGGTATCAAGAGCTGCGCGCGCGCGCGCTTGGCGGGATTGATGAGCTTTTGTCCGAGGTCGCTGTGATTCGCCGATAGCGCGAGTTATTTGGTTTAAAGCGGTACGGCAATTTT  
CCAACCTCGCGATAGGCTTTTCACTGCGCTTTGTTGGCGCGGTTATTGGTCGAGTACGCGCGCGCATCGCCATCTGCTGGCGATTTCGATGCTGGGGTATTCGCGTCCGCTATTTTC  
TCCTCACATTTCCGCAACCTTCGGATATGGAATGGCGCGCTTTGCGATGAAGCTGTGGAAGGAAAAAGTGCCTTTATCGGTGCGGGAACCATAGGTATCGCGCGGTTTGGACGCTTT  
TGATGCTGCTCAAGCAATGGTGAAGGCATGAAGATGCTGTTCAAGAGTTTTGGCGCGGTCGCGCGCTACAGAACGCGCGGAACAGGATTTCGCGCTAAAGCCATGATTTTCTGGGT  
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TTTTTGGTTCGCGCGCGCTGCGGTTATATGCGAGTTTGGTTCGCTGCTTCCAGCCGATTTCGCGCTGGCGCATCGTGTCCATCGTCTTATTTCACTGCTTTTGTGCTGGTAGGCG  
AATCCGAGGTTTGTGGCGGATGAGGCCAACCGCAATCTTACTGGCGTTCAGCCTTTTTCGCGATCGCGCAGTAATTCGCTGGCTTCGATTTCACAGCAACCTCGCAAGACTTGAA  
AACCGGCTACCTGCTCAAAGCTACGCTTGGCGCGCAGCAAGTCCGCTGATTATCGCGCTGATTCGTTGGTGGCTGGTTATTTTCGCGCGTGTGGAACCTGCTTACGAAACCTACGCGCTT  
ACCGCGCAATGCGCGCGGAAGGCATGGATGCGCGCGCAGGCTTGGCAGCCCTCAAGCGACTTTGATGACGACCATTCGCTGGGCAATTTTCGCCACAACCTCGAATGGCGGTACATCT  
TTACCGGTATCGCGATTGGAGCGGTATTAATCGTCTGCAATTGGTGTGAAAAATCATCAGCGCGTAAACTTGCCTGCGCGCTGCTGCGGTCGATTCGCGCGCTTTCGAAACCGCGCGCTATCGGTACGCTTTTC  
CGCGCAGCGCTGATTTGCGGTGAAAGCCTGATTGGTGAATATGCGGTTTATTTATGCTCTCTGTGACCAAGCGCGCTCGGATGCGCGCTCGCGTTGAATCTGCAAACTGGGATG  
CCGCGCTTCTGTTGGGCTTGGCGTTCTGTTACCGGATGTTTTCTTTGCACAGCGCTACTGAAGCGGTTAGG

## SEQ ID 8280

MNKSLSGSEVKEYRLTLRGMILGALITVIFTASNVYLGKVLTFASSIPAAVISMAVLKPKFSNILENNMVQTSAAAGTSTIIFVLPLGLIMAGYWSGPFWQTFLLCIAGGLGVIP  
TIPLRYAMVWKSLLPYEPGVAARILKVGHEEGDRQGGGKELAAAGALAGLMSFCSSGLRLVADSASYWFKSGTALPQLPIGFLSALLGAGYLVGLTGGAIIILGISIANGIAPYF  
SSHIPQPSDMEMAFAMKWKKEVRFIAGTIGIAAVWLLHLKPMVEGKMSFKSFGGGAATERAEQDLSPKAMIFWLSMMFILLGVSYFHYIGDSHTTGGMANLLVAVCTLLASVIG  
PLVAAACGYMAGLVGSSSSPISGVIVSTVVISLVLLLVGESGGLLADEANRKLALTLFCGSAVICVASISNDNLQDLKTYLLKATPWRQVALIIGCTVGLVISPVLBLLYEATGF  
TGAMPREGMDAAQALAAQATLMTTIIASGIFAHNLEWAYITGIAIGAVLIVVDLVLRKSSGGLALPVLAVGSGIYLPSPVNMPIVAGAVLAIVLKHIIIGKASNRBRLKNADRIETLF  
AAGLIVGESLIGVTHAFIIAFSVTNGSSDAPLALNLQMDAAASWLGALFFVTFMFFAPQVRLKGR

## SEQ ID 8281

TTGAAAAATAAAATATTTCACCAACGAACAAAAACAGCGTATCAGGGAGGTTCCCCGATACGGCTGCTTGTTCGGAACCTTAAATCAATCAACAAATCGCGCAGCTTGTCT

## SEQ ID 8282

LKIKTISKRTKFAVSGRFPDPAACFRTLKSIQIAQLV

## SEQ ID 8283

ATGAAATACCATCCGACCGCAATCCTGACAATAAAGAGCGGAAGAGAAGTTTAAAGAGTACAAAAGCGGTATGAAACTTTGTCCGACAAGGAAAGCGTGCCATGTACGACCACTATG  
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GTGTCAAATCTTTACGACGACGCGGACCGCGGATTGTACTGCCATATTTGTGCGAAAGCGCTGTCAATTTGACCGACCGTCAAAAGAGCTTTTGAAGAAATTTGAGCGGATTCTAC  
GGGCTTGAAGAAACCAAGCGCGCAAGAAATCGTTTTAGACAAGCTGCGCGGATTTGTTGAT

## SEQ ID 8284

MKYHPDRNPDNKEAEERFKVEQKAYETLSDKKRAMYDQYGHAAFEQGGQGGFGGFGGAQGFDFGDFISQMFGGSGRAQPDYQGEDVQVIGIETLLEAAKGVKKRINIPTYEACDVC  
NGSGAKPGASPETCTCKSGTWHIQQAIIPRQQTCTCRGAGKHIEKPCVKCRGVRNKAIVTVENIIPAGIDGQIRLSGEGGPMHAPAGDLIVYRIIRAKHIFQDGLDLHCELP  
ISFAMAALGGELEVPFLDGKVKLTVPKETGTGRMRVKRGKVKSLRSSATDGLYCHIVVEFPVNLTDROKELLEEFERISTGLENTPRKKSFLDKLRLDFD



## SEQ ID 8285

TTGATAAAGCTTACTGCTTTGTGTGCTTAATCCTGCTTTGTGTTTCAGGATTAAGTCGATACATCATCACCACAACTATGTTGTGTTTCTCTTGCAGAGGTTTTTATC  
CTTTGCAAGAAATAAAAAACAAACAACTATGCTTTGTGTTGT

## SEQ ID 8286

LILKLLALLCLNPAFCVSLSRYNHHPNTMFVFFSLRAGFYPLQRIKNQKLIIVFVC

## SEQ ID 8287

ATGCTTTTGTATTACGACAATTACGACAGTTTACTTACAACATCGTCCAGTATTTCGCAGAATTGGGGCAGGAAGTCGCCGTGCGCCGCAACGATGATATTACGTTGGAGGAAATCGAGG  
CATTTGAATCCGCAATATCTCGTTATCGGTCCCGGACCGGTGTTCCCTTAAGGAGCGGGTATTTCAGTAGAAGCCATGCGCCATTTTCCCGCCCGGTGCGGATTAATGCGGCGTGTGCTCGG  
GCATCAGACGATAGCGGAAGCGTTCGGTGGAGATGTGGTACGGGCAAAAACCTTGATGCACGGTAAGGTGTGCGCCGTGTCCTTCCATTGCGGCAAGGGTATGTTTAAGGGTTTGGCCCAATCG  
GTTACCTGTACCGGTTATCAGCGCTCGTTATCGAACGCGGACCGTGCCTGGAGTATGTTGGAATACCGGCGTGGACGGAAGACGGCGAAATATGCGGCGTGGCCATAAGGAATATGCGG  
TCGAGGGCGTGCAGTTCCACCCGGAAGCCCTCTTGACCGAACGCGGACATGATATGTTGAACAATTTTATGTTGAATTTCAAACCTTCAAACCGCAAAAAATC

## SEQ ID 8288

MLLFLIDNYDSFTYINIVQYFAELGQEVAVRRNDITLLEIEALNPQYLVIQPGPCSPKEAGISVEAMRHFAGRLLPMGVCLGHQITIGEPGGDVVRKTLMHGKVPVSHSGKGMFKGLPNP  
VTCTRYHSLVIERGTLPDCLLETAWTDEGEIMSVRHKEYAVEGVQFHEALLTERGHDLNLFVLEFQNFKPQKI

## SEQ ID 8289

ATGAGCACCTTCTCCGCGCAACCGCCCAAGCCATGACTGCCAAACACATCGGCCCTTCCCGCTATTGGAGTTGGACAGGTGATTGATTGGCAGCCGATCGAACAACTACCTGAACCGTC  
AAAAAACCGTTTACCTCAGAGACCGCGCGGCCCGCCCTATCCCTGTGCTGCTATGTTCAAAGCGTCTGCGCGACAAATGGCACAGCTCTCCGATCCCGAACTCGAACACAGCCT  
CATCACCGCATCGGTTTCAACCTGTTTTCGCGTTTTCAGCGACCGGGCATCCCGGTGCGAGCACCTTATGCCGTACCGTAAATTCGCGTATGCGCGGCGACCTATTTCGGGCTGCTC  
AAAGTGGGTGCGCAAGCCACCTGAAGGCGATGTGTTGAACCTGTTGAAGCGCCCAACAGGCTAAGTGCGCCCGCTGCGCGC

## SEQ ID 8290

MSPTFRQTAQAMTAKHIGRFLLELDQVIDQPIEQYLNRQTRYLRDRRGRPAYPLSSMFKAVLPQWHSLSDPLEHSLITRIGFNLFCRFDGPGIPGCSTLCRYRKFRYARAAYFGLL  
KVGAGSHLKMCLNLLKAAANRLSAPAAA

## SEQ ID 8291

ATGATACAAAAGATATGTAAGCTATTGTTTAAATTTGTAATTTTTCGAACTTCTCCCGCTTTTGCCCTTCAAAGCGACAGCAGCGCCCATCCAAATCGAAGCCGACCAAGGTTTCGCTCG  
ATCAAGCCAAACAAAGTACCACTATTAGCGGCAATGTCTATCATCAGACAGGATACGCTCAACATTTCCGCTCGCGCTCAACGTCAACGCGCGCGCAAGGCGCGGAATCCGTGAGGGC  
GGAAGGTTCCGCCGTCCGCTTCAGCCAAACGTTGGACGGGGCAAGGGACGGTGCCTGAGGCAAAACAGCTTACCTATTCTCCGCGAGGAAGCACCGTCTGTGACCGGCAATGCC  
AAAGTGCAGCGCGCGCGGACGTTGCGAAGGTGCGGTATTAACCTACAACACCAAAAACCGAAGTCTATACCATCAACGCGACGACGAAATCGGGTGCAGAAATCCGCTTCCAAAACCGGCA  
GGGTACGGCTGCTATCCAGCCTTCAAGCACACAAAAACCGAA

## SEQ ID 8292

NIQIKCKLFVLIVIFATSPAFALQSDSRRIPIQIADQGSLDQANQSTTFSGNVIIHQITLNIASRVNVTGKGKGGESVRAEGSPVRFSTLDGGKGTVRGQANNVTYSSAGSTVVILTGNA  
KVQRGGDVAEGAVITYNTKTEVYTINGSTKSGAKSASKTGRVSVVIQPSSTQKTB

## SEQ ID 8293

ATGAAAGTAAGATGGCGGTACGGAATTGCGTTCCCATTTGATATTTGGCGGTTGCTTGGCGAGCGTTCGCGCATGTTGGGCGGTATCAGCGAAGTCGAAATCGAGGAAGTCAGGCTCAATC  
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TTTTGATTGCGGCATCTGCTGTTCTTCCAAGAGGCAAGCTGTTGACGAAGTCGCGCAGCATGAAGCGGTTTACCATACCGAAGAAACAAACAGGTTCTTTTAAAAACAAACGTTGTGCTG  
ACCAAAACCGCGACGGCAGGCGGCGGCGGTAAGTCGAAACCGAAGAACTGCACGTCGATACCGAATCTCAATATGCCAAACCGGATACCGCTGTGAGTTTCCAATATGGCGCGTCCG  
ACGGTCAGGCGGCGGTATGACCTACAACACAAAAACAGGATGTTGAATCTTCATCTAAAGTGAAGCCGCGATTATGATACAAAAGATATG

## SEQ ID 8294

MKVRWRYGLAFLILAVLGSLSAWLGRISSEVIEEVLNDEPQYTMGLDGRFRDEQGYLKEHLSAKGAKQFPENSIDIHFDSPHLVFPQEGRLLYEVGSDEAVYHTENKQVLKNNVVL  
TKTADGRRQAGKVETEKLEHVDTESQYATDTPVSFQYGASHGQAGGNTYNHKTGMLNFSKRVKAAIYDTKDM

## SEQ ID 8295

TTGTCTTTGTTTGAAGGGAAATGGCTGGAGAAAGACCTGCGCTATATCGGGGAATGAATCGATGCAAGGAAATGCCGTCTGAACATGCGTTCGGGACGCGTTTTTATAACAAAACAC  
TTAATGGCGGTTGTTTTATACCTATCTAAGTTTTTGTGTCGTGCATATC

## SEQ ID 8296

LPFWKNGWRRKTCALSGNESMQRKRLNMRSGSVFTIKTLNGWFTYTLSPCVHII

## SEQ ID 8297

GTGGTTGTAGGTATACCGCCCGCTGACCGTGCAGCGCGCCATATGGAACATGACAGGCGTATCGGTTTGGGCATATTGAGATTTCGGTATCGACGTGCAATTTTTCGGTTTCGACTTTA  
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CTTGAAGAAGACAGAGATGCGCGCAATCAAAATGATGTCGCTGTTTTTCGGGAACTGTTTCGCACTTTTCGCGCTCAAATGTTCTTCAAGTATCCCTGTGCTGCAAAACCGCTTTCGCTC  
CAAGCCGTCCATTGTGTATGAGGTTGCTCGGGATTGAGCCTGACTTCTCGATTTCGACTTTCGCTGATACGCGCCCAACCATGCCGACAGGCTGCCAAGGCAACCGCAATATCAATGGG  
AACGCAATTCGTACCGCATCTTACTTTTCATTGATGTACCGTTCAAAGCCGCGCCCAACGTACCTTTTCGCGCGATAATCAGGTACACACTTCGCGCACCGCGCCCGCACCGCGCGG  
CGGTTTGGCAATA

## SEQ ID 8298

VVVGHTARLTVRRAILETDRRIGLGLRFGIDVQFFGDFTRLPPAVGGFGQHNVPKKNLFPVGMVNGFIAADVFQQPAPLEEHMERRIKMDVAVFGKLFRTFRAQMFQVSLFVKPPSV  
QAVHCVLRFVGLPDLDFADTAQPCRQAAQGNRYQWERNVSPPSYFHLMPFKAAPNVFPARLIIRSHTSRTAPAPPGLAI

## SEQ ID 8299

ATGCGCTTCGCGGGGCTATGCCCGGACGCGCTCCAGCTCTGCTGCGAAGCGCATTTGATGTTTACCGCGCAAGGAGAAGGCGCAGGAGAACAGCATACAGAACAATACAACATTT  
TTTTCATGGTTTTTCTTTAAGGGTTGCAAAACAACAAACCGCATCTTGCAGCATATGCGGATTAACAAAAACCGGTACGCGTTGCCCCCGCCCGCTCAAGGGAACGATTCCTTAAG  
G

## SEQ ID 8300

MAFAGPMPGSASSCCCAALMFTAAREKAQENSIQNFNIFPMVFLRVANNKPHLATIWRINKRYGVAPPRLKNDLSLR

## SEQ ID 8301

ATGGGAACGCAATTCGTACCGCATCTTACTTTTATTGATGTACCGCTTCAAAGCCGCGCCCAACGTACCTTTTCGCGGATAATCAGGTACACACTTCGCGCACCGCGCCGACCG  
CGGGGGCGTTTGGCAATATAGCGCGGTGTTGACAGGTAAACCAATGCGCGTGGGAGCGGCAACCGCAATCCGACGCGACCATCACCAGCAATGACACAGTCTGTCGCGGACAAAGG  
CGCACTGCGCTTCTTCAAGCTGCTGCGCGCGAGCTCTTATACGCGCGCGGTTTTCGCAATATGCTTTGAAGTAGTAATTTATGCCCACTGTTTACGCGGATGTCGCGGACGAGGG  
CGCGTCCCGACCTGTGATAATCGCAGTCTGCACGCGCTTGCCTGAAGCATTTTCAGGCGGTGCGCTCCAGTGTGTGAACGATTGATTCTTCGCGCGTCTGCGGATAAAGATGCGG  
CGCTCGGTCAAACCGCGTCCACATCAATATCAGCAGTTGATTTTGGCGGCGCGTGCCTG

## SEQ ID 8302

MTQPTFAILLSPDVFVQSRQRTFRADNQVTHFAHRARTAGAFNGIIGVLRKPMRVGDGNGRQSAHHHRQIDHVVDKALGFQACLRALQFIRGAFVRNAPFVVIYAQLFDADADGG  
RVPTCDNRSLHAACLKHFQAVSVQCKRFPFAVAVADKAPVQNAVHIOYQDFDGGACL

## SEQ ID 8303

GTGCTTCATCACTTAGGGAATCGTTCCTTTGAGCGGGGCGGGCAACGCCGTACCGGTTTTGTGTAATCCGCCATATCGTCGCAAGATCGGTTTGTGTTTGAACCCCTTAAAGGAA  
AAACCATGAAAAAATGTTGTATGTTCTGTATGCTGTCTCGCGCTTCTCCCTTCGCGCGTAAACATCAATCGCGCTTCGCGAGGAGCTGGAGGCGCTGCCGCGCATAGGCC  
GGCGAAGGCCATTCGCGAATACCGCGCGCAAAACCGCGCTCAAGTCTGTGGACGATTTGATCAAGGTGAAGGCCATCGGTCGCGCGGTGCTGGCGAAGCTGAAAGACCGAGCTTCCGTC  
GGCGCGCGCGCACAAAGCGCGCGCAAAACCGGTCTGCTGCGGTTAAABAAA

## SEQ ID 8304

VLHHLRESFPLSRGGATPYRFLIRHIVARCGLLPATLKGKTHKKMFLVFLMFLSCAFSLAAVNINAASQLEALPGIGPAKAIAYRAQNGAFKSVDDLKIKVIGIPAVLAKLKDQASV  
GAPAPKGPAPKPVLPAPVK

## SEQ ID 8305

ATGCAGGCAATTTCTCCGAATACAGGCACGCGCGCCAAATCAAACTGCTGATTTGGATGTGGACGGGTTTTGACCGACGGGCGCATCTTATCCGCGACGCGCGAAGAAATCA  
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AAATFACACTTCAAGGCATTTCCGACAAACGCGCGGTATGAAGAGTCTCGCGCGCAGGAGGCTTGAAGAAGCGAGTGGCGCTTTGTGCGGACGACGATGTCGATTTCGCGGTG  
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TTATCCGCGCGCAAGGTACGTTGGCGCGCGCTTTGAACGGGTACATCAA

## SEQ ID 8306

MQAISPELQARAANKILLIDVDGVLTDGRIFIRDDGEIKSFHTLDGHKMLQASGVQTAITGRDAPSVGIRVKQLGINYYFKGISDKRAAYEELRAQAGLEBAECAPVGDVVDLFPV  
MVRCLPFAVPAHWFYQLQHAAYIAKRPAGAVREVCULIRAKGTLGAALNGYIK

## SEQ ID 8307

ATGATAGTGTGGTCTTCCATGCGAAAGTAGGTCACTGCCAAACACCCCTTTCAGAAAACCCCGGATATCCGGGGTTTTGCTTTGCCCGGAAAAATGTCGGGATGGCGGGACGGCAT  
CTGTACGGTGTCCGGTCGGGTTTCGGGAGAACGGCTTGAACCTTTGGGATATTCATTT

## SEQ ID 8308

MIVWFFHAKVGHCTPFPQKTPGYPGVFALPGKINVDGGTASVRCPVGFABERLETGLYSF

## SEQ ID 8309

ATGCTTTACGCGCTTATCTCTCCGAATCTAGCTACCGGCTATGCAACTGGCGTTTACACCGGTACACCGAGGTTGCTCCACTCCGTCCTCTGCTACTAGGACGAGCCCCGTCAAAC  
TTCCAACGCCCACTGCAGATAGGGACCAAACTGTCTCACGACGTTTAAACCCAGCTCAGTACCACTTTAAATGGCGAACAGCCATACCTTTGGGACCGACTACAGCCCCAGGATGTGAT  
GAGCGGACATCGAGGTGCCAAACTCCGCGCTGATATGAACCTCTGGCGGGAATCAGCGCTTATCCCGGAGTACCTTTTATCCGTTGAGCGATGGCCCTTCCATACAGAACCAACCGAT  
CACTATGCTCTGCTTTCCGACCTGCCGACTTGTGCTCTGCGATTAGCTACCTTTTGCCTTGCCTATCAGTCCGATTTCCGACCGGACCTAGTAACTTCCGAACTCTCTCGTTAC  
GCTTTGGGAGGAGACCGCCCACTCAAACTGCCCTACCATGCACGTCGCCGACCCGGATGACGGGTCTGGGTTAGAACCTCAAAGACACCGGTTGATTTCAAGGACGACTCCACAGAG  
ACTGGCGCTCTGCTTCCAGGCTCCCACTATCTACACAAG

## SEQ ID 8310

MLSALISSELSYPMQLALQPVHQRVHSGPLVLGAAPVKLPTPTADRDQTVSRFPKPSRTTLNAGEQYFPWDRLOPQDVMSRHRGAKLRRRYELLGGISLSPYLLSVERHPPFHTPEPD  
HYVLLSHLPDLVSQSLSYLLPLHYQSDFRPDLGNLRTPLFRGRRPPQSNCLPCTVPDPDGGGLEPQRHQGGISRTTTPQLASLLPSLPPIIHX

## SEQ ID 8311

ATGCTTGCACATCTCAATTAACCTTCCGCGACCGGCGAGCGTACACCTTATACGTCACCTTTCGTTGCGCAGAGTGTGTTTAAATAACAGTCCGAGCCACTATTCTCTGCG  
ACCTTCCGGGGCTTACGAGGCAAGTCTTAACCTTAGAGGGCATACCTTCTCCGAAGTTACGGTATCAATTTGCCGAGTTCCTTCCCGAGTTCCTCAAGCGCTTAGAATTCTCATC  
CTGCCACCTGTGTCGGTTTGGGTACGGTTCGATTCAAACTGAAGCTTAGTGGCTTTCTTGGAAAGCGTGTATCGGTTGCTTCGTGTCCTAGACACTGCTCATCACTTCTCGGTGTTA  
AGAAAACCGGATTTGCC

## SEQ ID 8312

MLAHLQUTFRHRAGVTPYTSTFVLAECVFNKQSQPPLCDPPGLTEQVNLNRGHTFSRSYGINLSSFSRVLSALEFSSCPVSVCGTVRFKILKLSGFSWKRIGICFVSVDRHHSVL  
RKPGFA

## SEQ ID 8313

TTGCTAAGTCTTCCACCTACCGGCTTAAACAAGCTATTCACACAGCTTGCCAACTAACCTTCTCCGTCGCCACATCGCATTTGAATCAAGTACAGGAATATTAACTGTTTCCCATCGA  
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TCGCATTTCTGATACCTCCAGCACATTTACAATGCACCTTCATCAGCTACAGAACGCTCCCTACCATGCCGTAACCGGCATCCGAGCTTCGGTTATAGATTGAGCCCCGTACAA  
TCTTCCGCGCAGGAGCTCGACAGTGAATATTACGCTTTCTT

## SEQ ID 8314

LPKSSTYRLQAIPTACQPNLLRPHAFESSTGILTCFPTSTHFLCALGADSPYADERCVGNLGLSAGLPTRFIATHVNI RTSSTLYNAPSSAYRTLPHYAGKPAASAVIDLSPVT  
SSAQDDSTSELLRPL

## SEQ ID 8315

ATGGATGGCGGGGTTTGAAGGCTTATGCTACCCGATTGCGAAATTTGGGTAGTTTGTGTACAGCAAAGCGGATGGCAATGGCAGAAAACGAAAAATATCTCGACTGGGCGCGGAAG  
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CTCGGACGCGCTTGAAGGAGGCTTCGTGAGCATGAGCGAGAAAGGTTTGGGCTATGTCGCGTAACGAGCGGCAAGGCTGTGAAAGCGGCTTTACTGACGCGGATTTGCGCGCGC  
TGTTCGAAGATGCGACAATTTACCGTCTTTCGATAGACGAAGTATGATACACACCTTAAACCATCTTCCGCGAAGCGCTCGCCACCGAAGCGCTGAAAGTATGACGAGCAACCA  
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## SEQ ID 8316

MDGRGLKAYATPIRKFWVVLQRRNMAENEXYLDWAREVILTEAGLRBIAAELDENFVLAADALLHCKGRVVTGCMKSGHIGRMAATMASTGTAPFVHPAAAHGDLGNIVINDV  
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LGTPLKGAIVMSERKGLMLAVTDGQGLKGVFTDGLRRLFQECNFTGLSIDVMHTPKTISAERLATEALKVMQANHVNLVITDADGVLITGALNHDLLAARIV

## SEQ ID 8317

TTGTATCGACTTAATCTGAAACACAAAAGCAGGATTAAGACACAACCAACAGTAAGCTTATCAAAGTAGGGATTCAAGTTTGCTTACT

## SEQ ID 8318

LYRLNPETQKAGLRHNKAVSFIVKGISSLLF

## SEQ ID 8319

ATGACTATTTTATCGGACGTTAAAGCATTAGGACACAAATCTGGCTGGACAACCTTTCCCGCTCGCTCGTCAAAAGCGGGAATTGGCGCAATGCTCAAAACAGGCGTGTGGCGCTAA  
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ACACCGTCCCGGATGCCACGCTCAAGCCTTTATCGACACGCGACGCGCAAGAGCGACGCTGACCGAAAGCGCGGACGAAGCAAGCGCGCGCTCGCCGAAATTTCCCGCGCTCGGCATCGA  
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## SEQ ID 8320

MTILSDVKALGQIWLNLNLSRLSVQSGELAQMLKQGVCGVTSNPAIFQKAPAGDALYAEVAALKRQNLSPKQRYETMAVDVRAACDVCLAEHESTGGKTGFVSLVSPELAKDAQGTVE  
EARRLHAALARKNAMIKVPATDAGIDALETLVSDGISVNLTLFSAQTLLKAYAYARGIAKRLAAGQSAHIQVVASPFI SRVDSALDALTLPDLRLKGTALALAKAAYQDWEQYFTAPEF  
AALEAQGANRVQLLWASTGVKNPAYPTLYVDSLIGVHTVNTVPDALTAKFIDHGTAKATLTESADPEARLARLAALGIDVETLAARLQEDGLKQFEAFKLLAPLV

## SEQ ID 8321

TTGTGCTTAACTCGCCTTTTGTGTTTCAGGATTAAGTCGATACAATCATCAACCAATACTATGTTGTTTCTTCTCTGCGAAAGGTTTTATCCTTTGCAAGAATAAAAAATC  
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## SEQ ID 8322

LCLNPAFCVSGLSRYNHPMTMFVFFSLAKGFYPLQRIKQNKLIIVFVC

## SEQ ID 8323

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## SEQ ID 8324

LKADSNSSQLYQQSHQTSFQYAYDCPNRANFDRKG

## SEQ ID 8325

GTGATTAACCTATTGATTTATAATTTGTTTATTATTAACGCAATTTCCGATACCCCATCCATACCCCTTATATCTTAGCGTGCCCGATGCGCCCTCG

## SEQ ID 8326

VINLLIYNLFIINCISDTPIETPLYLVSVPDPS

## SEQ ID 8327

TTGGTAGAGCACTGCTTTGCAAGCAGGGGTCATCGGTTTCGATCCGTTTGCCTCCACCAAACTTTACAAATGAAAGCAAGTTTGTGTTTTAGCAGCTTATTTGATTTGCGAAGTA  
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## SEQ ID 8328

LVEHLLCKQGVIGSIPFASTKTLQMKASLFLAAYFDLRSRITTHRSLTNWKAEINKQRQ

## SEQ ID 8329

TTGGTAGAGCACTGCTTTGCAAGCAGGGGTCATCGGTTTCGATCCGTTTGCCTCCACCAAACTTTACAAATGAAAGCAAGTTTGTGTTTTAGCAGCTTATTTGATTTGCGAAGTA  
GAATAACGACGCATCGATCTTTAACAATTTGAAAGCGCAATCAACAACAAGAGACA

## SEQ ID 8330

LVEHLLCKQGVIGSIPFASTKTLQMKASLFLAAYFDLRSRITTHRSLTNWKAEINKQRQ

## SEQ ID 8331

ATGCCGCTGAAAGGCTTTACAGCGGCATCGCCCTTTGACCGGACACAGTCCGGCATATCAAGATCCGCCCTAAAAATATTAAATGGGCAAGAAGTTAATGCACGACATTACCCGCCAAC  
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## SEQ ID 8332

MPSERLSDGIALLTGHSAAVQGSALKILMGKKLMHDI TRQHKRK

## SEQ ID 8333

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## SEQ ID 8334

MGASLIQPCRVSEGLRVKDFCQGRKGRQYRRPMTVPRE

## SEQ ID 8335

TTGGTAGAAATGCAGGCAATGAGAGAAATGCGAGATAGACCTTCGATTTTCTCGCTGCTCTTATGGATGATTACGCTACCGAAGAGCAATATATGCCCTATATGATT

## SEQ ID 8336

LVENQAMRELQIEPSIFSRLLLMILPKSNIMPYMI

## SEQ ID 8337

GTGCGAGGCCAAGGCACTCACCTTATCGGTAATCTGTTTGTAAAGAGCGTTGCGAAATTATAAGTATCCCTTCCGCTGTCTAAGATATCTCTCGATATTTCCGACATTTCCGTGCT  
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## SEQ ID 8338

VRGPRHLSVICFVKERCELIKYPFRLSKISLDISDIPCTTFQVRRFGSGEBPNYTPAGENSQYQDRDFGKTRHVAWG

## SEQ ID 8339

ATGGCAAGCACTCGAAATCATTTACCCGATGAAATTTATTCAGATCTGATTTTAAGGATCCGGTACCTCCCACTATATATACAGAAATGATGAAACTGGTTGGTAGAAATGCAG  
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GGAATCGATAAAGATGAGATAACGGCTTTGATTAAATAGCTTAAA

## SEQ ID 8340

MAKALEIISPDRIYSDLPKDPVPPHTIYELMKLVGRNAGNERIADRAFDFPSPALMDSATTEEQYNALYDLTLLEPGRMELDKDEITLINSLK

## SEQ ID 8341

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## SEQ ID 8318

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## SEQ ID 8319

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## SEQ ID 8320

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AALEAQGANRVLQWLASTGVKNPAYPDTLYVDSLIGVHTVNTVPDATALKAFIDHGTAKATLTESADEARARLAEIALGIDVETLAARLQEDGLKQFBEAFERLLAPLV

## SEQ ID 8321

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## SEQ ID 8322

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## SEQ ID 8323

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## SEQ ID 8324

LKADSNBGLYQSHQSTFQTAIDCPNRPNDKTK

## SEQ ID 8325

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## SEQ ID 8326

VINLLIYNLFIINCISDPTIHTPLYSVPDAPS

## SEQ ID 8327

TTGGTAGAGCACCTGCTTTGCAAGCAGGGGTCATCGGTTTCGATCCCGTTTGCTCCACCAAACTTTACAAATGAAAGCAAGTFTGCTGTTTTAGCAGCTTATTTTGATTTCGGAAGTA  
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## SEQ ID 8328

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## SEQ ID 8329

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## SEQ ID 8330

LVEHLLCKQGVIGSIPFASTKTLQMKASLLFLAAYFDLRSRITTHRSLTNWKAEINKQRQ

## SEQ ID 8331

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## SEQ ID 8332

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## SEQ ID 8333

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AA

## SEQ ID 8334

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## SEQ ID 8335

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## SEQ ID 8336

LVEQANRELQIEPSIPSRLLLMIMQLPKSNIMPYHI

## SEQ ID 8337

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A

## SEQ ID 8338

VRGPRHSLSVICFVKERCILIKYPPRLSKISLSDIPCYTFQFVRRFGSGEEPNTYPAGENSQYFQDPFGEIRHVAVG

## SEQ ID 8339

ATGGCAAAAGCACTCGAAATCATTTACCCGATGAAATTTATTCAGATCTGATTTTTAAGGATCCGGTACCTCCCATACTATATACAGAATGATGAAACTGGTTGGTAGAAATGCAG  
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GGAAGTGGATAAAGATGAGATAACGGCTTTGATTAATAGTCTTAAA

## SEQ ID 8340

MAKALEIISPDEIYDLIFKDPVPPHTIYTELKLVGRNAGNERIADRAFDFFSPALMDDSATFEEQYNALYDL/LLLEPQMELOKDEITALLNSLK

## SEQ ID 8341

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ACTTCTCAGTAAATACAGGCGACCATCCGCAATATTGATGAAGGGGACTATGGATTCTGTGCCGATACGGGAGAACCTATCGCCTGAAGCGGCTGCTGGCAGCCCGACAGCCACTTTA  
TCCGTTGAGGCCCAAGAACCOCGAGAGAGGATGAAGAACAGTTTCCCGAC

## SEQ ID 8342

MVKLTEDQDILNWIGPEDDYMDHLAFRELLVKNQDELIENASVTTGHLQEHESAPDPADRATQEEYALELRTDRERKLLSKIQATIRNIDEGDYGFCADTGEPIGLKRLRLARPTATL  
SVEAQERRERMRKQFAD

## SEQ ID 8343

ATGTACACAGGACGCTTCGCCCCAGCCGACCCGGGTGCTCCACATCGGCTCTCTGCTGACCCCGCTGCTTCTATGCCGATGCACGTTCAAACCGCGGCAAAATGGCTGGTCCGTATGG  
AAGACCTCGATCCGCGCGCGAAATGCCGGGGCGCAAGCCATATCCTGCACACGCTCGAGGCATTTCGGATTCAAGTGGGACGGCGAAGTCACTATCAGAGCCCGCTTACGCCCTGTA  
TGAAGAAACCTATACCGTCTGAAACACCCCGGACTGGTCTATCCTGCCATTGCAACCGCAAGACTGGCAGGCGGGGCAAGCGGGGACAGACGGGTTCGTCTATAACGACGCGTGC  
CGCCACCCCGGCAACGCGCTGCACATGCAAGGCAACAGCGCTGCTGGCGCATCCCGCTCCCGACCGGACATCGGCTTTTCAGACGGCATCGTCCGAGTTACGCCCAAAACCTCGCCC  
CGGACATCGGCGATTTCCTCTGTTCCGTCGACAGGTTACTGGGCATACCACTCGCGCTGTCGCCGACGATGCCGAACAGGGCGTTACCCACATCGTCCGCGGACAAAGACCTGCTGCT  
TTCCACACCCGCGCAAACTATTTCGACGAGTGTTCGGCGTTCCGACACCGCAATATGCCACCTCCCGCTGCTGACCAACGCGCAAGGGCAGAAATGTCGAAGCAGACGCTCGCCCC  
GCATTGGATTAAACCGCGCGCAACACTTCTCCGCCAAGTGTTCGCTACCTCAAGCTGCCGGAAGCACCAGAACCGACCGCTCCCGAATTCGCTGACTGGCGGTGGCACACTGGG  
ATATGGACAAGTCCGGAACACGCCATTACCGCCCC

## SEQ ID 8344

MYTGRFAPSPTGLLHIGSLLTAVASYADARSNGKWLVRMEDLDPREMPGAASHILHTLEAFGFKWDGEVTTYSSRYALYEETLYRLKTAGLVYPCHCNKDWQAGARRGTDGFVYNGRC  
RHFGQRPALQKQPSWRIRVPDRDIGFSDGIVGSYAQNLRDIDGVLFPRADGYWAYQLAVVADDAEQVTHIVRGQDLLVSTPRQIYLLQQLGVPTPYAHLPLITNAQGGKMSKQTLAP  
ALDLNRREQLLRQVFRYLKLEFAPBETDRPARELLDWAHMDMDKVPKHATTAP

## SEQ ID 8345

ATGGCGCTGCCGTTGCCGGCGGATTTGGTCAAAACAGGGGATACCGCATCCATATAGCCAACCGTGGTGGCGAAAGCGCAACGTTTGGGAAAAGAGTTGGGGTGCAAACTTCGGCAA  
CCCTGCCCGAGCTTCATTCGACGATGTTTTAATCCTTCCCGTCAAAACCGCAGGATATGAAGCCGCGTGCAGAAAATATCCGACCAACCGCGCATTTGGTCTTTCTGTGCGACGCGGATT  
GTCCGTTCGTACGCTCAGCGTTACCTCGGGGAGCGCGCATTTGTCGGGTTATGCCGAATACACCCGGAATAATCGGCTGGGCGTATCCGCTATGATGCCGAAGCGAAGTATCG  
GAAACAGACCGCAGGATTGGCATCGAATCATGAATCAGTCGGTTCACCGTTTGGTGGGAAGTGAAGCGCAATGCAACAGCATTACCGGCATCAGCGCAGCGCGCGCTTATGTTG  
TTTATCTGCTGGACGATTGCAAAATGCCGCCATCCGACAAGGTTTGATATGCGAGAAGCAGCGCGCTCAGTCTGGCAACGTTTAAAGAGGCGGTTGCCCTTCCGAGCAGCAGCGGTGA  
AGATTTCGAGAAGCTTCAAAAAATGTAACTGCAAAAGCGGGACAAACCCAGAACCGTGAAGCCTTCAGACGCGCATCGTTCGCGAAGCCATAAGTGAGGGCGTTTGTGCTGTGTG  
TCCGTTCCGAGGAATGGAACCGCAATATCAA

## SEQ ID 8346

MAAAVAGGLVKQGGYRIHIANRGAERERLKGELGVETSATLPELHSDVLLAVKPDMEAAKNIRTNALVLSVAGLSVGTLSRYLGGSSRRIVRMPNTPGKIGLVSGMYAEAEVS  
ETDRRIADRIMKSVGLTWLEDAQMSHISITIGSGSPAYVYLLDALQNAIRGQFDMEARALSLATPKGAVALABQTGEDFEKLQKNVTSKGGTTHEAVEAFRRHRVAEALSEGVCACV  
CRSQEMERQYQ

## SEQ ID 8347

ATGGAAATTCGGGTAATAAAATATACGGCAACCGCTGCCGTTGTTTTCGATTACGGTTGCGAGGCTGCCCGCTGGCGGGGTGGTATGAGTGTTCCTTGTCCGGCTGGTGTAAAGCCGAGAA  
AACCTGCCCGCATCGATTTCCTGGGATATTTGGCGCGAGAGTCCGCTGCTTTAGAGGACTACGAGATACCGCTTTCAGACGGCAATCGTTCCGTCAGGGCAACAGAAATGAATCCGCGCA  
AAAATCTTACTTTTATAGGAAAATAGGGAAGTTTGAAGCTCGCGGTTTGGATTGCGCTACCGGTGACGGCAACCTTTGTTGAGAGGTTCAAACAGGAAGGTTTCGACTGTTTGGAAAAG  
CAGGGGTTGCGCGCAACCGCTGTCGAGCGCTCCGATGG

## SEQ ID 8348

MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAADPMDIGGESPLSLEDYEIPLSDGNRSVRANEYESAQKSYFYRKIGKPEACGLDWRTRDGLPLVERFKQEGFDCLER  
QGLRRNGLSERVW

## SEQ ID 8349

ATGTTTGAGTTAAAGAATGTGAAACCTTATGATAAAACAGGAACCTTATTGAACATAAAGGGAAGAGCGTTTATGCGTCGCCCGATGCTCGACTGGACGGACAGGCCTACCGTTACCT  
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GCAACTGGCGCGCAGCATCCGTCGATTTCGGCAAGCGCGCAAGCGCGCGAAGAATACGGCTACACAGAGTCAACCTCAACTGCGGCTGTCCAGTCCGCGCGTGCAGAAAGGCGG  
TTCGGCGCGTGTCTGATGAACGAAGTCGGGCTGCTTGGCGACTGCTCAACGCCATGACGACGCGGTGCGGCATCCCGTTACCGTCAAACACCGCATCGGTGTGGACAGGCGAGCGCAAT  
ACCAACCGCTTGGCGATTTCGTCGGCAGCTGCGCGACAAAACCGCTGCAAAACCTTCATCTGTCACGCGCGCAACGCTTGGCTGGACGGTCTTTTCGCCCAAGAAAACCGCATGTTCC  
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GTGATGCTCGCGCGCGGAGCATCAACACCGCATGGTGTGCGCGAATGGGACAGGCTGTTTACGGTGACAAACCGCGCCCGATCGAATACCGCGATTGTGTCAGCGCGCTCTACACAT  
ACAGCCAAAGTCAAAATCAAGCGGACGCGGCACAATCTGCGCCACATTGTCGCCACAGCTCGGGCTGATGACAGGTTTGAAGGCGCGCGGACTTGGCGCGGTATGCTTTCCGATG  
AACCTCTTGAAGACAACGACGCGCGCTGATTTCGAAGCGTGAAGAAGTGAACGGCAAAATACCGCGCA

## SEQ ID 8350

MFELKEENLMINKELIEHKRRRLCVAPMLDWTDRHYRLARQITRNALYSEMNAGAIYVGDKDRFLMPNEGEQPVALLQGGSDPSDLAKAAAEYGYNEVNLNCGCPSPRVQKGA  
PGACIMNEVLVADCLNAMHDVGIPTVVKHRIQVDRQTEYQTVADPVGLTRDKTACKTFIVHARNALDGLSPKENRDVPLKYDYVYRLKQEPPELIIINGGITNEALAGHLQHDVG  
VMVGREAYHNPVMREWDRLFYCDNRAPIEYADLVQRLYYSQVQIQAGRGTTILRHIVRHSGLMHGLKGARTWRRMLSDATLLKDNDDGLIFPAWKEVERANTRE

## SEQ ID 8351

GTGCGAGGCCCAAGGCACTCACACTTATCGGTAATCTGTTTGTAAAGAGCGTTGCGAAATTAAGAATATCCCTCCGCTGTCTAAGATATCTCTCGATATTTCGACATTCGGTGTCT  
ATACTTTTCAGTTCGTCGCGCGCTTCGGCAGCGCGGAAGAACCAACTATACGCCCGAGGGGAAACAGTCAATACTTTCAGCGGGATTTCCTGGGAAATTCGTCATGCTGCTGCGG  
A

## SEQ ID 8352

VRGPRHSLSVICFVKERCKLIKYPFRLSKISLDISDIPCTTFQVRRPGSGEFPNTPAGENSQYFQRDFGEIRHVAVG

## SEQ ID 8353

TTGATTAAAGAATTGATAAAACAATGGGTTTGAAGTGATTTCGCCATTTTGGCTTCCTGTCGATTTCAAAATTTTGTATTATATAACATTGCATTTTATATCATAGATTTTGA  
GAATACTCAGAGGCAATAGGCAAAAGTTTTCAAA

## SEQ ID 8354

LIKRIDKTMGLSVCAILASRRISKFCYYITLHFLYHKILRLRGRHQKFPK

## SEQ ID 8355

ATGGTGCAAAATGGCAACAATAACCAAGCGCGCAATCCTTCGCGGAAACAGTATATCGGGTTACAGGTACGGTTCGCGCAAGAAAGGCTATCTGCTTTCATAGAGAGCAGGAGTTACGTA  
AAAAGGCTTTGGCGTTCGAATGGGGGAAGAAACGGGAGCGGAAATCGAAGCGCGCCAGAACTGCTTTTCAAGCGCGCAAGGTCAAGATGATGACGCTGTCCGAAGCTATCGGGAAGTA  
TCTTAACGAAACCGTTGGAAGCGGTCGCTCAAGAAAATGGGCTTCGCTTTTCATGAGGAGTTCCGATTCGCGCATCGGCATCGATAAGCTGAAACGGTCTGATTTTCGCGGAACCGTT  
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AAATAGGCTGGCAGGAATTTGGATTTCGCGGCAAAACGGGCTGAAACGCTCGAATATGTTGGCGAAATCTGCAATCAGGACAGATTCGCCGACCAGGAAGAACTGCAAAACCTGACAACTTA  
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AAAAATGATTGTACCCGGCCGGTCTGTGATTAAAAAATCCGAACGGCAGCAGCAGGGAATAATAAAGGAGTTTGATATTCTGCCTATGGCTTTGCGCGTCAATTGACGAGCTGCCGAGGAAT  
CGGTGAGGAAGCTATGCTTTCGCCAACAAAGGCATCGCCGACAGCTGCTTACCGTGCACCGAAAAATCGGTTTCCGCGCTTGGACGAGGGCGTGCAAGGTTCTTGAATTAAGACTTGGC  
CTTCCACGATTACGCAAGCAGGCTTCCCGTATGCTGGTGAAGCTGGTCTTACAGTTCGCAAGATGAACCGGTAAACGCTGCATGACGGTTGGAACAGCCTCCAGAGGTATGTGAGCGTA  
CGCAAAACGCTCGACGCGGCTGGATTTTAAAGAGGCAATGATGCAGGCGCAAGCGATATAAAATCCGGAAG

**SEQ ID 8356**

EVQMATIKRRNPSETVYVRVQVRVGKGYPAFNESTRTPSKKALAVENGKKREARTEAGPELLFKRGKVRMMTLEAMRKYNELTAGRSKRNGLRFLMEFPIGGIGIDKLKRSDFAEHV  
MQRRRGIPELDIAPIAASTALQELQYRSVLKHAFYVWGLEIGHQELDPAANGKRSNMVAKSAIRDRLPTTELEQLTITYFLRQWQSRKSSIIMHLLIMLAIYTSRRQDEICRLIFDDWH  
KNDCTRPVRDLKNPNWGSTGNNEKFDILPMALPVIDELPEESVRKRMLANKGIADSLVPCNGKSVSAAMTRACKVLGIKDLRPHDLRHEAATRMEDGFTTPQMQRVTLHDGHNLSLQRYVSV  
RKRSTRLDPKAEMNQASDIKSGK

**SEQ ID 8357**

ATGACGGTGTGCAAGAACGTTATCGTGAGGTGTCGACCGGTATCGGAAAAATTGGTTCTGCAGGCGGGCAGGGAGCCGCAATTCGTCAGCCTGATTGCCGTGACGAAGACCTCCCTTCAG  
ACGGCATCCGCGAAGTTTACGCTGCGCGGACAGCGTGATTTCCGGCGAGAACTATATATTCAGGAGTGTGTACGGCAAAACGGAGGAATTTGCGGATTTGACCGACATCGTGTGGCAGCTCATCG  
CGATGTGTCAGTCGCAACAAAACCAATTTGTCCGCCAAGCGCGCGCATTTGGGTGCATACCGTATGCCGTCTGAAGACCCCGTCCGGCTGAGCAGGCAGCGTGCCTCCTTAATGCCGCCCTTG  
CAGGTGTGTGTCAGGTGGAACATTTGGCGGCGAGCGGCAACCGGTGTGTCGCGCCCAAGAAAGCGGTGCTGCTTTGCCGTGAAGTGGCGAAGCTGCCCAACCTTGTGTGCGCGGACTGA  
TAGTGTGCTGCCAAGGCCAACGACGAGTGAACGAGGTGTGAAACTCAGTTTCAGACAGTCGAAAGCTGCGTCTTGGCAGCTCAATCGCGCTGGCTTTAAGGCGGACGTGCTGTCTATGGGAT  
GTCGGACGATATGCTCTGCCCATTTGAGTGCGGTGCGACACAGCTCCGTATCGGCAGCGCGCATTTTCGGGAAAAGGGGC

**SEQ ID 8358**

HTVLQERYREVSDRIGKLVLAGREPHSVSLIAVSKTPPSDGIREVYAAGQDQFGENYIQEWYKTEELADLTIDVHVHVIDGVQSNKTKFVAERAHVHTVCLRLKTAVRLSRQRSLAPFL  
QVCVEVNLAGEAAKHGVAPEEAAVALAVEVAKLPNLIVVRGLMCVAKANSSETELKQFQTMKLLADLNAAGVKADVLSKGMDDMPAAIECGGATHVRIGSAIFGKRG

**SEQ ID 8359**

ATGCAGATTACCGACTTACTCGCCTTCGGCGCTAAAAACAAAGCATCCGACCTTCACTCTGAGTTCGGGCATATCCCCATGATTTCGGGTTCACGCGGACATCGGGCGCATCAACCTTCCCG  
AAATGAGCGCGGAAGAGGTTCGGCAATATTGTAACCTTCGTGTATGAACGACCACAGCGGAAATCTACCAGCAAAATCTGGAAGTCGACTTCTCTGCTGCAACTGCCCAAAGCTCGCCCGATT  
CCGCGTCAACCGCTTCAACACCGCGCGCCGCCCGCGCCGCTTCTTCGCAACATTCCCACACCGCTTCTATCGCTTGGAGAAGATTGAAAGCCCGGAGCATTTTCCAAAAAATTCGCAGAAATCG  
CCGCGCGCATGTGATTGATTTCACGGGCTTACCGGTTCCCGTTTCGGGAATTCGACACAGCTCTGCGCGGATGATTAATCATATCATGAAAGAACCCAGCGCGGCACACATCTGACCATCGAAGACCGGA  
TCGAATTTCGTCCACCAAAGCAAAAAATCCCTGTATTACCAACGCGAGCTGCACAGCACACCTCAGCTTCGCCAACCGCGTGAAGTTCGCGCATTCGCGGAAGAACCCGAGCTGATTTCGT  
CGCGAGATTCGCGGACCCGAAACCATTCGGCTTGGCACTGACCGCGCGCGGAAACCGGACATTCGGTTTCGGGACGCTGCACAGCAGCCGCGCGGCAAAAACCGTCGACCGTATCTCGGGAC  
GTATTTCCCGCGAGGAGAGAAAGAAATGGTGGCTTCCATGCTGTTCGGAATCGCTGACCGCGCTCATCTCCAAAAACCTGCTGAAAGACGACAGCGGAGCGGCGGTGTGCTCTGCACGAA  
TCTGATTTCGCAACCGCGCGTTCGCAACCTCATTCGCGAGAACAAAAATCAGCATATTAATCTGCTCTGCAAAACCGGCGGGCGAGCGGTATGCAGACGATGGACCAATCTGCTCAATC  
GCTGGTGGCCAAAGGCGTGAATCGCACGAGGACGCCACAGCGAGACCGCGCAAAACAGCAAGAAATGATGATTTTC

**SEQ ID 8360**

HQITDLLAFGAKNKASDLHLSGSGISPMIRVHGDMMRRINPEMSAEVEGMMVTSMNDHQRIYQQNLVDFSPFLPNVARFRVNAFNTGRGPAAVFRTPSTVLSLEELKAPSIQRIAES  
 PRGMVLVTGPTGSGSKSTTLAAMINYINETQPAHILTIEDPIEFVHQSKSLINORELHQHTLSFANALSSALREDPDVILVGMERDPETIGLALTAAETGHLVFGTLHTTGAARTVDRIVD  
 VFPAGEKEKVRSMLSLSLTAIVISONLLKTHDGDGRVASHEILLIANPAVRNLIRENKTIQINSVLQTRASGMQTMDSQSLSVRQGLIAPEATRRRAONSNSNF

**SEQ ID 8361**

ATGAACATCAGTAAAGAACAAGGGCTTTTAATCGCATACGGCGGCGCCCGGTATATCCCGCCGAGGGAAGTACACAAAGACTTTTTTGGCCATATCGGCTTTAAACGCGTTAAAGCATCGG  
GGTGGCGTGCGAGCTTCCGTTCCGATTTCCGATTGTCCGACAGCCGAAAATCGGAATATTTCGTACAGCTCCGAGAGCTTGCAAAGCAATCGCAGACAAGGAGGAAAAGCCAAAATC  
GGAATATCGGAAATTCGGTCT

**SEQ ID 8362**

MNI SKEQGLLIAYGGRPYI PPREVHKDFFAHIGFNAFKASGVRCELFPPIFRLSDSRKSEYFVSVRELAKAIADKEEKAKSEYRKPRS

**SEQ ID 8363**

TTGCATCAAGACGGGAATTTCCGATATTCGGATTTTGCCCTTTTCTCCTTGCTCGCATGCGCTTTCGCAAGCTCTCGGACGCTGACGAAATATTCCGATTTTCGGCTGTTCGGACAATTCGGA  
AAATCGGAAACGGAACTCGCACCGCACCCCGATGCTTTAAACGCGTTAAAGCCGATATGGGCAAAAAGATCTTTGTGTACTTCCCTCGGCGGGATATACGGCGCGCCCGGTATTCGCAAT  
TAAAGCCCTTGTTCTTTACTGATGTTTCATATATACCTCTTTCTGT

SEQ ID 8364

LHQDRNFRYSDFAFSSLSAIAFASSRTLTKYSDFRLSDNRKIGNSSHRTPDALNALKPIWAKKSLCTSLGGIYGRPPYAIKSPCSLLMFIYTSFC

SEQ ID 8365

ATGTAATACCGGATAACCTGCACGACATCTTGACGAAACGGTTCAAGTGTATTCTCAAAAAAACAAGCCGATCCGAAACCCCGCGCGGAAATCGGCACACACTTCCACCCGCTGCTCGACC  
GCCCTGTGCGAAACCCGCAGAGCAACAAACGGGTCGACATCTTATCAGCAAAAGGATTCGCCCTCGTTGAAAATCAACAGCGCATTAACCCCGCAGCGCAAAAGGCTCTGACGGGCGA  
GGAAACCGCGCCCATCGCCGATCGACGATGAACGCGCGAACAATCGGAAATATTCGCGCGCAGCGCGAAATCAACTACTCCGCTCAATCGCGAGCGGCACGGCTACCGCGCGCAACGCC  
TACTACATCGCAAGGCGCGCGAGGTTTGGTTTTCGCGGCATCAACCAGCTATCTCCGCAAAATCGGGAAATTTGGGCTTTGCCGAAAAAAGCTCAAAGACCTCGCCGTCGACCGCGCGGGCTG  
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AACAGCAACCAAAATATCTGATTGACATCGCCCTCAATCTGACCGGCATCATCTGCCAAGCCCTCGCCCTCAAAAAGACAAAACGGCGCAGGACGCGGTTGTGCACTTGTCTATCAACAC  
GCCCGCCATCCAGGACTTCATCTTGAAGGGCAGCTGATGAACATCAGTAAATCATGGAACCCGCAAAACCGACGGAATGCAGACGATGGAACCAAAACCTTTTCGAACTGTGACGTCAC  
GCTCATCATGATGTACGAAGAAGCCGTGCGCGAGTCGTTTTCGCAACAACTGCGATTGCACATCCAATGCACAAAGAAGGCAAAACGCCCGAACTCTTTACGACAGGGTCAACGGTC  
TCAACTCATTTCC

SEQ ID 8366

MNTALHDILDTVQVVSQKKQSRSETPAEIGTHFHPFLDLRLCETAEAQNASDILISKGFPPSLKINSALTPQPKALGTEETAALAASTWABQSEIFREDGEINYVSQSRSGTRYRANA  
 YYSQGSAGLVLRRINHVIPQMRGLGPELKKDLAVAPRGLLIIVGPTGSGKSTTMTMLBHRNKLPGHIVTTEDPIEPIYKPRRCIFTQREIGVDITNWQTAVDNAMRQSPDVCIGEV  
 SRESMEYAMLAQTHGLCIFTLHANTAPQSLERILINFYKPEQHQNILIDIALNLFGIICQRIALKKDKTGRATAVVDLLINTPAIQDFILKGDLMNISKIMETARTDGMQTHDQNLPELYR  
 GIISYEALRQSVSANNRLHILHQHKEGKTPELLYDRVNGNLIS

SEQ ID 8367

TTTAGAGGAGTGGGGTTTTTCATGGTTTTACCGGTTTTATTGTTATGAAGTGAATAAAGTGTGGCCATGAATGGGGCGGATAAAATCATGCCGTCTGAAAACGGGGATCGGTTTTTCAGACGGC  
ATTGGGTTTTTCGGGATCAGGAAA

**SEQ ID 8368**

LRSGVFMVLPVYCYEVNKHWHMNGADKIMPSENGDAVFRRHVLRIRK

**SEQ ID 8369**

ATGAAACCACCCACTCTCTCAAGCCTCTGCTCAITACCTCGCTTCGCGTTTTCGCCAGTGTCTTTACCGCGCCTCCATCGTCTGGCAGCTAGGCGAACCAAGCTCGCCATGCCCTTCGTAC  
TCGGCATCATCGCGCGCGCCTGTGTGCAATTGGACAACACGCCCTGACCGGACGCGCTGAAAAACATCATCGCCACCGCTCGGCCGTGTTACCTCTCTCTCGCTACGGCGCAAAAGCACCTCGG  
CACAGGGCTGCCCTTCATCTCGCATGACCTGATGACCTTCGGCTTTACCACTTTTAGCGCGCGGTGGGCTGAAATACCGCACCTTCGCGCTTCGGCGCACTCGCCGTTCGCCACCTACACCC  
ACGCTTACCTACACCCCGAAACCTGATGGCTGACCAACCCCTTCATGATTTTATGCGGCACCGTACTGTATCAGCACCGCCATCATCTCTGTTCCAAATCATCTTGGCCACCAGCCCGGTCC  
AAGAAGCGCTCCCAATGCTACGAAGCATCTGGCGCGTACTTCGAAGCGAAGCGCACTTCTGCACCGCGATGAGGACCGCTGGATAGGCAACCGCCACCATCGACCTTCGCATGAGCA  
CACGGCGGTTCATCCAGCCCTTCAACCAATGCGGTTTCGCGCCTGTGTTTACGGTTTGCGGGGCAACACCGCACCGCGCACCGCGCAAAATGCTCGGGCTACTACTTCGCGCCCAAGCAATC  
CAGAACGCATCAGCTTCGCCACGTCGACTACCAAGAGATGTCCGAAAAATTCAAAAACACCGACATCATCTTCCGCATTCGCGCCTCTGCTCGAAATGACAGGGGAGGCGTCCGCCAACA  
CGGCCAAGGCATCGGTTCGGGCAAAAGACTAGCTTTACAGCAACAGCCCTGGAGCGGCCATCGAAGGCTGCCGCCAGTGCCTGCGCCTCTCTTCAGACGGCAACGACAGTCCCGACATCCG  
CCACCTGAGCGCGCTTCTGACAACCTTGGCAGCGTTCGAACAGCAGTTCGCCCACTCCGACACAGCGACTTCCCGCGCGCAAAAGACCGCATGGCGGACACCCGCATTCGCGCGCTTCGAA  
ACCGGCAGCTTCAAAAAACCTTGCAGGCAACTCGTCCGCGCACTGAACTCCGAATCATGCGTATTCCGCATTCGCCGTTCGCGCTGTCCCTCGTCTGTTCGCGCGCGCTTGACCATCTGTTCGAAG  
CCCTCAACCTCAACTCCGCTCTGCTAGTACTGCTACGCGCCCTTTTGCTGTTCGCAACCAACTACCGCGCCACCAAGCGCGGTGTACCAACGCATATCGCGGCACCGTACTTCGGCGTAAT  
CGTTCGGCTCGCTCTGCTCCCTACTCTACCCCCCTCGCTCGAAACCAAACTCTGGAATTGTCTACGCGGTACCACTCTGTCTTCATGACCGCGACATCATAAATCAAGCTTTCTCCACTCTCTTC  
ATCACCATTCAGGCACTGACCAAGCTCTCCCTCGCAGGTTTGGACGTATACGCGCGCATGCGCGTGCGCATCATCGACACCATATATCGCGGCATCTCTTGCTTGGCGGGCGGTTCAGCTACC  
TGTTCGCAGACTGGAAATACCTACAGCTCGAACGCACCGCGCGCTTCGCGTATGACGACGCGGCACATACCTCCAAAAAATTTCGCGAACCGCTCAAACCGCGCAACCGCGACGACAT  
AGAATACCGCATACACCGCGCGCGCGCCACGAACACACCGCGCGCTTCAGCAGCACCTTTTCGACATGAGCAGCGAACCAGCAAAATTCGCGGACAGCTGCAACCGCGCTTTTACCTTG  
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CCCATCTTCTCAACACTGTCCGACATGGAGTACCGACGACACTTTTCAGACGGTATGGATACATGCGCGGCAACTTCGCGACCTTCGCGACACCGCGCAGCGGAACAACAAAGCCATCTCT  
CTCCAAACAGCTTCAACTCATCGCGCGCAACTCGAAACCTTACTACCGCGCTTACCGACAAATTCGCGCAGCGCAGCCCAAAACGCGAGCC

**SEQ ID 8370**

MKTPLLKPLLLTSLPVFASVPTAASIVWQLGEPKLAAMPFVLGI IAGGLVDLDNRLTGRKLNIIATVALFTLSSLTQAOSTLGTGLBFFILAMTLMTPGFTILGAVGLKYRTFAFGALAVATYTT  
 TLYATPEFYVWLTNEFMLLGGTVLYSTAAILFQIILPHRPVQESVANAYEALGGYLEAKADFPDDEAWIGNRHII DLANSNTGVI TAFNQCSALFVRLRGKRHRPFTAKMLRYVFAAQDI  
 HERISSAHVDYQEMSEKFNPTDITFRIRRLLEMMQGAACRNTAQAIRSLNGQVYSYKRLGRATIEGCRQSLRLLLSDGNDSPDIRHLSRLLDNLGVSVDQQPRLRHSDSPAENDRMGDTTRIAALE  
 TGSGFNWQAIKRLNLNLESCFVRHARVILSLVAWAEITAEALNLSKGLWITLLTALFVCPQNPYATKSRVYQRLAGTVLGVIVGSVLVPYTPSVETKMLVILAGTLLTFMTYTKYSFSTFF  
 ITI QALTSLSLAGLDVYAVMPVRNIIDITIGSLAWAVSYLWPFMDKYLITLERTAAALVACSSGGTQIQIAERLKTGETGDIDIEYRI TRRAHEHFAALSTLSDMSSEPAKFADSLQPGFTL  
 LKTGYALTGYI SALGAYRSEMHEECS PDPTAQFHLLAEHTAHI FOHL PDMGPDFQTALDTLRGELGLTRRSSGTSKHLLQOQLIARQLEPYTRYAYROI PHROPQONAA

**SEQ ID 8371**

TTGCGACAAACGGCGCCGGCTTCAGCTGCTTCAACTGGACCGGAACATTTCAAACGGACGGCAAACTTGATCAGCTCTCATGCACAGGGAAGCGCGGCATGAGGACGCACATCCGAACCTGCG  
TGTATCAGGATTCGGCGCAAAAGGCTCTAAACACGGCATCAGGCATAAGCGGCACGGCTGCCGGCGCGCGGGAACAAGCGTTTTTCAGCGCGCGGAGAGCGGCAAAACCGCAGCGCGCTCAGC  
CGCATCCGCAAAACGCTCCGCCACACCCGGACAGCCAAAGAACGGACGAAACCCTATGACGTTTCAAGGACCAACAACCGTAAAAAGCCGGCGGCTACGCCAATACATCATCGGGCGCG  
CCGTAGAGCGCGCTTCCGCCCAAGTCCCGCGATATTCGCGCGAACCAACCCGGCGATTTCAGCGCGCGCGAGGAAGCGGCGCATGGAGACGCATACGAACCTGCGGATTTCCCGC  
ACGTTAGAGCTACAGGCGGGAAGCGTTGAAGCTTTGTGCAAACTACCCCTCGCGCAAGATGTATCAACAACAGCGTTTTTCCTTTATACCGACGGCGAAGCTCGCAAGCTCAGCGCTCATGAA  
TCCGCCGTTTTTCATCAAGCTAAAGGATTTGAGCGAAGACGAAAAAGCGGTATCGCACAGGAATACCCGTGGAAGAAATCGGCGGTAGCCGATGAAATCTCTGTTTTAAAGGATTGGAA  
AAGCCCGCGCGCTTCGGATCTTTTACCTCTGTTCCCGGCATCGCTACCGCAAAAGCGAGCAGCGATTCCCGGAAATCATCGGCAACCGGCTGGCAGAACTCAACCGCATACAAAACGCGT  
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AATCGAACCCGGACTTTGGGCAAAACCGTGAAGAACCCTGCACCCCGCAAGGAAAAAGGAAGACCCCGTCTCTTTGGAACACGAATGCCGTGACGCAGCGGCAAGCGGATTGCCCGGGAATTG  
AGGTTTACCAAAATGTGTACAGAGATGAAGCGCTGGCGCATGCCGAATTTGACGGCTTTTGCGACCGCTGTGCAACCTGTATACGGCAGAGAAATACGAAAAAAACACTACTTCCCGT  
CGAGCTCGCCAAATTTCCAGAGGGCGCGCGCGC

**SEQ ID 8372**

LRQRRLQLLLQDRTPTQDGGKPDQPHQAQSGSGMRTHIRTCVYHDSGKSGNSATSGISGTAAGAABQAPPSAAKTANRSASASAANAPPHFDPKPKNGKPMPTFGQHNHNRKKAAGGYAEYITGG  
SLRRLVAAKVRRYCEHPGVFDGAAGSGQLEQYIEPSDFRAVEIQAEACKALLQNYPAKVYNTSLPLYTDGEPQDCTVMNPPFSIKLKDLSDEKSRIAQEYFWKSGVADEIFVLKGL  
NARRFGFFILPFGIAYRKSEQRFEIIGNRLAEINRQIQADEFDPIEVLILLVIDKDKTDGGCIRELYDCKDTLLAADTWQIEPDLNQTVQEPAPPKKEKEDPVILLEHBCRDAAAKRIAREL  
RFSKMVNRTEGPHAEFDGFCDRICNLQIAEKYKGHYPPCSLPLFGGAAG

**SEQ ID 8373**

TTGGGCATTGAGAGAACCGCATCAAAAAATCGAGAAAAAAATGCAAAACAGTAGCAACAAAAACCGACGGCAAAACAGATGCTTGCCCGCAAAACGCGCGGCGAAGGAATCAACGCGGCAGG  
AACGCGCCGCTCAAAACGCGCGGGACCGTCAGAAACGTTGACCGGAACCGCGCTGCCGCCCGGTCAAAGGCGCAAAAGAAACATCGCGCCGATGTGTGTCGCGCGCAAGGTATCGGAAGA  
CGAAGCCGCTGACGTGCGGCATCATGATCGCGCTGCCCTCGCAGGATATCGCTATCGCTGCAATCAGGAACTTAATCAACTTCGCGCAACATATCTGTCACAAACAGGTGCAACGCTTGGGCCAT  
TACTGCAACACTGACGACCCGCGCAAGCGGGAAGCGGTACTGTTGCCCTGCGCGAAAGATTCGCGAGCGCGCTGCGCAATCAAGTAAAGATTTTGACAACTTAAGCGCCGAATCGCGCCAAC  
TCGTGTCGCTCCGCTGTCAAACTCTTTCGCCGCGTACGAAGAATTCTTGAAAGACGCGCTGCACGGCTGATAGCCGAAGTATCGGCATACTCATTGGCCGTGCGGGTTGCCAAGAAGAC  
CATGGCGTTTTTAGAGCTTTGACGCGCGTTTGATTTTGGCGGTTGGCAAAGTCGTCAACGCGCGCGATTTCGCGCGCGGGAAGCCCGCCGCTTAAATATGCGGTACGCGGAATTTACAGGCCG  
ATCTTACACGCCCGCAACCTGCTTTACGATGTGGGCATTTCAGGCGGCAAGGAGCTTTCGGCGATGTACGCGCAGCCGCTGAATCCCGTGGCGCCCGAGCGGATAGCGACGTGCGCGCGC  
ACATGATGAAAATGCTTTGTCGCGCAACGCGCGCGCTGCTTGTCTCGCGCGCTCGGAAGACGTCATCCGGCATTCGCGACACGCGCGCGCGCTTCAGCTGCTTCACTGGAACGA  
CGAATTTCAAAGCGGCAACCACTTCAGCTCATCGCTCAGCAGGGAAGCGCGCGCA

**SEQ ID 8374**

LGIERTASKNRENKMTVATKPTAKQLAAKRAAKESTRQERAVRKAGTVRNVDNRNLSARSKAQENIARMLSGAKVSEDEALTGCGIMRLSLQDMRYCQELINFIAEHIVKQVQRLGL  
 YCMTDDPANGESVLFACREASQAVQMTKDFINLSPNQRLVLRPLNSLPAAYEEFLKDPARLIAEVSAYSLAVRVAKKAMAFLELDGGLISAVGKVVNGADSRABRRLKMPYAEFTGR  
 ILHAANLLYDVGCIQADKELSAMYGKPLNPPVRPRRI SDVRRPMMKLVDKGGALVRAVKDSEDVIRHCNGAGFSCPNTEHPKRTANLISLMHREAAA

**SEQ ID 8375**

GTGGGCTTGGAAACGGTCAGCGTCGTGGGCAAAAGCCGTCCGGCGCGCACTTCGGGGCTGCTGCACACTTCGACCGCCCTCCGACAAAATCATCTCCGGCGATACTTTGCGCCAAAAGCCG  
TCAACTTGGGCGACGCTTTGGACGGCGTACCGGGCATCCACGCTTCGCAATACGGCGGGCGCGCATCCGCTCCCGTTATTCGCGGTCAAACGGGCAGACGGATTAAGTATTTGAACCATCA  
CGGCAAAACGGGCGATATGGGCGGACTTTTCTCCGATACAGCCATTAATGTTAGATACCGCTTGTGCGAACAGGTTGAAATCTTGCGCGGGCCGGTTACGCTCTGTACAGCTCGGGCAAT  
GTGGCGGGGCTGTCGATGTTGCCGATGAAAAAATCCCGGAAAAAATGCTCGAAACCGGCGTATCGGGCGAAGCCGGATTGCGTTTGAGCAGCGCGCAATTTAGAAAAATGACATCCGCAG  
GCATCAATATCGGACTGGGCAAAAATCTCGGTGGCATACCGAAGGCTTGTACCGCAAAATCGGGCGGATTACGCCGTACCGCGTTACCGCAATCTGAAACGCTTGCCCGACAGCCATGCGA  
TCTCGCAAAACGGGCAGCATCGGGCTGCTTGGGTGGCGCAAAAGGCTTTATCGGCGGCAGCATACAGGACCGCTCGCAGCCGCTACGCGCTTGCTGCCACAGCCAGAAATACGATGATTG  
CACCGCGCATCATCTGCGCAAAAGATGTTGATACAAACACGTAATTTGACGCTTATCCGCATCTGTTGACCGAAGAAAGACATCGATTACGCAATCCGCGGCTTGAGCTCGGGCTTCCACG  
ACGGCGACGGTGCACACGACACACCCACAACGGCAAAACCGTGATAGACCTTGCAGCAACAAACGCTACGAACCTCCGCGCGGAATGGAAGACAGCCCAATCCCGGTTTGAAGCCCTCGCGG

ACATCTGAACCGCAATGACTACCACCAGACGAAAAAGCAGGCGATGCACTAGAAAACCTCTTCAACAACAAACACACACGCGCGTATCGAGTTCGCCACCAACCCATAGGCGCTCTG  
AAAGGCAGCTGGGGCGTCAATATTTGGGACAAAAATCCAGCGCGCTTTCCGCCATTTCCCGAAACCGTCCAAACACCGATGTTGATTGACAAATGTCGCCGCTTACAGCTTTTTCGGTG  
TAGAACAGGCAAAATGGGACAACTTACGCTTGAAGCGCGGTACGCGTGGAAAAACAAAGCTCCATCCGGTACGACAAAGCATTGATTGATCGAGAAAACTACTACACAGCCCT  
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CAAGAACTGTACGACACGCAAGCAGCTCGCCACCAACCTTTGAAGTCGGCAACAAACCTCAACAAAGAGCGTTCCAAACATATCGAAGTTCGCGCTGGGCTACGAAGCGGACGCT  
GGCAATACAACTTCGGCAGCTTACCGCAACCGATTTCGGCACTACATTTACGCCCAAACCTTAAACGACGGAACGCGCGCCAAATCCATCGAAGACGACAGCGAAATGAAGCTCGTGGCTA  
CAACCAATCCGGTCCGACTTCTACCGCGCGAAGCGGAAATCTACTTCAACCGACACCGCGCTACCGCATCGGTGTTTCCGGCGCACTATGTACGAGCGCGCTGTAAGAAACCTGCGCTCC  
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TCGATGCGCAATTTGGACTACTACCGCGTTCGCCCAAACAACTCGCCCGCTACGAAACGCGTACGCGCGGACACCATATGCTCAACCTCGGTGCAAACTACCGCGCAATACGCGCTA  
TGGCGAGTGAATTTGTCAGTCAAGCGGACAACTGCTCAACCAATCCGTTTACGCCCAACAGCAGCTTCTCTCTGATACGCGCAATGGGCGCGAGCTTACCGCGCGGCTAAACGTA  
AAGTTT

## SEQ ID 8376

VGLTVSVVVKSRPRATSGLLHTSTASDKLISGDTLRQKAVNLGDALDGVPIHASQYGGGASAPVIRGQTRRIKVLNHHGETGDMADFSPDHAIMVDYALSQQVELLRGPFVLLYSSGN  
VAGLVVDVADGKIFKPKENGVSSEAGLRSSGNLEKLTASGINIGLKNFVILTEGLYKSGDYAVPRYRNLKRLPDSHDSQGTSGLSWVGKFGFIAAYSDDRRDRLPAHSHEYDDC  
HADIIWQKSLINKRYLQLYPHLLTEEDIDYDNPGLSCGPHDGDGAHHTHNGKFWIDLNRKRYELRAENKQPPFGFEALRVHLARNDYHDEKAGDAVENFPANKTHNARIELRHQPIGRL  
KGSWGVYQLQKSSALSAPETVQPHLIDNNVHRYSFFGVEQANWDFLTLEGGVREKQKASIRYDKALIDRENYNQLPDLGAHQRTARSFALSNGWYPTPHHKLSTASHQERLPST  
QELYAHGKHVATNTPFVGNKHLNERSNNIELALGYEGDRWQYNLAAYRNRPKNYIAQTLDNRGPKSIRDDSEHKLVRYNQSGADFYAEGEYFKPTPRYRIGVSGDYVRGLKNLPS  
LPGREDPYGRKPLAQADQAPRI PAARLGFHLKTSLTRIDANLDYTRVPAQNKILARYETRTPGHMLNLGANYRNTRYGEMWTVKADNLLNQSVAHSSFLSDTPQMRSPFTGGVNV  
KF

## SEQ ID 8377

CGTTTCGCTCAACGGCAGATACCGCTTGAAAGCTGATTCAAAATAGCGGGCAATTATATCAGCAAGCCATCAGGGTACATCTTTTCAGACGGCATATGATTGCCCGAACCGCGCAACTT  
TGACAAACAGGCAATAACAATACAATGCCCAATTCGCACAATGGTGTGCGGATATTAACCAT

## SEQ ID 8378

RFRQTADTA\*KLQIAGNYISKALRVHLFRHMLIARTQTLTKQANNWYMPNPAQHCADINH

## SEQ ID 8379

ATGCCGCTCAAGCGCCGAGTTTCAGGCGCATATTCACAAAGCGCATCAGCGGAGGAGAAGAGGAGGGGGGGTGTGGAGGCGCGCAGCGTTTGGCGGAGATAAAAAACCTTATC  
CGACAGCGACA

## SEQ ID 8380

MPSEAPSFRRHLHKGASAGGEEGGVVGGAFAFGDKKPYPTAT

## SEQ ID 8381

ATGTCCTGATCTACCTACCCCTCTATTTCCGCCCCACATCGTCGAACCGCGCTTTTGTATTTTCAGCAGGACAAGGTTCCGGATGTCCAAAAAATTTCTTAGGCGCTTATCGGCGCA  
AGGTATTCGATTTCGAAAACTAT

## SEQ ID 8382

MSRIYLPFLFPPIHVERGLYFQQDKVRDVQKISLGRYRAKVPDSENY

## SEQ ID 8383

TTGTTTCGATGATGACGATTTTCATACGCGCGCTTCGCCAAGATGGAGGAAATTTTCGGATTTCGGAATCAITGAAAAAGCCAAAGCATTTCGGCGGGCGTTTCTATGAAGGCTGCTGGCTGA  
TGGGAACGAAAAATGCCAATACGGCGCGTCCATTACGGCGGCCAAGTGAACGATGTTGGTTGAATTTGACGGCGTAGGCTGCAATGCTGCAAAATTTGGATGGGAATCAAGGCTTTT  
TGATTTTCTGCAAAATGCGATTTCGTCAAAAATAACGCGCGTTGACATTGCAAAAGACTTTTCAACGGAGAGTACAGCCCGAATCAGGCAAGAGAAGACCGCAATAAAGTTTGTATTACG  
TGCCATCAGCTCAAAACGAGGGCGAGTGTCTTGGTTCTGATTGGGAGGAGAGACGAAACGCAAAATGACGAGCGGCAAAACCTACGGCATAGGTTTCGCGTGAATCTTCAAAATATGTAC  
GAATCTATGAAAAAGGCAAGCAGCTTGGCGATAAAACAGCACATGGACCGCTTTGAAATCGAATTCAAAGCGAAGACATTGTAATTTCCCTTTGAAGTCTTACAGACACCGCGGAGTA  
TTTCGGCGGAGCATACCCGATTTCGGAACGCTTTACAGGCGAGTGAACCGCTATTGAAGCGGTCAAAAGCAAGATCATGATTGATTTCGATACCTATATAGAAGGCTGAAAAAGCAATC  
GGACGAGGAATCAATGATCGAAGCAGTGTTCGGGACAAATCCAAACAGAAATTTGTTGAAGTCTTACGCGGAAACATGATTTTTCGCTAAAAAACTGAGCTTCGGAATTTACGATT  
GCAGCGAGGCAAGCTAACCCACTGCTGAAATTCCTCGCTTCTAAATTTGACCAATACGGCATGTGGATGGATCGATATTTTCAGCGTCAAAAAAGAGGGGAAGAGCAGGCTTATTT  
AGAGAAGATGATGACAAATACGCAAAATTTACCGATTTCATGGGCT

## SEQ ID 8384

LPDDDDPIRAASAKMEEIPFGGIIIEKAKHSGGRFYEGCWLMTGTEAAYQVRVHYGGQRETMLEVELTAVGCNAANTGWESRLFDPLTNARFKITRVDIADKDFPNGEYSPNQAREDRNKGLFT  
CHHWKPKGBCLGSDEEEDAKMTSGRTYIGISRESSKYVRIYKQKLGDKTSTWTFEIEPKAKDIVIPFVQLTPGEYFGGAYPICERTFGSANRIEAVKSKIMIDFTYIRLKKQI  
GRGINASKAVFPDKSKQELFEVLBPKHDFLPKKLSFENYDCSEAKLTPLEHIPSILKFDQVGMMDRYIQQRKEBQRYLEKMYDKYANLPISEA

## SEQ ID 8385

ATGAGCTATTTCGAAGATGTAACAAACGCAATTAAGGTAATAGATAACTTATGCAAGAAGCATTAAAGAGCGCTGAATCGTTAGAGGTTATATAGACGAAATAGGGATAAAGCAGACG  
AAGCGGATACCTCTTTTGAATTTCTAAAGGATGTAATAAATATTGTTATAGCGATTAAAAAAATGTAATTGAGGTGTTTGAAGATTGCGTT

## SEQ ID 8386

MSYLEDVKNALRVINDNLCKEALKRPESLEGYIDEIRDKADEADTSLEFLKDVINYGISDLKNVIEVPEDCV

## SEQ ID 8387

ATGCAGCTGCGGTTTATATTTTACCAAGCCAACTAATGGCAGCTTATACATTGGCGTTACATCTGATTGTTGGTCAACGTAATTTACCAACATAGGAGCATTGATTGAAGGATTACAT  
CACGCTACACGTTACTATGCGCGTTTGGTATGAATGCACTCTACGATGGAGAGCGCAATTTACTCGGGAACACAGTTGAAGAAATGGAACAGGCTTGGAAATTCGAACTGATTGAAGA  
AAATAATGTTCTTGGCGGATTTATGTTTGTATTTAT

## SEQ ID 8388

HQPAVYLASQRNGTLYIGVTSDLVQRIYQHREHLIEGFTSRYNVTMPVWYELHPTMESAITREKQLKKMNRANKLQLEENNVSWRLHFDII

## SEQ ID 8389

TTGCTAAATATAAACCGCAGCTGCATATAATACCTTTTGAATTTTAAATTTATATTTCCCGGCAACCAATCCGGTGAATTAATTAACCTTCGTTATCCCATAGCTTTCCATCAT  
TCCCGCAACTCTTCGTCATTTCCCGGAAACGCGGAATCCAGGACTCAGGACCTGAGAAACCTTTTACCGGATAAGTTTCCGACCCAGACAGCCGGATTCGCGCTGAGCGGAA

## SEQ ID 8390

LLKYPQAAVNYLWYLNLYSREHHPVITLIRYPHSFPFQFVIPAKAGIQDSGPEKPFYPIISFRTRPGPPPERE

## SEQ ID 8391

TTGTTTCTCTTTTGTAGGAATGATGAAATTTGAGTTTATAGGAATTTATCGGAAAAACAGAAACCGCTCCGCGCTATTCCCGCTCAGGCGGGAATCCGGTCTGTGCGTGGGAA  
CTTATCGGTAAGGTTTCTCAGTCC

**SEQ ID 8392**

**LVFCFCRNDEILSFRNLSEKTETAPPSFPLRRESGSVGAETRVKRFIRS**

**SEQ ID 8393**

TTGCTGTGTGTCACGCTCTAGATTCCTCCGCTGCGCGGGGAATGACGCGTTCATTGTGCGCCCCCTCCGAAAAACGCAAAAAATGCCGTCCGAAGACTTTCGGACGGCATTTGCGGAA  
AAACCGCGCGCGCGGGCGGGTCAGAAGAAGACTTCGCCACGCT

**SEQ ID 8394**

LLLSHVLD SRLRGND AFHLPPPPEKRKKMPSEDLSDGICGKTGRAGGSEEDFAPA

**SEQ ID 8395**

ATGACCGCCCTCACACTCTACCGGTGGCGGCAGACGTACAGGCGGCCTGGATTACTACTTTGACACGGAACCGAGCGCGAAGACACGCTGGAAAGCCGTATCGGGCAGTTCGAGGTC  
AAGCGCAATCCGTTATCGCTTATATTTAAACCAAGAAATCACGGAAAAATGCTTGAGGGCACATCAGGCAGATACCGGGGAAGCTCAAGGCGCGAAAAGCGCGGAATCAAAGCCTGAA  
AGACTCTTTGGCGCGCAATATGCAGGCGCGGGCATTCACGAAATCAAAGCGGATGACGGCAGCTTTTAAAGCCCTCGTCCGCAAAATCCGAAGCCGTGCTGATCTTAGACGAAGCACAAATC  
CCCGCCGAATTTATGCGTGAGGCGCTCAAACCGAACCGGACAAAACCGCCATCAGAAAAGCGATTGAAAGCGGTGGCAAGTAGCAGGCGCGAAGATTGAAGGGCGGAAGAAATTTGCAGA  
TTAGA

**SEQ ID 8396**

MTALTYLRCAADVQAALDYDFDSETEREDTLEAVIGQFEVKAQSVIAYIKNQEIETEKMLBGHIRMNTGKLKAAKARNQSLKDYLRNMQAAGITEIKADGTFKASFRKSEAVVILDEAQI  
PAEFMREAVKTEPDKTAIRKAIESGRQVAGAKIEGRKNLOIR

**SEQ ID 8397**

TTGCAACTGCTCTCGGACGGCAACAGAGAAAGGAAACAAAAAATGGCAACATCGACCTGACCCAATGGGACGGGAAAAACCATTGGCCGCGCCGCCAATCCGSAACAGGGATACATCAACA  
TCACCATCGGCAGCGACGACCTATTTCATCAACATCGAACAGGCATACGCCATACAACGCCGCGCTTGGGGAAGCGGTTGCCGAATATGAGGGAGGGGCACAA

**SEQ ID 8398**

LQLLRTATEKGNKKMANIDLQWDGKTI GAAANPEQGYINITIGSDDLFINIEQAYAIHAALGEVAEYEGGAO

**SEQ ID 8399**

ATGAAACGCGCAAAATCTGCCGAGGTAAGTGGGGCAGTCTATTTCATCAGCGCCAAAAAAGACAGGGAGCGCCAATTTTACCCATACAAAATAATTTTAAATCAGAAGAAACACAACATATATCATTTCCGATATATACCGATAACGTTGTGTCTAAAAGGCGGTATCTGTGTTTTTCGGGGCGGCGACTTACTTGCGCCCTACGGCAAGGTTTCCGGTTTGTATACCGATAGTCTGAAAGGCGCGGCAATGCCGTTTGATTAGTACGACCCGCCGGGGTGTGTAGGCTACAGCTACGAAATGTCACTGCCACAACAATCTTTCGCCCCAGCAGAGGCTGCCCTGAAAGTTGCTATTAAGAACCCAAATTACCTTCGGTCAACAAGAGGTTGCAGAAAGAGGCGGCAACAAGCTGGATATATACGAAGACAAGAGCGGCAATTCGCCCAATTATAAATTCGTGGATTATCTTTGTGGGCGTGTCTTTCAATTGTAGACGACGAGAGCTTGTCTAAGCAAGAAAGACACATATAAAGATATTTTATTTTTAACGAGGATGTAGCAGCCAAAATATGGGAACCCCAATACAAAGACCAAAACCTCGTTTATACGACAGCGCAGGTAATAAATATTTCTCCCGTTATGTCTGGGCAGAAAGAACACTCCGCCATCGCTTTTATCTGAAGCGCAAATCTGTGCACTGCTGTGATATAACCAAAATCAAGAGATATACGCAAGGCAAAACAGTTGATTGTGGTACCTTGAACCCGCGCATCGAACTGTCTGAAAGGATGAAAAACAGGCTGGATAGATTTTTTCTAGGTAATTGGAGCTTGAAGAATAAAGAAAGTCAGGCTCAATCTAGGCCCTGCCCGAAGTCAAAGCAGGCCGTGCATCAACAAACAGAACCCCAATAATAATACCAAGGCCCTTCGCCGGCACTGACCGCCCCCGCTGTGTGTTGCCGCTTGTCAAAATGGCAAGTCAGAGTGATTTCCGTTTCGGTTTCTACCTACCCGACAGTTTCGAGCGCCGATCTACCTTTCAAAATCTGAAAAGAAACACTGTAATCCGGCAAAACCGGCCGTATTTCCCTCTGTAACCTTGAATGAGATGATATAAAGATAAAGAGCGAGTTCTATGGGGCGGAAACAAATCATCGCAATGTGATAGCGCGCTACAGCTGTATCAACTGAAATAGAAACAAGGATGAGGTCGTCACTTTTGGAAACACCGGCAACAACCGGCACTTTTCGGCATTGTTAAGGAAGCGAAGCTCAATCTTAAAGCCGACGAGTGGAAAAAAGCTGCTGCTGCCCTGGACAGGTTCTGCTCTGCCGATCAGCGGTGATTAAATCAATTAAACCGAGATCAGACAAATACAGCCAAAGATACCGCATTCGCGCAAAACCGCAATCGGATTGGGCGACATCTGCAACAGCCCGATTCGCGGTCGCGCGGGTATTGGCAAGCCGCCGCAAGCAGGGATGGTCATTTCAAAAAAACCGCGCAGTGATGAACGCAAGCTACAATCTGAGGCTTCAGCTACATACCCCGCAGATGTCCGCGCAAGGATATGAAAGACAGCAATTTACACTCGCCAAAGAGCTGCGGCTTTGCGCCGAAAAGGCTATGGTGGCGACCGCTTGTCTTTCGCGCGCATTACAGATGACCAAGACAAGCAAAACATTTCTTATGTTTGTGTGATGGGTTTGGCGGAGAGCGGATATGCTTTGATTTAAGCAAAATCAGCGAAATATCAGCGCGCGCTCCCTGTTTGTATGTCTAAAAATGGCGATAATAACCGCAAAATCCGCTGAAAGTGAATTAGGCTACACCGTCGCGCAGCGCAATCGGCAAAACCCAAACCGCAAAATACGCGCGCTTCTCTGCTTTCGGTTATGCGGCTAAAAATTTGGCAGCGCGATATAAACCAGCGCTGTATGTATATTGGAACCGGCAATGTGTAGTCTGATTAAAAAATCGAAGTGCAGAGCCGCAAGGGCGGCTTTCTGCTCCCACTGCTTCCGCTCCCAAGGATCCGAGGATCGGGCAGTAAGGGTGGTGTAGTGAAGCTGAAGGAAGGACAACGCTTACCGTCAACCGACCGTGTATTGCGTACCGGATTTTGTACCATCCGCACTATACGGTAATGACAAATGGCGCGCAACAAACCGCCATTTCGGGCATCAATACCGCGACGCGCGCAATTGACTTCGGAAGCGCGCGCCGATTTGCGCGGATACCAAGGCTTCGCACTATTTCCGGCATCAGAAATGAACCGCAAGTCCATCCCACTAGGCTGCATGTGGAAGAACCGGCAAAACCGCTTCGCCGAACGGATATGTTTACGACAACACCGGTTAATGTGGCTATCTGGCAGCAAAAGAACAGAGATTTCCCGCTCGCGCAGCAGTGTATGAGCGTACAGGCGGCAACATCAAGAGGTTAAAAAACCCCGCCGCAATAACCGTGCTTCTCCGAAAAGGTGTGCGCACCTTCTGTATGAACGATTGGACAGCTTGGATATTACCGGCCGATGTGCGGTATCAACACGCTTAAGCTGGCGCGAAGTCTTCTTCT

**SEQ ID 8400**

MNAQNLPPEVKWQGSYSSAPKKDRERQFHTHNNFKIRRMTTISFDNTDNVVAQKGGIVVFGAATYLPYPYKGVSGFDSDLKGRGNADVWISTTRPGLVGYSYENVTCHNNYFAPSRCGPPEV  
KYTQTPQGOGLQRKAGNKLDIYEDKSRDNSPIYKISDYFWLGVSPNLSSESLSVKERKRNKIPFPNEDVTQQNSGNPQYKDQNLVYTTGDGNKYSRRYVQGNHSAIAPYLNAKIHLK  
YIKQIDITQKGTVDLGTLPRIELSKQWKNLDRFLPGLNWTLEDKGVSVNLGLPQVKAGRCINKPNPNNYKAPSPALITAPALWFGFPVQNGQVMYSASVSTYPSDSSSRILYQNLKRTKTE  
SGSKPGRYSLTLENENDIKSEKPSMGRFTIIRLDSVGLIKLARNKDEVTTFPGTGNNGTGFVKEANVNLKADENKWKVLFTWVRAAADAGGRFKSINRESDKYSQRYRIRENGNRDLCDI  
VNSPIVAVGGYLATAANDGMVHIFKKNKGSDERSYNLKLISYTPGTPRMDIESNDSTFLAKELRAFEKGYVGDRYVGGVFLRRITDDQKQHFHFMFGAGGPGGRGALDLKSIDNY  
PAAAPLFDVKNKGDNNGKNRNVKVELGYTVGTTPQIGKTQNGKYAAFSLASYAARNIGSGDNKTALVYVDLENGSGSLIKKIEVGGGKGLSSPTLVOKDLGTVDIAYAGDRGDDGLSDIGY  
SNSPKWSVRTIFEGDKPITSAPAVSRLLADKRVVIFGTGSDLTEDVDLNTGEQYTYIGIFDDDKGTFVKVTVQNGTGGGLLEQVLKEENKTLPLNKGSDSGSGKWVVLKEGQRVTVKPTVVL  
RTAFVTLRSYTGNDCKGAQTALIGINTADGALTPSRAPRPIVPDNGVAQYSGHGMKNGKSIPICGMKNKGKTVCPNGPTVYDKPVNRYRLDEKKTDDFFMTADGDAGDGLYFKBGKKPARN  
RCFSGSGKVTLLMNLDSLDITDPMGCKIKRLSREVF

SEQ ID 8401

ATGGGAAAACATCAATATGGCGGCATAAAGCGCGGTATGGCGGAAAACTGCCTTTCAAGTTTATTTCATATTTTATTCCTTAAGTTTGCCTTCGCGGACGGCGCGCGCGCAACGGCG  
GGGTTCGG

SEQ ID 8402

MGKHQYGGIKRGMAENLPFQSFTHILFLKFAFAGRRAANAGVR

SEQ ID 8403

TTGATTTTATGCTGTGAAAGACGAAAGCAATTTTCAAAACCATGCCCGCAGGCAGGCATCACGCCACCTGCGATCCGCATCATCGATTGGGTACGCAGCTCGTCGAGTACCAAACGAAACAA  
AGCGGCAGCAGCAAGATTTTATGTCAGTGGGAAATCGACCTGGAAGCGGATCCGGAAATGCTGATGCGGACGGCAGGCCCTACTCTCATCAGCCGACGATACACGCCAGCCTGCACAGCAA  
TAGCCAACTGGCAACAGACCTCAAAAGCTGGCGGGGAAGGGACCTTTACACGGGAAGAACCGGACAACTTCGATTTCGCCAATATTTTGGGCAAGCCCTGCCTGTGATGATTCGCCCAACAA  
GAAAGCATGTACGGCAAAACCACTATGCCAACATTCGCCCATCAGCAACAAGATGAAGAGCTACACCCCGAAACATCCGGACAACGCGCGTTTTCCTCTCGACCTGTCAGACCCCGGATT



GGGCGAATTACGGCTCCTGAACGAGAACTGAGGAGCAGATTGCCAAAAGCCCGAATATGCCAAGCCGTAAACGGCCGCAACCGCCGGCCGCGCAGAAACAGGCCCAAGCGGC  
GGAAGGCGCGCGGAACACCCCAAGCAATGCCCGCTGCCGAAGACATCGAGGACGACATCCCTTTTAAT

## SEQ ID 8404

LLLSVKDESNTKPCPAGSHHATCIRIIDLGTQVEYQNEQKQKILVQWEIDPEGDPEMLPDGRPYLISRRTASLHKSQSLATDLKSWGRDFTPEERDNFDLNLGKPCLLSLAHQ  
ESSDGKTTYANIPAINSKMSYTPKHPDNAVPAFDLSDPDWANYGLLEKLEQLAKSPEYAEAVNGRQPPAPPQQAQAAEGRPEHPQGNAAPEIEDIPFN

## SEQ ID 8405

TTGCTTTTCGTCTTTCACACTTAAATCAATGACATTTTCGGTCTCCTGTAAAGGTCGTTCCTCTATCGGTCTCGCGCTGTTTTATGCTTGCCTGCGCGCGGTATC

## SEQ ID 8406

LLSSFTLKINDIFGLLLKVVSSIGLALFYALRGVI

## SEQ ID 8407

GTGCAGGTTTCGTATGGATGGATTCGTATCCCGCGCGAGCGGGAATCTAGACCTTGGGACAACAGCAATATTCAAAGGTTATCTGCGCGGTTCG

## SEQ ID 8408

VQVSVHMDSSFPRRRESRPWDNSNIQRLSAVC

## SEQ ID 8409

ATGAGCTTCCATCCGAAACCCGTTATAACGGCGCGGAGAAACAGAGCCGTACGGACCAAGCCCCGAAGAAATCAAATACCGCAAAGCCCGGAAACCCCGAAACACCGCGGATGACCG  
AAAAACAGGCAGAGGCCACATTAAGCATTTATCAGA

## SEQ ID 8410

MSFHPETAYNGGETEPYGPSPPEIKYRQSPETAETREMTKQABGHKSTIR

## SEQ ID 8411

GTGCGGATTTAAACATAACCTTTATGGAGTTGAGTATGTACCGGTCGTAACCAACGGCGGCAACAGTATAAGTTTCCTGCGCGAAGAAATGAAAGTAGAACAGATACAGCCCAAC  
TCGACAGCCAAATCGAAGTACGACGAGTTTGTATGATTCGTACGCGCAATCTGTAAAGTTGGCGCACCTTTATCGAAGTGCAGAAAGTAAAGGTAGTGGCACACGTCGTGG  
CGAAAGTCCCGCATCTTCAAATGCGCCCGCAACACATACCAAAAGCCCAAGGCCACCGCCAAATTTACCCAAATCGAAATCGTGCAATCGCC

## SEQ ID 8412

VRILITITLMLSMYAVVKTGGKQYKVSVEKLVBQIPAQLDSQIELTEVLMADGESVKVGAPFIEGAKVTAKVVAHGRGEKVRIFKMRRRKHYKQKQHRQNTQIEIVAIA

## SEQ ID 8413

ATGGGCAACATATTCCTTTAGGTGTAACGGGCGATTTTCGGCGGTATAAGTCTTCGCGAGTTGGTGGCAGTCTGTAACCAACAGGGGCGATTTCGGTTACGGTGGTTATGAGCCGCTCGGCCA  
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TTTTCTGATTCGCGCGCAAGTATGAATACCGTGGCAAAATCTGTAACCGGTGCGCAGATAACCTACTGACCAATCTGGCAGCGCGACGGAATGCCCTCTTGGCATTCGCTCCCGCATG  
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GGATGCCGGAACCTGCCGAATTCGTGGATTTGCTTCCAGACTTTGGGACACCGAAATTTTAAAGGACAGAAATCTTGATTACCGCAGGTGCGACATTTGAAGCCATTGACCTGTCTAG  
GGGCATCACAAATACCTCCAGCGGAAATATGGCGTAGCTTTGGCGCGGGCGTGGCGTCCCGCGCGGCAATCAGCCTGATTACGGGACAGCTTCAAACACAGCTGCTTTTCGGCATA  
TCCGATACGGTTCAAGCGCTCAGTCCGAAGATATGCATCGCGCAGTACATCGTTTGAATGAAACCAAGATGCTTTTATTTCTGTTGCGCGCTCTCAGACTATAAGGTTAAACACAGGA  
GTACGCAAAATTCAAAAAGATAAAATGCCAAACGTTATCCATCGAATTTGGATGAGAACCCGATACTTTGGCTTCTATTGCTCATTGCCGAACCGCGCTTCGTCATCGTTTTCG  
CGCTGAACCGGAGATGTATATGGCATATGCGCGGAAACGATATTAAGAAAAAATACCGGTGATAGTTGCCAATGATGTTTCAATCGCGATGGGCAAGACAAACCAAAATTTGTTATC  
ATAGATGATGATCGCGAGTTGCTTTCCCGCAACAAAGTAAGATGAAGCGCAATCGCGGATTTGTGAAAGGCTTGGCGTATATTTGAACAAA

## SEQ ID 8414

MGRHILLGVTSIAAYKSCLEVRLLKKQGHSTVVMRSRATFVSPVLTQALSGNFVLTDTHTGNGSGMGEHINLTRNDVFLIAPASHNTVAKICNGVADNLLTNLAARKCPLAIPAM  
NVMMLNPNANRNIQIVSDGTVVMPGLGEQACRENGMRPEPAELLDLLPDLWPKILRDKKILITAGATPEAIDPVRGITWTSRGMVALARACRAAGAEISLIHQQLQTLTPFI  
SDTVQAVSAEDMRAVHRLIEQDAFLSVAASDVYKVNRSQPKFKDKKNAPLSIELDENPDLASIASLPNPPFCIGFAASTENVMAIAREKRIKKIPVIVANDVSIAMGRTTNQIVI  
IDDDAKLSFPFETSKDEAMRIVERLAVYLNK

## SEQ ID 8415

ATGCAGAAAAAAGACATTCGCGCGCACACCTTTTCATCCCAAGTTCACAAACACATTTCCGGCTTAAATATCCACAGCATTCCCGCTTCAAAGGCAACCGGAGCCATTTCGGTAAAGA  
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TCAGATGATTTTAAAAATAAAAAAGTTACCCACAGAAAAATCCCATATCAATATAATCATCGTTTATTATTATAACCTTATATTTTATTAACCTTCAGGGAAACCGGACCGGCA  
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## SEQ ID 8416

MQKRHSRHLFIPTSSKHISGLNIHSIPVLKGTGSHSVKSGMSSAQANYPNLPPTKNNPVCTKGNPPYRHPFKTAIQMLIKIKKSYPKIPHINIITVLLFKPYLIFTTLQNGTA  
KRGIFSKN

## SEQ ID 8417

GTGCACCGCGCGCAACCGGCTTCTTCTTCGCAATTAGATGCGCTCTTCCAGCAAACTCGGCGCTCAATTCCGCAACCTGCGCTGCTTTTGAGCCAAAGCCATACGCAATTGCGCA  
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TTCTATTTCCTTAATTTAAAGGTTTAAATGCGCACCGCGCTCCGTAAGGATGTTACGACCGTGGCGCTCGGGTTATTGCGGCTTAAATCTACAAAAACCGCGCGCGCCACT  
CCCGGCTGACGCGCGGCAATTCCTATGCCCGCTATGAATTTGCCAGCTTGGCGATGTTCTCGCCACGCGGAACCAATCCCGCTGCTCTATGGCG

## SEQ ID 8418

VHPATGFFFRIQMPLFQPNLGAQFNLRLLSQRHTRCNIGGFLSCTASASLGESEGLARRQYRQYRELKRNIPCLHFFYFLNLKGFNCAPRPLEMVRTVRRRGYLRLEKSTKTAAPT  
PRLTARHSYARYEPASLPHPSASANHSRSSHA

## SEQ ID 8419

ATGGGCAAAACCTGATTTTGAATATGAACGATTGCGGATTTAAGGTTGTGCTACCAACCGGACAAATCGGTAAAGTGGACGAATTTTAAACGGTGGCGGCAAGAGACGGGCATTATCG  
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AGGCGACATCATTATCGACGCGGCAATGCCAATTAACCGGACGACGCGGCAACACTTACCTTGGCGGAAAGGGAATTTGTTTGTGCGCGCGGGGTATCCGCGCGGCAAGAAAGC  
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TCCTATGCCCTGCATGGCTTCGGCGATTACGTTCTTGGACGGCTATACGACCGAACGCTGCCCTGCCAACCTCTGCAGGCACAGCGGACTACTTCGGCGCGCACACTTACGAGCGCAC  
CGACAAACCGCGCGCGAATTTTCCATACCACTGGACGGGCAAGGGCGGAGATACCGCTTGACACCTACGATATT

**SEQ ID 8420**

MGQNLILAMNDGFKVYVAYNRTIGKVEFLNGAAKETGIIIGAYSLQDLVDLAKPRKIMMVRAGSVVDDFVEQLPLLEBDDIIIDGNANYPDTTRRTHYLAKGILFVGAGVSGGEEG  
ARRGSPIMPGDKRAWEAVKPIFQALAAKTPOGEPCCDWVGKDAGHFVKMWHNGIEYDMLICRAYQFMKDLGLSYDEMHRVFAEWNKTRLSYLIETAAILGYKDEGGEPLAKIL  
DTAGQKGTGKWTGINALDLGILPLILSEAVFARCVSSFKEDRVQTLKLFARTATPVEGGKQEWVEALRQALLASKIISYAQGFMLIREAGESYWGWDYGTALLWREGCIIRSAFLGNIR  
DAYEANFDLVFLGADYFPKNILLENCLPAWRKVAKAVECGIIMPMAASAITFLDGYTTERLPANLLQAQRDYPGAHTYERTDKPRGEFPHNWTGKGGDTASTTYDI

**SEQ ID 8421**

ATGCCGGGCGACTTCGGAGCGTTTGTCCAAATAACGCCGTATCCATATCGCGCGAAGCAGCCACAATACATCATAAAGCCATTGGAACATCTTTCTATTTCCTGCAAAACAAATGCCGTC  
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ACAGCGGAAGCAGTTGTTGCACAAATCGTCAACACCGCAACCTGCGCGAACCATCATGATTTCCTCGGTTTTCGCGCTTATCGACCAAGCTTCGAGGGAATACGCCCGGATAAT  
GCCGCTCTCTTTTCGCCGCAACCGTT

**SEQ ID 8422**

MPGHFRSVCNNVAVSISAQATIIHKAIGTSFYFLQNKCRPNSSDGISATESNIVGCRSGISALARPVMGKFAARFVGALVSVRAEVALCLQEVGRQAFGRIVQERNRRSHAGHRDA  
FDRLGNHILACRQAVFQNIPEIRITQEHQIGIGLIRVADIAQKRAADDAFAPQQRSAVAVQTPAVTFAFPADQHKALCVGNDFGKQSLPQRIDPPLFAAFDGRGSGEQLAGLHALFF  
ERRNTAGEYFGFQNRQNAQIQGIDARPPARAFPLCRIEDFLQRFAPVLLAQNCRCDFNQIQLGFIPLGKHAHVHVVGGPQPTVPHKLVRFANQLHIAVDFDAVHHFDPKMSRAILADP  
VATRFALRRPFGNRLNRLDRFPALIPARHGRPAAPFAAGYARADKQNPFSGKVMCPFCRVGVIGIAAVDNDVAFQQRKQLFDKVVNHRTCANHHDFSRFCQLIDQVLQGRADN  
ARLFCRTV

**SEQ ID 8423**

GTGCAGGATTCCGTTTTCGCCCTCCCAACCGTCCAAAGCCTGCCGCATATCTCCCGCGCTAATATCTTCCATCCCCCAATCGGGCTGCGGTAGCGCGCGTCCGTAATATTTCCACC  
GCCTTCGCTCTTTTCGTTTGAAGAAACCGCGCGCAGCATTCATGTTTCGCCGTCGCGCTTCGCCCGCTTGAAGTTGCTATCTCATCGCTTTTGTCTATCCCGCGCTTCGCAGATATAGC  
TTTCGGCGCGTTTGTACTTACAAAACATCATTCGCTTATCTTTTAAAGCGCTCTTTTAAACCGTAAAGTAAAGCGGTG

**SEQ ID 8424**

VQSVFRLPTVQSLPHILPRVISFHPPIGAASRRRAVIFHRLRFFLRKPPAAFTVSPCRCPALKFDTSSLCAIFGLADIAFGRFVYTKTIALSFKPSFLTVKVKAV

**SEQ ID 8425**

TTGATTCGTTGCCGAAATGCGGTCGGAACCGTTCGGACGGCATTGTGTTTTCAGGAAATAGAAAGATGTTCCAAATGCGCTTATGATGATTGTCGCTGCTTCGCCGATATGGAATACGGC  
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TATCTGCGGAGGCGCGGAATGCGATGCGGCGCGCTGCGAGCTTTATCGCACACATCGCGGAGCGGCGGAGAAATCGCGGAGCGGTGCGGGAAGCGGTATGCGGACATCGGGG  
GCGA

**SEQ ID 8426**

LIFLPCRPNRSDGICFAGNRKMFQWLYDVLNLLAPITWIRRYLDKRSGPSAPYRAHRDERFGKPHNPTGAVMIHAVSVGETRAAQFLIRELRRRFPDAPLMTQHTPTGRETAQVLFPD  
AQCRYLPYDKKFWVQFLRHRPMPGILMETEIVNPLMKRRCRAGVPLFLANARLSEKSLNGLYLVKRLIRPAASLTGCLAQTREDAARLAKLAGASVQVGNTRYDLMPSEDMKTLAGQ  
FEKRIGRPPVAVCGSTRVYRGEDEAKLLAAWQYRGDALLAVVRHPEHPTTETAKRPFKVRQRRSDGLPVEPTQVWVGDMSMGLYAYYLCAADVAFVGGSLVGGCGQNIIEPLSCGV  
TTTGFSTYFSEACRHALASGAIVQVESADANREAVEKTLSEGGGMQJQARVDGFIAQHRGAGARIAEAVREAVCGHRGR

**SEQ ID 8427**

ATGAACGAATTAATCAGCAAAATAACCGGTCGCGCGAGGGGAAAGGACGGGCAAGCCCTTTATTTGAAAGTCGGCGAAATCTGCCGAGCGCGGGGCAACTTTTACCAACCGGAAAAA  
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**SEQ ID 8428**

MNELISKINRVGAREKDGQSLLLKVGIEICRDAGATPTTRKSESINHTAFTTFTVKDGLKDKAMIVL

**SEQ ID 8429**

ATGTCCGCATACCGCTTCCCGCACCGCTCGCGGATTCTCGCGCCGCTCCGCGATGTTGTGCGATAAAGCCGTCACGCGCGCTGCATCTGCAATTCGCCGCCCTCGCCAGA

**SEQ ID 8430**

MSAYRPFHRLGDSRARSAMLCDAVHARLHLHSAPLAR

**SEQ ID 8431**

TTGGAGCATGTTAGTATTATGCGCTCGCGCACATCCACCTGTATGCGCCACCGCTTTTTCGCGCGCGTGTGTTTGAAGTGCTGGTTTTCGCTCTGCATACGGGACGGG  
TGTGCGCGGAGCGCGCGCGGAGTGGAAAGGCAATGCTTACCGCGCGCTCAGGTTGATGCGCTTTCGCGTGGCTGCTGTTGCCAGCGGCATGATGAGCGGCAACCGCTACCT  
TCTTATATCGCGGCAACCGTTTCCACTTCTTTCGCGCAATGCTGACGCTGAAATCTGTTGCGCTTCAGCGTGTTCGCGCACTTCGCCATCGCGCTGCTCAAAATGGCGCTTCCAGC  
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**SEQ ID 8432**

LEHRMSIYVAHIHLHYCATAFVGGVFEVLVLSVLHTGRVSRREARREVEKAMSYRAVRVMPFVGLLPSGIIVMAANRYLPISEFPATSPGTMLTLKILLAFSVLAHPAIAVVKMARST  
LIVGMSKYIHAVVPTHMLLIVFLAKAMFYISW

## SEQ ID 8433

GTGTTGGCAGCTATTGACCGGATGGGATGAGCAGGCATGCGCTTGCTGCAATTGCCAGGATTGAGGCATACCGCCCCCTACCGAAAGCGCGATTGATG

## SEQ ID 8434

VLAAIWTGNDQACALPALPRLRHTAFYPKARLH

## SEQ ID 8435

TTGTTTACCATCTAGTCAATCCGTGTATCTGCCAACCGTGGAAATAAGCCGAGGTCTTCTTGTCGGCATTTCTTCCGTCCGGGCAAAATATCCATATGATAATGCTGCATCATCA  
GGCAGGAGAACATCTTTTGTCCGACATGACAGTTATGTCCGCTACCGTGATGCAAGGATTGATGCCGTCGAACACATAGAAAAACCGTGTGCATGAAGGAATATTCTCCGTAAAACACC  
ATGTGGCGAACAACTGTTGAAGCGTATCATTTGCCGGGCTTCAACATCAGGATATGCCGCGAGGAAGTTAAGCTTCTGATTGAAAAATTTGCTATAGCA

## SEQ ID 8436

LFTLLVNPCLIPNRGNKQVLVSGISSVRANIPYDNACIRQGEHPFVRSDSYVRYRDARIDAVEHIENRVHEGIFSVKPPCGEQLLKRIIAGASTSRVAGREVKLLIEKFAIA

## SEQ ID 8437

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AAAACAGCGCGCTGGCGATTTTTTCGCAATCTCTGACGGTAAAAAATTTCTCGCCGTGAAACCGCGTCCGACCGGAACGACTTCTTGACGGCATCAGCAGCGCTGCTGTTGCGCAAAATC  
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CCACAAGCCGCTCCATGCCAAGGTTTCTTTGATGCCGACTTTATGGCTGCCGTTTCTTTCAGCGAAAAACATATCCAAGGCAATCATGACCAGCACTGCCGCAAAAAAACCGCGTAAAC  
AACGGCGACCCGATCCCGGATATTCTGTCATGGTTCAATCTCC

## SEQ ID 8438

VYPHHQHFTDKTQHECQAVFQEDKAFRHIHQEIHRRPQTONSENIGSQHDKRIGGNGKDGDTVHGKNDIAQFNHNQHQKRRGDFPAILDGKFLAVKRRADRNDLFDGIQQPAVCQI  
LFLISFLHHVYTSIEDERAKQIQNPLKLPNQCRADENHDGAQYQCAQYAVQQHVLKLRCDFEVAEYHQEHENTVDCQRFQNVAGKEFYFFFCGRAVAGIAGEFEIQPACEQAGYGN  
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## SEQ ID 8439

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TAA

## SEQ ID 8440

MTEYPCIGSPLFYGVFAAVLVMIALDMPSLKNGSHKVGIKETLAWSLVAVSCLPAGWLYPELAGNPGYGAAAAKEKVLFTTGYILEKSLAVDNI FVFLMIFGYFKVAPQFQHRVLL  
YGVLAGLVLRTVMIFVGAALVRQFEMILYLFAGFLYLYTGIMMKPEDEEDLANSLNVAKKVVPVGTAFHGEKFTTENGKLIATPLFLVNLINIELSDVVPFVDSIPAVFATVTDPI  
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## SEQ ID 8441

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## SEQ ID 8442

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## SEQ ID 8443

ATGCATAAAGCATCACCGATGAAGGTTGCAGAGCGGAATTATAAGGGATTTCGGGAAAAATACGGAAGCCGACCAAGAAATTTGACGAAATGCCGCGCTTTCGGAACAAGGATTGTC  
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## SEQ ID 8444

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## SEQ ID 8445

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CATCCGCTTACACCGGTTCTGAAGAA

## SEQ ID 8446

MASKAGGSTRNDRSEAKRLGVKAYGNELIPAGSIIRQRGRTKPHAGDNVGMKGHDHFLAKIDGYVEFRKLGALNRKTVSIRPTTSEE

## SEQ ID 8447

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AATTCATTCGGTTTCAGCGCTTTCGGAATAATACCGTAACGTTAAGTTCCCGGATTCCTCATTTTCGTGAACATAAAGGTTGAACATTAGCAAAATTCAAAAACCAAACTTCTCATTT  
CGT

## SEQ ID 8448

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## SEQ ID 8449

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## SEQ ID 8450

VDLKLSANGFLANGITVSGAKNAALPLMCAGLITSGTLRLKNVPLADVATTQKLLQNGARVLTDNISEFEINGGTVMNTCAPYELVTRMRASILVLGPTLARFGEAQVSLPGGCAIGS  
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## SEQ ID 8451

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## SEQ ID 8452

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 LAKAALLTMNQA

## SEQ ID 8453

TTGAATAGCTAGACGTTATTCGCTACTCAAAAGACGGTGGTATAAGTTGCAACAATCCGGAGGCCATTTCGAATATAAGCACCCAAACAAAAAGGCCGTGTAACCGTCCCGCACC  
 CGAAAAAGACTTCCCGCAGGTACTGTAAAAATATCTATAAGCAAGCCGTTTGAAG

## SEQ ID 8454

LNSLDVIALLKQDGYKVAQSGSHSYKHPTKKGRVTVPHPKDLPTGTVMITYKQAGLK

## SEQ ID 8455

TTGCTGCGGCTGACAGCCCTCAAGACCGCCCGGTATGCGGGCTTTTACACCTTCCCTGCAACTACTGCGGAAGATATTTTACACACAAATACACA

## SEQ ID 8456

LPAAADSPQDRPRYAGFLHPSLQLLPKDIPTHTYT

## SEQ ID 8457

ATGGCATTTTAAACTGACCGAACAAACGTGCGGGGCAAAACCGTCTCATCCGCGCGATATGAACGTCCGTTCAAAGGCGGCAAAATCAGCGACGACACCGGTATCCGCGCTCGC  
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 AACGATTTAGAATCGGCAAGCCTACGCGCTTGTGCGACGTGTTGTCATGATCGCTTGGCACCACACCGCGCCCAAGCTTCGACCGAAGCCGTGCGCAAGCGCGCGCGTGC  
 CTTGCGCGCGCTATTGATGCGCGCGCAACTCGACCTTTGGGCAAGCCCTGAACACGCGCGCGCTCCGATGTTGCGCGGATGTTGCGCGGACGAAAGTGTCCACCAAGCTGACCATCTCT  
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 TCGAAAAAATTTGCGGAATGCGCGCAAGGCGGCTTGTGCGCGTGGCGACCGATGTCGTGTCGCAAGCCCTTTCGCGCGGATGCGCAAGCGGTGTTAAAGACATCGCGGAGC  
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 ATTGCGAGCGGTACGAAAGCCCTTCCGGAAGCCATCGCCAAAGCAAGCGTCTCGATTGCGCGCGCGCGACACGCTGGCGCGGATGCGCAAAATCGCGGTTACCGAACAAATCGCG  
 TACATCTCCACCGCGCGCGCGCTTCTTGAATTTTGAAGGCAAGAGCTGCTGCGGTAGCGCGCTTTGAAAAAAGCGCGGAGTAACAGGTTTGATA

## SEQ ID 8458

MAFLKLTQNVGRKTVLIRADMNVPFKGGKISDDTRIRASLASVKYCLONGASVIMTHLGRPTTEGEFHPEDDVAIPAHLGGLLKGDVKVILNDRNKPALNAGDVVMLQNVIRINKGEK  
 NDLELGKAYAAALCDVFNDAFGTAHRAQASTFAVAQAPVACGVLNAGELDALGKALKQPARPMVAIVAGSKVSTKLTILESLADKVDQLIVGGIANTFLLABGKAIKGLAEHDLVEE  
 SKKIMAKMAARGGSVLPDTPVVAKAFADABAVKDIADVAEDEMILOIGPKSAAALADLLKAAGTVVWNGPVGVFEFDQFAGGTKALAEALQSKAFSIAGGGDTLAAIAKPGVTBQIG  
 YISTGGAPLEFLEKELPAVAALEKTRRVNGLI

## SEQ ID 8459

TTGGAGCATCTCATGAACCGATATGCCATGCGTTTTCGCGTCATACGGTTTATGCCCTATGTCACAAAGCGCGAATTTGCCAACATCGGCATCATATAACCCACCGCAAGCGGCTGCT  
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 CTGAACCGCTGTTTGGATTATTGTCGCGCGCAGCTTCGCCAAAAACCAACCGAAGCAGAACTTACCGACAAATACAGGCAATGTTAAAGCGGCTTCAGACGCGATACCCCTTCAAG  
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 CATCTATTACAGTCTGATAAGCGGATTGCGCGCATAAACCGTTGCGCGCGCGGATACATCGACCGCTCTGAAATATTGTTTTCGCTACGAAACCGCGGAGCGTCCCGACAGGCAACAA  
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## SEQ ID 8460

LEHLNRYAMRFAVIRPMFVQTRFANIGIIITHPSGCFDFKIEHYSRLSRFFRRFPDPAKYAATRAFEKELQIRINLAHSPDQIRAMPDHLTPREALIMAAQPGVTLPDRQGE  
 LNRLFDYFVARSPAKNQPEALTRQIQAMLKPLQATYPPKESTIGDPSGFHASIPLVQKAENGIRKIIKPIYFGRKDPADIIYKSDKRIAGIKRLRRGGVIDRSRLFAYEPPERPKAQ  
 EKALLDVSGDLBQGIQIADNRSEKIIIRNFACG

## SEQ ID 8461

ATGAAAAAAGAGAAATTAATGAAATGAGACGCTGAATGTGCGGAACATAAAAGAAATTTTAACTCAAAAAAGAAAGCTTAAGCTAACCCAAATCAAGCTGGCAGAGCTGTAGGAG  
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 AGAATAAGCAGTATGTCCTCATCGCATTTGATGAGATAAATGCTGGCATGCAAGCAGACATTCGACACCAACCATTCACCTCAACTATACGATCATCAGCAGTTGCGGTCTAT  
 GGGGTAGTCAACCCGACTATCCGCAACTGCTACGCTCGATTGAGATTCCCAATGACGCGCTATTTCGAGCTTTTGGGACAAACATCTGACAAACGTCGAGCTTTATGCGCGCGGACGCG  
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 GTTTTGGCGCTTGATTTTATGACCTT

-633-

## SEQ ID 8462

MKRELNIEITAECAELKRI FNSKKEELKLTQYKLA EAVGVTS AVNHYLNGTNALNASIASQPAKILQIPVSDPSLR LAEEISSMSIGIDGKLLALQADNLDNTNITNLVDVSASCGH  
GVVNPDPQLLRSLIEIPNDALFELLGTNNLTNVQLMPPDGSMEPTIPQKSTILKIDVSKFQTGGIYLFITFDGYTYIKRLSRKGGAHATSNDRYAKSDFLINPEADKPHINGKPHK  
VLPDLFDL

## SEQ ID 8463

ATGCTGACACCCGAACAAGTCAAGGCCCTGATTGACAGCGGTGGCAAAATGCGAACACATCGAAGTAGAAGCGACGGACACCATTTTTTCGCCGTCATGTTTCATTAGAAATTGAAGGCA  
AGGCACGCTCGCGGCCACCGCTGATTAAGACGGACTCAAGGCCCACTGGAAGCAACGAATGACGACCATTTCCATTTCCGTTGCGGCACTCCGCGGAATGGGCTGCCAAGC  
ACAA

## SEQ ID 8464

MLTPBQKVALIAGVAKCBHIEVSGDGHFFAVITVLSLEFGKARLARHRLIKDGLKAQLESNELHALSISVAATPAEHAAKAQ

## SEQ ID 8465

ATGAAGAAAATTCGCTAAATGAGTATGTTGAGCAGCACGGACAGCGGAAAAACAGCAAAAGAAATCGCGTTACTCAAGGAGCAATTTCAAAGCATTGAGGTCTGGCGGGCAATTTTTT  
TATTTTCAGACGGCAAAAGAGTGAAGGCTGAGGAAGTGGCGGCTTCCCTCGACACGCTG

## SEQ ID 8466

MKILPLNEYVEQHQAKTAKEIGVTQGAISKALRSGRATPLPSDGKRVKAEVRAPPSTR

## SEQ ID 8467

ATGCGCTCTGAACGAAATGGTTTCAGACGGCATTTTTGTGTGGCGGTATTTGTGCTTTGGCAGCCCATTCGCGCGAGTGGCGGCAACCGAAATGGAAGTGGCTGAGTTCGTTGCTTT  
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TTCGCAATTTGCCACGCTGCAATCAGGCGCTTGACTTGTTCGGGTGTACGATAGTGGGAGTCTTATTTGGGAAATGCGCCATTATACCGCAAAATCGAAATTCGCTGTGAAAACGGC  
TTCAGACGGAATTT

## SEQ ID 8468

MPSETKWQTAFLCGGYCALAAHSAGVAATESACSSLLSSNALSPSLIRWRARRALPSNSETMTAKKWCPSPTSMCSHFATPAIRALTCSGVSIVGSPTWGNAPLYRQIIPSENG  
FRNF

## SEQ ID 8469

TTGGGTTACAGACGTGTGAGGGGAAAGCCCGCACTTCCTCAGCCTTCACTCTTTTCCGCTCTGAAAAATAAAAAATGCGCGCCAGACCTCAATGCTTTTGAAATTCCTCT

## SEQ ID 8470

LGYYRVEGKARTSSAFTLLPSENKKIARPDINAFETAP

## SEQ ID 8471

TTGGCGCGGCTTTCAGCATCGCTTTTTAATCAGCGCTGTCTTTCTTCGACAGCGGTTTCTGTCTGCTTCTTCATTTTTTCTTTCCGTTAAATTCGGGATGACTTCCGCTTCAA  
TTCGTTATATCAATTAACATCTGACCCGACGGCTTTTTTATTTGGTTACAGACGTGTGAGGGGAAAGCCCGCACTTCTCAGCCTTCACTCTTTTCCGCT

## SEQ ID 8472

LAAAFSIAFLISRLSFFDRRFLSCFPFIFLSGKLKMTSASIRLYQLTSDPTGFLGLQTCRGESPHFLSLHSFAV

## SEQ ID 8473

GAAGCAAACGCTTGGCGTTAAAGCCTACGGCAACGAGCTGATTCGCGAGGTTCATCATCGTACGCCAACGCGGTACCAAATTCACGCGAGCGGACAACTAGGTATGGGCAAGAC  
ACACTTTGTTTCGCAAAATTCAGCGTTATGTGCAATTCAAACCAAAGCGCGCTGAACCGTAAACCTGTCAGCATCCGCTCTTACACCGGTTCTGAAGAATAATTCACCGGATACCTGAA  
GCCGATCTTTTCAGATGCGGCTTTTACATACCCATACCCGATTGATACAC

## SEQ ID 8474

EAKRLGVKAYGNELIPAGSIIVRQRTKPHAGDNVGMKDHLTFAKIDGYVEPKTKGALNRKTVSIRPYTGSEEFNRYLKPHLFTMRIFTYPIPDLIH

## SEQ ID 8475

ATGCGCGCCCCCAACCTTCGCGCCCTTACGACCCCTGACGCGCGAAGCGCGTACCTGCTTTTCCATACCGCCCTCTACCTCAAGCCCGAGCAACAGCGGAGCTTGAAAAAGCTGTG  
CCTATGCGCTTTCGCGCCACGACGGGCAAAACCCGCAAAAGCGGGATCCCTACATCAGCATCCGATTGCGGTTCGACGCGAGCTCGCCCTTTGGCATATGGACATACAGGCTTGTGTC  
AGCGGTGATGACGACGCTATTGGAAGATACGGCGGTGACAAAAGGGGAAATGGCGCGGTGTTTCGGCAATCTGTTGCGGAGATGGTGGACGGGCTGTCCAACTCGCAAAATCTCAATTT  
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CGATGCGCCCGGCAAAACGCGCGGATTCGAAGGAAACCTTGAAATCTACGACAGATTCGCAACCGCATAGGTCTGAATATCGGTATCGGAGCTTCAGGATTTATCGTTCCAA  
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GCCGCTGCGTACGAAGCTCAAAACCGGATTCGTTGAAATTTATCATCCGAACAGCGCAACCAATCCCGCTGGTTGAATTTCCGCGTGTCCGCGAGGGCGCGCATGCCATACGC  
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ACCTTGGCGATCTCAACGACAAACAGACTTCAATTTGAGGAAGTCTGTACAACGTCGGTATGGGCGATACCTGCGCTGTTATGTGCGCATCATATCGCGCAATTCGCGAGGAGCAATTT  
CGGACGCGAGGTCAGGCTCAGTTCCATTAAGTTGATGGTCAGGAAAGCGGCGATATTCATTTTCAGAGTGTGCCACCTGTTCCCGGCGATTCCATCCGTTTGTGTTGTTAAGGGA  
AAAGGCGATGATTTCATCGGATACCTGCGCGAGCTTGTGAAAGTCCGATCCGACAGCAGCTGGATCGAGACTGGGAAAAATGAAGCGGCAAGTACCGGTGTCGCGCTTCAAGTCC  
AATCGGAGACAGCAACGCGCTGTGGCATTAATGGCGCAAGCGATTTCGATTCGCGGTGGGACATCGAGTCCGTCGAAACACCGCTTAAATCCGAGTCCGGAACGGAAGGTTTGTGCA  
ATTCAATCTTATTGAAGTCAAGAATTGGATCAGTTGAATCAGATTATTCAAAATCTGCACAGCATCCCATATATCCGCAAGTCTACAGAAGT

## SEQ ID 8476

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EDHAHQAESFRKLI LAMTKDVRVIVKLDRLNHRITLGSMPDKRRRIAREFLEYAQIANRIGLNAYRELQDLSFQNLHPNRYETLKKAMDKSRKNRQDVVGVKILRAFGRLVIGANI  
EAKIRGRENLYGIHQKMAKRLFAEVNDIYGRVIVNSIPACYAALGTLHTLYQPKPRPKDYLAIPKSNQYQSLHTILVGPYGLPIEVQITRENDVAEAGGVGVHGSYKSDSETVDQ  
AVLHTNQWLNLIDLOASSANAIEFLEHVKVDLFPNEIYILTPKGLILPLKPGATFPDYFAVHTDIGHRTVAARVNMVMPLETRKLTGDSVEIITSEHAKFPNWLNFVSGRSASIR  
QYIKNLNRHDAVVLGESLLQKALSSLLPKDVLSDGIEKYLADLNKQTSFEVLYNMGHTLPPYVAMHIAELAGEHFGSEVRLSSIKVDGQESGHIHFAECCHFPVPGDSIRLLLVKG  
KGMITHRDTCPTLLKSDPEQLDADWENMGQNYRVGLQVQSEDSHGLLALMAQAISDSGADIESVETPSKSQSGTEGFVEFKFLKVKNLQNLQIIQLHLSIPYIRKVRIS

## SEQ ID 8477

ATGAACCGCTTTATCCCAACCGATTATCGCCGCTGAGGCTGGCGGATTATCGCGCGGCTTTGGCTTTGAGCCTGCTGGTGTGATGTGCTCGGCTGGTGGTCTTTGCGGTTTGGG  
TGTTTACCGTATTTCAGTTTCAGTTTTCGCGACCTCGCGGTGAAATTCGCAAAATCTGAAGCGGTGTTGAGTCCGCTTACGCGCGGTATCGTGGTGGTTCAGCGCGCACCGGATCC  
GTATCGTGAATGATGCTTTGAAATCAGTATTTTATGAACGTGTCAACGTGATTCGCAAAATCGCCTCGCGATTGTACGGTAACGAAAGTGGCTATATAACAAAGCAAAATTCGTT

AATGCGGATTGACAAAGCAGCAGCGAAACGAACGCAACGCGTTTGGCGACTACGGCTTCCGGTGTGAAATTACTTTTGTTCAGTGGCCGGTCTGGTGGCAGCCGATTTTGT  
GTTACACCCCAAGCAGGTGCGAAATGTCCCGCGCGAAGCGTATGGCTTTATCCGCTTCGGTTCGCGCGTGGATATGTATCTGCGTGTGATGCGCAGGCGCAAGTGGCGATTGGTGATAA  
AGTAACCGCGTAAACCGTATTGGCGGTTCGCGCTGACTGATTCCTCAAGCGGATCTGTTTCAAGCTGCTTCGGTGAACAGCGGCAAAACCATCTGCGCAACAGCAGCAATC  
GAAGCGCGCGGCTAAGATTGAGCGGCTGTGCAAGATGTGTGAAGAT

## SEQ ID 8478

MNRLYPHPIIAREGWPIIGGLALSLLVSMCCGWSLPFWVTFVVALQFFRDPAREIPQNPBAVLSPVDGRIVVVERARDPYRDVDALKISIFMNVFNVHSQKSPADCTVTKVYVYNGKFFV  
NADLDKASTENERNAVIATASGREITPVQVAGLVARRILCTQAGAKLSRGERYGRIRFGRSDMYLVPDQAQVAIGDKVTGVKTVLARLPLTDSQADPVSQAASVETAAANPSAEQQOI  
EAAAARIQAADVQDLKD

## SEQ ID 8479

ATGAAGAAGCAGGACAGAAACCCCTGTCGAAGAAGACAGACGGCTGATTAAAGAGCGATGTGAAAGCCGCCCAAGGCTGCGATGAGGTTTACAAAATCGCGCCGGTTTGAAG  
ACGGCTTTGAATTACTTGGAAAGCAGCCGAT

## SEQ ID 8480

MKKQDRNRLSKDRRLIKKAMLKAAAKGCDEVYKIAPGLKDGPELLGKQPD

## SEQ ID 8481

ATGAGCATCATCCTACTTCTCGCTGCAATCCGCGCGCTCCGCACTCAACAGCTTCTCGGCCAACCTTCGGCACACTGCTTACCTCATATAATGCTTGGCGTCGCGATGACCC  
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ACGCGAGCTGCTGACGCGCGATAAACGGCTCGACAACATCCGCTTCATCGGCAAGGAGAGCGTTTGGCGGAATTACAGTCCAACCTCGACCAAAATCTGATTTCATGCTTGACGGCAAC  
CCCTGCGCGGATGCTTTATCGTTACCCCGACCCGCGCAACACGCGCCGCAAAATGCAAGCAATCTACCGGGACATTACCAAGCTGCTATGTCGGAATCCGCGTCTATGGATACCGAAT  
GGGTGCAAAACGCTGTACCAATCAACAGTTTCATCCGCAAAATCTTATGTTTCTTCCCTGACGCTGGGTATGGCTTTCGCTCTTGTGCGACACACACCATCCGACTGCAAAATCTCTAG  
CGCAAAAGAGAAATCGAAATCAACAACTCTGGTGGCGCGCGCTGTTTATCCGCGCGCTTCTCTTATCAGGCTATGTTGGCAGAGTATCTTCTCGCGCGCGTACAGCTTAGGCTT  
TGCGGTGGCTGCTCTGCGCGCGCGCTTGGTGCATGCCATCTTCAAACTTACGGCTTGAACATCGGCTGGCGTTCTTCTACGTCGCGCAACTCGGGCTGGTGTTCGCTTCGCTCA  
TCGCGTGGCGGTATTGCGCGCGTGGCTTGCCACCACACACCTGCTCTGCTTCAAGCCAAAAA

## SEQ ID 8482

MSIHYPSLHVESARSALKQLLRQPPGTLI/LIMLAVAMTLPFMYLGIQSGQSVLGLKLNESQITVYMETAAQSDSDTVRSLL/TRDKRLDNIRFIGKEDGLAELQSNLDQNLISMLDGN  
PLPDPVIVTDPDATTAPQMIAIYRDIKLPVESAAMDTEWVQLYQINEFIRKILWFLSLTLMGAFVLVAHNTIRLQILSRKEEIRITKLLGAPASIRRPFLYQAMWQISPSAAVSLGL  
CGWLLSAVRPLVDALFKPYGLNIGWRFPYVGEGLVFGFVIALGVFGANLATTQHLLCFKAKK

## SEQ ID 8483

GTGAAACCCGGTTGCAACGGGTGACGGCAATCGAAAGACGGCTGACCGCCCGACAGACGGGCGCGCGATAAAGAAAAACCCGACGGGGCGGTAATCCCGCTGAATTCAGGGAA  
CGCGTTGAGGTACCGGCGAAAGCGATTA

## SEQ ID 8484

VETRLQRDCKSERRLTARTDGRPIKKNPHGAGNPPELQSGSGNGEREL

## SEQ ID 8485

ATGCCGCCCTTCTTACAGGACCTCTATGATCCGTTTCAACAAGTTTCCAAACCTATCCCGCGGTTTGAAGCCCTGAAAAACGTGAGCTTCCAGATCAACAAAGGCGAGATGATTT  
TATCGCGGGACACTCCGGTTCGGGCAATCCACGCTCCTCAAGCTGATTTCGGGCATCAACAGCCGAGCATGGGCAAACTCTGTTTAAACGGACAGGACCTCGGCACATTGTCCGACAA  
CCAAATCGGCTTTATGCGCAACACATCGGCATCGTGTTCGAAGACACAAAACTCTCAACGACCGCAATGTCTGCAAAACGTATCTTCCCGCTGCGGATTATCGGCTATCCGCGCGC  
AAGCCGAAGAAGCAGCGCCGATCGCCATCGAAAAAGTTCGGCTTGAAGGACGAGAAATGGACGATCCCGTAACCTCTCGGGCGGTGAACAAACAGCTGTGATCGCCCGCGCGCTCG  
TCCACAGCCCGGCTCTGATGTCGCGGACGAACTCCGCAACCTCGACCGCTCGATATTATGGAATTGTCAAAACCTTCCACGAAGCGGGAACACCGTCACTCGTCGC  
CGCATGACGAAACCTGATGCGGACTACGGACACCGCATCTCGCGCTCTCGAAAGGACGACTCGCA

## SEQ ID 8486

MPFLTPPNIIRFQVSKTYPGFEALKNVSPQINKGEMIFIAGHSAGSKSTVLKLSIGITKPSMGKVLFPNGDLGLTSDNQIGFMRQHIGIVFQDHLILNDRNVLQNVILPLRIIGYPPR  
KAERARIAIEKVLKGRELDPPVLSGGEQRLCIARAVVHQPLLIADREPSANLDRAYALDINELFKTFHEAGTTVTVAHDETLMDYGHRIILRLSKRLA

## SEQ ID 8487

ATGCCGTGCGACTTATCTTCTACTATTACCAAGAGCTTATCCGACGCGGTTCTATCCGCTTAAAGGGCAGTACGGCCAAAGGACAAGCCGAGAAATTGGCGGTATTTCATCCGAACACTTC  
ATCAAAACCCGAAGAATCGGAGCCAAATACCGATAACGAATATTTAATCGGGCTGCTTTCCAAG

## SEQ ID 8488

MPDLSPILTKELIRSGSIRLKGSTAKGQAGELAVFIRTLHQKPESEPTINEYILGLLSK

## SEQ ID 8489

ATGCCGTAAACGCGGATGCCGTCTGAAGCGCTTCAGACGGCAATTTCGCGCCCGGCTTCGGTATCCGCCAAACTTATCCACTATCTAAAAACAGCGGAATCTTTATAATCGGTACT  
GTCTTACCTATTGTTCAGACGGCATATCCCTGCGGACGCAACCGCCGAAACGATATGCCGCCCTTCCCTTACAGGACCTCTTA

## SEQ ID 8490

MPLNAGCRKLPLQTAFSPAPFIRQTYPLSKNRRNLNRYCLFYCSGDISLRTQPPETICRPSLDLL

## SEQ ID 8491

GTGACGACGTTGCGGCACGGATAACCGACTTGAAGGACAGGGGCTTCGTGTTTGCAAGCCGCGCATGAAGGCGGGCGCGCGGGAAGCCTGTACGCATTATTTCGATTGTCAAAAAAG  
GAGCGAAGTA

## SEQ ID 8492

VTQLAARITDLEGRGFVFAKPRMKAGGRGKPVTHYSIVKNGAEV

## SEQ ID 8493

GTGAAAATTGATTTACAGACATGACATTTCCCTACTTCTGCAAAATCCCTTATTATCGGCTTACGAGGGTTTACTCAATACCCCGCTCCAAACGTTTACAATACC  
CGAATCGACATACAAAGGACAAAACGATGAACGCTTGAATCTCGCCGCAATCGCCCTTGGCCGCAATTTGCGGCACATACCGCTCGGCAGACGAACTGGCCGATGGAAAGACAAATAC  
CCGCAAAACCTGCAATCGCTCAAGCCCGCTCGGCATCGCAACCTATGGGCGACTTGGTGGTCCGTGTCGAAAGAGATGCCCGCATGTCCAAATGGTACAAAGCGCAGAAAAA  
GGCAGGCTCATATGCTCGGCATCGGCATCGGCATCGCAATATCGGCAACTTCTCAAGCAGACCCCGGTGAGTACCCGATTTGGCGTTACACCGGGCGAACAGCCGAACTTTA  
TGAAATCTACGGAACAAATGTGCGGCTACTGCCCTTACCCTGCTGAGACCCCGAAATGCGGATACAGGACAGCAATTACAGGAGAGGTGAACGAGAAAAAGCCTGACCGAAGCCGCTCAA  
ACTGCCCAATCAAAATGCCGT

## SEQ ID 8494

VENFDPRHDSILLDNPLIIGLRRVLNTPPTVFNGLQYPNRHTKDKTMKRLNLAIALAATFAHTASADELAGWKDNTFQNLQSLKAPVRILANLWATWCGPCRKEMPAMSKWYKAQK  
GSVMVGIALDTSINIGNFLKQTPVSYPINRVTGANSRNFMRSGYNNVGLPFTVVEAPKCGYRQTTGVEVNEKSLTEAVKLAHSKRC



**SEQ ID 8495**

TTGTTTGTCATTGCGTTTGTTTTGATTCAATAATGCGCTTTTCGCCGTACCTGAACCGCTTCCCTGCAATTTCAGGGGGATTACCGCCCGGTGCGGGTTTTTCCTTTATCGGCCGCCGCTCTG  
TCCGGGCGGTTCAGCCGCTCTTCCGATTTCGCGTCACCCCGTTGCAACCGGGTTTCCACACACCGCCGAACGGAG

**SEQ ID 8496**

LFALRLFLIHNRLSPLPEPLPCNSGGLPAPOGFFFIGRPSVRAVSRLSDLPSPRCNRVSTQRPTE

**SEQ ID 8497**

ATGAGTGCAGGGCTGATGGGGATGGCCTTTCAAACCGGGTATCCCGAGGGGGCAGCGTTTGTGTTTTGGTAAAGTTGTGCGACTGCGCCAAOCAGCATGGCTTGTTTATCCGTGCGAAGAAA  
CGCTGGCGGAAGATA CGGGCTTCGCCGAAACCGCCGTACGGCAGCATATCAAGTGGCTGAAGAGTAACAATTTCATCAAGTCCGCCCGCGCAGAGGGGGGGGAGAGAAGTCCGCAT  
CTACCGCTCAACGCTCCGCTGCTGAAAAATGCTATGCGAGGGCGGCAAAACCGAGGGCGCGCGCAGGCAAAAATGTGGGAAGAACCATTGGATTACGAACCTTCGGATTTTGAACCG  
TCGGATTACGAACCTTCGGATTTTGAACCGTCGGATTACGAACCTTCAAAATGTAGCGCTAAGAACCATCAGATTTTGAGCGATGAACCATCAGATTTTGCGCTAAGAACCATCAGATTTT  
CGCTAAGAACCATCAGATTTTGAGCGCGCAACCATCAGATTTTGCGCTAAGAACCATCAGATTT

**SEQ ID 8498**

MSARLMGMFAFKTGIPRGQRFVLVKLCDCANDDGLCYPSQETLAEDTGAETAVRQHIKWLKQNFIKSARRQRGRERKSDIYRINVALLEKCYAEAAKRKAARQAKNWEEPLDYEPSDFEP  
SDYEPSDFEPSDYEPSDFDAKNHQILSDEPSDFALRTTRFCAKNHQILSGEPSDFALRTTRF

**SEQ ID 8499**

TTGAGCGGTGAACCATCAGATTTTGACGGTTCCTTATATGTAGAACCGTCAGTAGAACCGTCAGGATCAAAATCGCGCGGGCGCGCGCCCTGCCGACCCGACCCCTGCGAAACCGCAAA  
CGCGCCCTCCGAAACCGCAGCGGGCGGCGAAGCGCAAAAACCGCGAGGCACGAAACCGAGCTTTTCGCTGCTTGGCAGTACCGGATACAGGGGACAGGTGGCGCGGACATTCTCGAAGT  
CGCAAGGC AAAACCGCAGCCGCTGACGGAACGGCAATCGCCCTGATTTGCCGCCGATGCGGAGAAATGCGGGATGACGGCGCTGCAGGCGCGGAGTACGCCATCGCCAGCGGCTGGGCC  
ACCTTCTCGCGCGGAATGGCTGCAAAAACAAACTTTGCGGGGTCTGAAACCGCGCGGGCCGACGCACAAACCAACCGCGCCCTGTCTGGATCGGGAAGCTACGGCGATATGCCGACGA  
CGGATTTT

**SEQ ID 8500**

LSGEPDFDGLSYLVEPSEVPEPGSNARGARAPAGPHPAKPQTAPPETA AAAAKAKKTGRHETELSLADYGITGVAA DFLQVRKAKROPLTETAMRLIAADA EKCCHMTALQAAEYATASGWA  
SFRAEWLONKTPGGSGNRRGPTTHNQTA AVL DAGSYGDMPTTDF

**SEQ ID 8501**

ATGTCTGAAATCAAAATTTTCCACAATCCGCGTGCAGCAAAATCGCGTGCCGCCGTGTCCTTATTGGAAGAACGCGGCATTGCTGCCGAAGCGGTCAAAATATTTGGATACGCCGCCGCCGACT  
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**SEQ ID 8502**

MSEIKIFHNPRCSKRAAVSLLLEERGLAAEAVKYLDTPPDLSELKDI FNKLGLSARGMVRVKODLYKELGLDNPDLNDALLRAIADHPALLERPTVLANGKAAVGRPLENIEAVL

**SEQ ID 8503**

ATGGCTTTGAGGAACGCGCTGATTCTCTGGGGGCTTACGGCGCGCGCGCTGCGGGTCGAGCGAGGCAATGCGCGGAACACGGCGGATACGCGCGCAAAAAGCGTTTTCGCGCGCGTGTGGA  
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CCCGGGTTTCAGAAATCGCGGATGTAAACATCCGCTGAGGATGATGCATCGCGGGATGGCGAGCGCAAGCGCGCGCGCGGATGATCGCGCAAACTTCGCGGATTTTCGGTTCGACAGC  
GGCGGGAGCATGATTTTTTCGGCGAGGAGGGCACGGGCAAAAACCACTTTCCTGCGGCATCGCGCGGAGTGCATCGCGCGCGCAAAAGCGCGCTCATCAGCGTGGGCGCATATATGC  
TGCAGACGGTCAAGAGACAGTTTCGGCGCGCGCGCGCAGCGCGGGCGGCTCGGGATTTTCGTGAAGCCCGATTTGCTGTGTCTGGACAGTTCGCGCGCGGCGAGTCTGTGGAAACCGGACGG  
CGGATATTTGTTTTCGCTGTCACCGCGCTGACGCGGCTGATCCGATGCTGCTGTGCTGACCAACTGACGGCGGAAGCTTTCGCGAAAACACCGACGCGCGGATCAGGGACAGGCTG  
CGGAGTCGCGCGCGCAAGCTGATTCGCTGCTGCTGAGGAGAGCTACCGTGGC

SEQ ID 8504

MALRNASDFLGAYGGGVVRVERRQCAEHGGYAAKSVLRGVWTCGPACRKLKLEAADEMAAYATFLRRGAMRDALKRIGRSGIAPPRFNCRIENIYAVSDSIPGMARAKAAAAEYAAANFADVLQT  
GRSHIFSGRRGTGKNHLACGIAREVIAAGKSALVITVGDMLRTVKDSFGGGGEGAGVGIIVKPDLLVLDEFGAGSLSETDGRILFSVNNARYERLMPMLVLTNLTARAFRENTDARIRDR  
RDGGGKLIPFDWESYRA

**SEQ ID 8505**

GTGTCGGGTGGGTTTTGAAATCCCGCTACTTGCAGAAAAAGCAGGTTTACGCACGGTAGCTCTCCAGTCGAAACGGAATCAGCTTGC CGCGCGCGTCCCGCAGCGCTGTCGCGGAGAGCTTCGCCCGTCAGGTGGTTCAGCACACAGCATCGGCATCAGCCGCTGTAACGGGCGTTGACACGCGAAAAACAAATTCGCCCGTCCGTTTCCGACAGAC  
TGC CGCGCGCGAACTCTCCAGCAGCAGCAAAATCGGGCTTCACGAAAAATCCCGACCGCCCCCGCTCCGCGCGCCGCGCGAAATCTGCTTTCAGCTGCTCCGACGATATATCGCCCAACCGTGAT  
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GACGTTTGGCGCATCTCGGGCGGCGCGCGCTTCGCCCTCGCCATCGCCGGGATGGAATCGCTGACGGCGTAGTTTTCACATCCCGAGTTTCTGAAACCGGGGCGATCGCCGAACGCCCGA  
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TTTCGCGCATTCGCGAAGTCTCGCGCGCACCTGCCCGGTATGCGCTAGTCGGCAAGCAGCAGGAAAGCTCGGTTTCGTGCTTCCCGGTTTTTTTCGCTTCGCGCGCGCTGCGGTTTCGGA  
GCGCGCGTTTTGCGSTTTCGACGGGTGCGGTCGGCAGGGGCGCGCGCGCGCGCATTT

**SEQ ID 8506**

VSGVWLK SAYLQKKVSRVTALPVERNQLAAAVPQVPDPFRVGVFAEGFRRCVQGHQHRHQPLVPGVDGKQNPVFRQRTARAELVQEQIGLHENPRPRLAAAAETVLDROPQHIAHRD.  
 DQRAFAGGDDFAGDAAGKVVPARAPPARKNHAPFRLQHI GEVCRILGGGLRLPRHPDRDIADGVVFNPAVSEPRGDARTPDFAFFQRVAHRPAAQRFVRCRHFRRLQLPAGRAARPHAAQN  
 AFRFVSAVFRALPLDPHAAAVSQEIRRVQPSHIRTPPSKIRRRHIAVASRI OHGGGLVVRRAAAVSRPAESFVLQPPGAEAGPAAGDGLRLRLQRRHFAFLRIGGNQAHCRFRQRLEPC  
 LADLQEVRRHLPRDAVVGKQRKLGFVPAGFFRLRRRCGFRRLRFRVRSVSGRGAARA I

**SEQ ID 8507**

ATGCGCGAAGGGCGCGGAATCGCGAAGACGGGGCGAAGCATTACCCGCGAACAATCCGTGCGCGCGCGGGGGCGTTTCAGACGGCATCGGGGGCGGCAGTCGCAAAAAGGACGGCGGTGCTT  
GGGGAAATATCCCCCCCCCAATGCGCGCAATT

**SEQ ID 8508**

**MREGAECGRAGEALPANQSVRRRGVSDGIGGGSRKKGDDGGANGISPPAHRI**

SEQ ID 8509

GTGAACAAACGGCTGTTTTCGACGCGCAACGCGCTTCGCGTATTACCTGTTGGGCGGTTCTGTTTGAGTGTTTTCCGCTTTTTCGTGGTGTTTGCCTCATCCGTTTGGGCGGTTTATCGGA  
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ATCCCTGTTTGAACACATTCGCGCAACACTTATGAAAACCTGAACAACATCCGTCGCGTTTTCGCGTCCCAACGCGTATTCGCAGCGTGGTGATGTCACGCGATCCCTACCATTTCGCGCGGG

CGGCGGAAATGGCGGAGGATTGGGTGTCGCGGTTATATGCTGCCACGCCGACCAGCGGTTGATCGGGGAAATAGAAAAAATCTTTATGCTGCAAGAGGGGTATGCGTTATCCCT  
CTACCGTTTGGAAAAATGGGCGAGCCGCTTTTGGGATGGCTGTCTGAT

## SEQ ID 8510

VNKRFLPCSRNLKRYLLGGFCLSVFPLLLVFPASSYVAVYRTGGQVLPYVRADAALVLGAAAWDKRPSVFRFRINHAIALYQSRVVGKIVFTGGRTKKGYMTEAFVGRYALKQGVPARN  
ILFENTSRNTYENLNIPIVLRANGIASVIVSDPYHLARAEMAEDLGVRVMSATPTTRFDAGNKKKIFMLQEGYALSILYRLKNGSRPLGLWLS

## SEQ ID 8511

TTGATACACATTAAAGCTGAAAGTAAAAATCCGCATACACCCCTCCCTGCATATTCTTCAACAACGGGTTTTGATATAATCGCTATCTGTTACAGATAGTTCAAAACGGCATTCAAAACCT  
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CGGACGCGTTTGAAGGTACTCTGATCGAACGCGCCACTGACTGTTCTGCAAAATCTCCCTATGACGAGCAGGAAATCGCCCTGACCCATTTTTTCCGCGAAATCATGACGCTT  
GGTATGTGGGACAAATTTCCGAAACGAAATCTACCCCTTGCAGGATGCCAAAGTGTGAAAGCGGACGTTCCGACTACACAGCTCCACTTTCCCAACCGACTGAAGCGCGCGCGAGCTG  
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CAGCAGCATCCACCATACCCCTTGTGCGCATGATTGCCAAACGTTTCTACGCAACGCGAGCGGCTGATCGCGCATGCGGCTGTCGCTATGCAACCGCTAACGCGACACGCGTTCAAC  
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ATCCGCTTTATCAGCGCAACATATGATGCTGAAACTGTTTACCAACGAAACCGCGCGCAAACTGTTGCGCGGTTTGGTATTACGAGCGCGCAACACTTCCCGCGCTGAAAGAGCT  
GATTACCAACAACTGACCGGT

## SEQ ID 8512

LIHILKVKIRIHPPLHISSTTGFDI IAYLLQIVQTA PKPLQMPSEIIGIRLCKGYFMSIHSIDLIVVGAGPAGLSFAELAGSLKVTLIERSPLFVLQNPYPDGREIALTHFSREIMQRL  
GMWDKIPENIEYPLDARVLNGSDYQLHFPQTEARGEPADCLGLYLISNHNIRRAAYEVVSVQLDNVSILDTAVKEVTSNDAQVFLNGDILTRILLAAADSRFSQTRRQLGISIDMH  
DYSRTHFVCRMKHTLSNQHTAYECFHYGRTIALLPLEKRLTNTVITVDTRKINSVQNLSPLELAASVKEQLKRLGDMELVSSIHYPVVGMIAKRFYGRKSALIGDAAVGMPHTAHGPN  
IGLSSADILAKLILEAQQRQDIGAASLLEKYSKHLMLHAHPLYHGTNMLKLTNETAPAKLRGLVLRAGNNFPPLKLLITKQLTG

## SEQ ID 8513

GTGGGGATAAGACGGTTCATTTTGTCTACCTTTTATTCAAAATATATTAATAGCGCAATTATAACGGAATCCGCGCGCTTCCGCGGACAAATGCCGCTGTAAGCGCGCTTCAGACGGCATC  
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## SEQ ID 8514

VGIKTVHLSFYSLNLSIDIITSAAFRRQMPSEGRFRHPRKCYNI GFPLFFQAAISIMCNHPRHSHNDITIRGARTHNLKNIDLDIPRKLIVVTVLGSGLKSLAFDITLYAEGRR  
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FARVRVDGEVYQLDEVPLKLEKNKHNDIVDVRVKADIKQRLAESFETALRHGNERALAMEMDSGEHMFSAFACPVCSYSLPELEPRLFSFNPMPGSCPTCDGLGNTPDFPEKVV  
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ARYVVGGEPLHEVSAWPLTKTRHFETLDDGNKKQIAEKILKEITERLGLFVGLDYLNLRSBAETLSGGEAQIRLASQIGSGTGLVMYVLDDEPSIGLHQNDRLLATFLKRLDGL  
NSVIVVEHDEADREAFVVDMPGAGEHGNVLIADTPENVAKCEKSVTGQYLGKKSIAPVSERTFPVNPGRMLVLKGARGNNLNKNTLELPLGLITCTIGVSGSGKSLINDTLAKITA  
RELNRAQEPAPYDIDIRGLEHLKVINVDSPIGRTPRSNPATTTGLFTPIRELFAVGLSRERGVNVRFSFNVKGRCEACQDGVIVKEMHFLPDVVPVCEVCHGRYRNRELEIQYK  
GKNIQVLDLMTVEAREFFDAVPTVSRKLQTLMDVGLYIRLQSATTL SGGEAQIRKLALBELSKRDTRGTYLDEPTTGLHFADIALLEVI GRKKGKNSIVITIEHNLVDIKTADMTV  
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## SEQ ID 8515

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GCCGCGCTGCTTGCCTCATCTCCGCGCTTATTACATCCGGGACGCGCAAGCAAAATTTGCGTGGCGCGCGCTGTGTGCAAGATTGTGTGAAAAAATGCGCGCTGAAGCGCGCGG  
CCCCCACCCTGAAGCCGATGCGCGCTGAAGCGCGCGCGGAGGCAATT

## SEQ ID 8516

LKTKLKKRFRKYGTVRNTQTSTVTRTAAPQGGNTNFGYKNRAFCVGFQYLNFLNLGNAFKYIWRHKEKGGREDLEKALRYLERQAGAPKFKLKHRRYERMYAGLKDGCDFDGT  
AALLAVISAAYIIRDEGNFANAAACVEDLLEKMPFAGRAPHPESPMPPETAGGGI

## SEQ ID 8517

TTGATGCTTAAGCAGGTAAAAACAGTAAATAAACGCTTTCAAAGATTTTCGAGCCATATGACCGTCAAAACCGGTTTCGCCCCAGCCACCGGTTACCTGCATCGCGCGGCTTC  
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GAAATGGGTCGCTCTGATPACGACCAACGCGACACGCTGTTACCAACCCCGGTTTCGACCGTTATAAAGAAGTCAATGCGGAATCTTGGCAAAAGCGGATGCTACTACTGCTAT  
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## SEQ ID 8518

LMPHKGNKSNKINAFDGAIDMTVKTRFAPSPTGYLHIGGVRTALPWFARHHRKGFLLRIEDTLARSTAESVNIILDMKRWGLDYDNDNVVYQTRRFRDYKVEVIAELLARGDAYCY  
CSKEELAMREKAEKEGTATYDRWRPEAGKTLPEIPAGVQPVVRFKTPLDGVTKWTLVKGESIPNEALDDLIARADGTPPTNFCVAVDDYDMGVTHIRGDEDEVNTPKQINILKAI  
GANLPEYGHLPMLNBQCKKISKRSQDTVAITDFGAMGILPEAMLNVLARLWAGHDDDEFTTEQFIENFDLKDVSFSPSRMDLKKLYWINGEHIKITPDGLITELVKPRALRDITHEK  
PALEDVLALVKDRAQDLNALADECLYFYKQVPAEADVAKHMDDEAARMRFARERLEGLDWNKAITHDLFPFCDEBEGIKMGKLGMPRLRLAVCGTAKTPSVDAVALISKEVILKIRIA

## SEQ ID 8519

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CGGTTTACGCGCGAGGGAAGCAAGCGTTCGGGGAAT

## SEQ ID 8520

VRAMPDVCMRLQTAFRRLNKKILYFLMFVSTSVWAGGAEDNLLSIQSGYRALLQKQNNLDGKIIGMSOLEDARRRLQAAQADIARLEAEIPAAMAQKARQAEEMRQIGVRLDHAN  
AVYGAGERKRRGN

## SEQ ID 8521

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AGGT

## SEQ ID 8522

MNSLFDVNTVFIIRLKAGHIGRLVQALFEEMHGFEWSSVDKIRAYYGRCLKDDPLAPAAVDSTGLIGSAVVRHDMENFPQYEWLGDVFLPEYRGKIGRLVAHCIGAARSLGI  
KFLYLTPDVQIFYESFMAVVRHFNHNGEWTVVRLLDVVKV

## SEQ ID 8523

ATGGGCGATGCGCTGAGCTGTTTCGACGCGCATTTTTATGTTTGAATAATTCCTGTGATATAGTGGATTAAACAAAACCGGTACGCGCTTGCCCGCCCGGCTCAAAGGGAACGG  
TTCC

## SEQ ID 8524

MGRCLSCSDGIFVVKFVVRYSGLTKTGALPRPGSKGTVP

## SEQ ID 8525

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## SEQ ID 8526

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## SEQ ID 8527

ATGGCAGTATTACCAACGAGACTGTACCGGAAAAATTTCAACCATTTTGACCTGACATTGGTAGCGGCGCGTCGCGGCCCGGAGCTTGAATAAGCAATACCGCGCTTGTGGACGATG  
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## SEQ ID 8528

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## SEQ ID 8529

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## SEQ ID 8530

MIDMLAAVKIIVHFLYPPVVKTFKYPVPV

## SEQ ID 8531

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CAATGGTACGGAACCGGTTGCGCGGTGCTTGGCGCTTACGGAACCGTTCCCTTTGAGCGCGCGCGGCAACCGGTACCGGTTTTGTATTAATCCACTATATC

## SEQ ID 8532

VQIRLISVGGAAASHNEKSVDKLYGGLTKIRTRRAAGSTNGTEPVRPVLGRLEFPPLSRGGATPYRFLLIHYI

## SEQ ID 8533

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## SEQ ID 8534

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## SEQ ID 8535

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TTGAAA

## SEQ ID 8536

LRFYAEVLLHHWNGGFGHGAALLLGKRYCSKRFLRRNETDRKPVNKVVETNRKTAKLSIRIILSQRTSTLIJCLIRQALNSNLFNKKVMKILDICLYTTSRAITKIIKILKSNIECAP  
LK

## SEQ ID 8537

TTGTTTGACGCGAGTGAATTTGCTATTTCAAAAACGCGCATTCATATTGTGATTTTAAATTTTAAATGATGATTTTGATGATTTGCCGACCTGCTTGTGTATAAG

## SEQ ID 8538

LFDAGEFRYPKNAHSIFDFKILMMILMIADLLVYK

## SEQ ID 8539

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## SEQ ID 8540

VECSFISEYNTGIGLYFTTGRNMSIKVAINGFGRIGRLALRQIEKAHSEIYVAVNDLTPAEMILLHLFKYDSTQGRFQTAELKDDAIVVNGREIKVFANPNPEELPWGELGVDVVECTG  
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VIPELNGKLDGSAQRVPVATGSLTELVSILVERPATKEINAAMKAASSESYGNEDQIVSSDVVGLIEYSLFATQTRVMTVGGKQLVKTVAMVDNEMSYTCQLVRLTLEYFAGKI

## SEQ ID 8541

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## SEQ ID 8542

LNKRLLFVRHKPQYVTDKQRLNAMCSDGIVLSTGLFKP

## SEQ ID 8543

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## SEQ ID 8544

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## SEQ ID 8545

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## SEQ ID 8546

MNRPAVSISLADGLQIRIRQMFQAEKHNKNKASEQSEALLSN



## SEQ ID 8547

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CCGGTTTT

## SEQ ID 8548

LGSGHFRRLSGCMCFIISNRRTARRQSVSACVSGRIYLLRVNSVPICPAAISLKAFTVGLLLRTSSTSGVLFPSSHARRAATNVRSKHLEIFPVQSSVIRAILFAFPQKYLNHETGYF  
RGF

## SEQ ID 8549

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## SEQ ID 8550

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## SEQ ID 8551

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## SEQ ID 8552

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## SEQ ID 8553

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## SEQ ID 8554

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## SEQ ID 8555

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## SEQ ID 8556

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KNEAKVI

## SEQ ID 8557

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## SEQ ID 8558

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## SEQ ID 8559

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TGTATCGGTCTCAAAACAGAGGATTTTTTAGAGGCTGTGTTGGTTACGGGACGGAGGAATGTAAAAAATGCTTTATCAAATTTATGAGGGCAAGCAGTTTGTGTATCAATGGA  
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## SEQ ID 8576

VKTFLLHTQKRNFLDGLSLHDCYRTAKVBEGRNVCFDFEDGFVLDNNPNQAGKHLKTFDSRVVLTHENRNAEDYLDIFEDIVFLGKRLPTVRKFLDPSLELLEMINAQGYTLEFLYLYE  
CIGVKTSDYFLEAVLVTGRSRECKCFIKIMRASSFVYQWNNLRNLSKIV

## SEQ ID 8577

ATGAAACCGTATGCGGAAAAAACTCTGATTTCAACTTATACACAAATTTATCCATAAGCCTTATTATAAAAAATGCCGTCTGGAATACTGAAATATCAGCAATTCAGACGACATTTTGCCA  
TTCCC

## SEQ ID 8578

MKPYAGKNSDFNLVTNLSISLILKMPGILKYQHFRHFALP

## SEQ ID 8579

GTGAGAAAAAACGGAATCTGATGATTTTCCAAGATAAAAAAGTTGTACCAATCTGAAACAAGAAGCTTTTGCCAAACACCCCGCATACAAGACTGCCATTGCCGAGTGGGAAATCCACT  
GCAACAACAAACATACCGCTTAAGTTGCTACAGTTATTTGATACAAAAACAGGAAATTTCCACACAAACTACACAGCCTCTTCCCTCCGCCGATGAGCATCTGTCCGGGACATT  
AACTGAAAAACAATATGAAACCGTATGCGGAAAAAACTC

## SEQ ID 8580

VRKGNLMTIPQDKRVVFNLKQERFANTPAYKTAJAEWEIHCNKTYRLSSQLPDTKNTEISTQNYTASSLRPMSILSGTLTEKQYETVCGKKL

## SEQ ID 8581

TTGGGAAACCGGATATTTTGCGCGTTTTAGGAATTTTCCAACAATCTGCAATAAATCCAGTTGCCGCGACCTTTTCAGACGGCAGGCATTCACAAATGAGCAAAATCCCGCTCCGCC  
TTCTCCAGGTCTGTCATTGACACGACAAAGTCGAACAATACGAGCTGTTCGATTTTCATGCTTTCCTTCGACAGCCTCTTTGGATAACTTCCCGACTGTCCGTCCCGCGCTTTGAGGC  
GCGCGGCAAGCAGCTCGAAGAAGGCGGAGGATAAAGATACGACAGCTCCCGCAGCGCGTTGCGAACCTGCGCGCGCGCTGAACGTGATTTCCAAAATCAGCTCATAGCTGCCGC  
CGCAACGCATTACGCGCTCCGTGCTTGTGCCGTAAATAGTTGCCGAATACGCTCGGTATTCCAAAAAGCCTCTCGCGGATAAGCGATTCAAACTCTCTTTGGAAACAAAGTGATAA  
TGTACGCGCTTTGCTTCCCTTACGCGCGCGCGCTGATGCGACACGGAACCGCGCAACCGTTATGTTTGGCAACAGCGCGACACAGCGTGGTTTGGCCGTGCCGGAAGCGG  
CCGAAATGATAAGATGTTGCCCTTTTCGATAAGCGGACATATTTTACCTGTATTTTCCAAACCGATTGTATCACACGGACACCCCTATTTCATTTTGGCGATGCCCATATTTTGGCG  
CTATTGTTT

## SEQ ID 8582

LGNRIFSRPLGIFQOICNKSQLPFPQTAGIHNKQIPLRLQVVIDHDKVEQYGLDFMPCLRQPPLDNFPTVRPAFFEARGKHVERRRQDKDTSFRQRVANLRRALNVDFQNHVIACR  
RQRHIALRACAVIVAYVCPVQKSLLRDKRKLFPGNKVIMYAVCPAFTRRRRRMRHNAQTVMVCCQPRHQRGFARAGSGRNDKDVAFSISGHIPLYIYPQIVSQRTPPYIPADAHILL  
LLF

## SEQ ID 8583

ATGAAGCTTTTGGAAATTTTTTCCGCGCGCGCGGTTGGCAAAAGGCTTGAACCTGCGAGGATTCACATGCTCTTTATTTGAACCTCAATAAGATGCAATTCATTTAAGAAGCA  
ACTTTAACCCCAAGCTTGTATTATCAGGAGATGTGGCAGATTTGATCTTTCCAGTCAAGAAGGATAGAAAGTCAATTCAGCGCGTCTCTCTTCCAGCGCTTTTCATTGGCGGGGAAACA  
CCTTGGCCATGAAGACAGAGGGATATGTTTCTCATGCGGTGAGATATGTGGAGTATTACCGCCCCAAAGCTTTTATCTTTGAGAATGTAAAAGGACTTTTAAAGAAAATCATTCGCTGAT  
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CTATGAAGCAAACTCTTCAACATATCCCTGAAGAAATTTGTCATTTCTGGAGCTTTGGGAGAAGCAATGCGACAAATGGCAATGCGGTTCTCTGTCAAATTTGCGGAAATTTTAGGCA  
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## SEQ ID 8584

MKSLEIFSGAGGLAKGLELAGFQHASFIENKDKACNSLRNPNKLVYQGDVDFDLSSQEGIEVIAGGPPCQPPSLGGKHLAHEDRDMPFHAVRYVEYRPAKIFENVKLLRKSAD  
YFETILLRLTYPNLIGLQNEWKHGLTLKLEIEPNLYKGIKYSYQLLNAADYGVQPKRERVVIVIGRADLDIDWPKRTHSEDRLNWKEYVTGEYWEKNEPKRFNKDIAELKQKYG  
IFPEPKPWQTVRDTLSDIPHLGNHKITGHEYRDGARIYPGHTGSGIDEPSTKIKAGGHGVPGENMIRYDDGTVRYFTSYEAKLLQTFPEEFVLSGAWGEAMRQIGNAVPVKLSLILK  
HLMGVLSKSSILHN

## SEQ ID 8585

TTGCCGTTTGAGATTGTGCGGATATTTTCCATCGGGCAGACTGTCCGTGTGCTGCGAGCGGTATCAAAATAGGGAGTAAACGAAAGATAGGAAGATTGGGCGCATTAGGGTTTCTT  
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CGTATGGAGAAATATGCTCTCTTTGAAGAGTGTATTATGATGAACCTGCCGA

## SEQ ID 8586

LPPEIVPIFSHRADLSGLVQAVIKIGSKTKDRKIGRIRVSLIIEIRSFKNLGGGRNAVCEMRQIWEIDAFAVFYVFIYSVWRNMLLLKSVLMMXR

## SEQ ID 8587

ATGGAGGAATATGCTGCTTTTGAAGAGTGTATTATGATGAACCTCCCGATAACAGTAAATCGGTTTGTATTGTTTCCGTCAGCTTATGCCGTC

## SEQ ID 8588

MEEYAAFECCINDLPITVNRFDLPAYAV

## SEQ ID 8589

TTGATTGTTTCCGTCAGCTTATGCCGTCTGAAGCCCTTTCAGACGGCATTTATTTGAAGTTCTGGTTGTTTTCGCCAGTGATATTTGATGGTT

## SEQ ID 8590

LICFRQLMPSEALS DGIYFEVLVVFASDILHV

## SEQ ID 8591

ATGGTTCAACCAAGAAAAACCGAAGTAAACGTTATGAAAAATGCCGCGATATTGCCCTGCTTCTTTCCAAACATCAGGACGGGAAACACCCCGGCGAGAAGATTTCCATATATATGC  
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## SEQ ID 8592

MVQPRKPEVNVHKKCRDIALLLSKHQDRETTPEKISTYMHLLFCPHCREYKRLQTIKISLAKTTRTSK

## SEQ ID 8593

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CGGTATCAGCAGCTCCAACCTACCAACCAATATGACCCGCGCGGAGAATCATTCGCCCAATGCTGCAAAATCAAAATGGTTCAACCAAGAAAAACCGAAG

SEQ ID 8595

**SEQ ID 8596**

SEQ ID 8597

**SEQ ID 8598**

**SEQ ID 8599**

**SEQ ID 8600**

**SEQ ID 8601**

**SEQ ID 8602**

SEQ ID 8603

**SEQ ID 8604**

**SEQ ID 8605****SEQ ID 8606**

**SEQ ID 8607**

**SEQ ID 8608**

SEQ ID 8609

TGTGTTGTTGAGCTGGTTGATTACTTCGGCTCCATGATCTTTGTTCTTTCAAATTTTAGGGGCGTATTGTACGGGATTCGGGTATTTTTTCTATGGAATGAAGCCCTTCGGAAACACG  
 CTCGGACGGCA

## SEQ ID 8610

VLLSWLITSAHLSFPQNFGRVLYGIRVFFSMDEAFWKHVRIA

## SEQ ID 8611

ATGGCGTTAAACATCAAACCTGGAACACGCAATGCTGCTTCATCCCGAAGCTATGAGTGTGCGGCGCTTGCCGACAAAATCCGCAAAATCGAAAACCTGGCCGCAAAAAGGCATCTTAT  
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 TTGTCGAAGCGCGCCATTTTGAATTTACCGACCTTCAAGCGCGCAAGATATCCGCGCAAGTGGCGGCGCTTATTTACCTGCTTCAAAACGAAGCTGATGAAAGGC

## SEQ ID 8612

HALKTSLHMLVHPEAMSVGALADKIRKIENWPQKILFHDITFVLQSAEYRLLVDLLVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGLPFETVSQSYALEYGEAA  
 VEIHTDAVKPSRVLLVDDLVATGGTMLAGLELIRKLGGEIVAAAILEFTDLQGGKNIRASGAPLFTLLQNEGCMKG.

## SEQ ID 8613

AAGAAAACAGATGTTTTCGCGGGTAAGCGCGCGGATGCGGCATCTGCGGAACGTTTGCAGGTGCGGAACAGATGGGCGCGGTTATAGCGGATTTTCGGAGCTTCTGCATTCAAAATG  
 CCGTCCGACATATTTCCAGTATTTTCAGACGGCATTTCAA

## SEQ ID 8614

KNRCPARVSRPSAASAEIRLQVRNHWGAIADFGSPCIQNAVRTYFYQYQTAFO

## SEQ ID 8615

TTGTTGGACTGATGTTTCCAAACGACATTTGAGGCGCTCTGAAAGCACTAGCTTCAACGAAGTTAAAGTTGAAACGGCAACCGCTCAATCAAGCAACCGCTGCGTACCGCACACCG  
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## SEQ ID 8616

LLDLHFPNDIGRLKALASTKLKLVETANRQSSNRVETAHTQWAG

## SEQ ID 8617

ATGAATATATCGGCGGACATCTCAAAGGACACCATAGACGCAACATTCATATAAAACAAACGGAAGTATCCATTACATTAATTTAAGAATAATGATGATGGATTAACACCTTTAGAT  
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 CAAAGATGTAATATCTGTCATCATGCGCAAACTGGCGAAGCCCGCTATTACATGTTTAAACCGCCAGCTTACGATGCGGAAGACACCGATTGAATCAA

## SEQ ID 8618

MNLIQPDISKDTIDATLHKTNGSIHYIKFNDDGLKQFRLMIKGNIRKVIYIMEATGIYYEKAADMLSSYYTVYVINPLKIKDYGKSRFNRTKTDKADSNLIADYIKRHQDTLIPYQIP  
 RNKALQKLNKLNQLOOQQRQIKNRLHSTEDFIRNIHQDLIDTIQDKMEQVKIAISEQIKKQTTNNHYRNLQTPISIGKDTASVLYAQLPEKHFKTANQVSYAGLSPALIQSGTSVRGR  
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## SEQ ID 8619

TTGCCCCGTTTTTGGAGATTGCAAAATGGGAGATAAGCAAGGGATGACAAAGCGGTGCGCGGCTGATGACGGACCGCGCGGCGGAGCGGAGCGGCAACCGCTTCAATCTTCCCC  
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## SEQ ID 8620

LPVFEDSQHDKQGTAKAVAGVMTDAPADGRKPATASNLPFYLTVGVQPKRRAGFRKSSNVTKRT

## SEQ ID 8621

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 AAATAGGAGGGTAGGTAGATACGGGACATGGTTTCTTCCAGGAGTTGTTGAAATATGGGGAATTTACTGGTTGGGCGATGTTTGGGGAGAGGGGTGGGAATTTCTTGTTTTGGGAAGT  
 GGAAAGGCTGCTGAAATGGGTTTCAGACGACCTTCTGTGAAATGTGCATT

## SEQ ID 8622

MPNSFPNRIQPNALRKFFGHREPCPAENTKGRVRCGAIEIGVGRYGTFWASKELLYGFTGLGDVWGEWELFCEVEKGRLLKMGFRFPCEMCI

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